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OM protein : protein search, using sw model

Run on: May 30, 2003, 14:32:12 ; Search time 19.6974 Seconds

(without alignments)  
40.589 Million cell updates/sec

Title: US-09-643-260-2

Perfect score: 40

Sequence: 1 LDMSWL 6

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: /SID52/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:\*  
2: /SID52/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:\*  
3: /SID52/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:\*  
4: /SID52/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:\*  
5: /SID52/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:\*  
6: /SID52/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:\*  
7: /SID52/gcgdata/geneseq/geneseq-emb1/AA1986.DAT:\*  
8: /SID52/gcgdata/geneseq/geneseq-emb1/AA1987.DAT:\*  
9: /SID52/gcgdata/geneseq/geneseq-emb1/AA1988.DAT:\*  
10: /SID52/gcgdata/geneseq/geneseq-emb1/AA1989.DAT:\*  
11: /SID52/gcgdata/geneseq/geneseq-emb1/AA1990.DAT:\*  
12: /SID52/gcgdata/geneseq/geneseq-emb1/AA1991.DAT:\*  
13: /SID52/gcgdata/geneseq/geneseq-emb1/AA1992.DAT:\*  
14: /SID52/gcgdata/geneseq/geneseq-emb1/AA1993.DAT:\*  
15: /SID52/gcgdata/geneseq/geneseq-emb1/AA1994.DAT:\*  
16: /SID52/gcgdata/geneseq/geneseq-emb1/AA1995.DAT:\*  
17: /SID52/gcgdata/geneseq/geneseq-emb1/AA1996.DAT:\*  
18: /SID52/gcgdata/geneseq/geneseq-emb1/AA1997.DAT:\*  
19: /SID52/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:\*  
20: /SID52/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:\*  
21: /SID52/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:\*  
22: /SID52/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:\*  
23: /SID52/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	40	100.0	6	23	AB08725
2	40	100.0	6	23	AA08530
3	40	100.0	6	23	AA08530
4	40	100.0	6	23	AA08534
5	40	100.0	6	23	AA08534
6	40	100.0	6	23	AA08535
7	40	100.0	6	23	AA08535
8	40	100.0	6	23	AA08536
9	40	100.0	6	23	AA08529
10	40	100.0	6	23	AA08532

11	40	100.0	9	23	AA08533
12	40	100.0	10	23	AB077313
13	40	100.0	10	23	AA08528
14	40	100.0	10	23	AA08531
15	40	100.0	11	23	AB077311
16	40	100.0	11	23	AA08506
17	40	100.0	11	23	AA08525
18	40	100.0	11	23	AA08525
19	40	100.0	13	23	AA08640
20	40	100.0	13	23	AA08641
21	40	100.0	13	23	AA08642
22	40	100.0	13	23	AA08643
23	40	100.0	17	23	AA08638
24	40	100.0	17	23	AA08639
25	40	100.0	17	23	AA08643
26	40	100.0	17	23	AA08644
27	40	100.0	18	23	AA08628
28	40	100.0	18	23	AA08629
29	40	100.0	18	23	AA08632
30	40	100.0	18	23	AA08633
31	40	100.0	22	23	AA08630
32	40	100.0	22	23	AA08631
33	40	100.0	22	23	AA08634
34	40	100.0	22	23	AA08635
35	40	100.0	22	23	AA08636
36	40	100.0	22	23	AA08637
37	40	100.0	28	23	AB08740
38	40	100.0	28	23	AA08523
39	40	100.0	36	23	AA08652
40	40	100.0	220	22	AA08488
41	40	100.0	552	21	AA08488
42	40	100.0	745	19	AA08490
43	40	100.0	745	19	AA08532
44	40	100.0	745	20	AA08900
45	40	100.0	745	20	AA08902

#### ALIGNMENTS

##### RESULT 1

ID ABB08725 standard; peptide: 6 AA.

AB08725:

14-JUN-2002 (first entry)

IKKbeta NEMO binding domain peptide SEQ ID NO 2.

IKKbeta: IKKalpha; NEMO: NEMO binding domain; NBD; NF-kappaB; NF-kB; kinase activation; leukocyte; inflammation; E-selectin; osteoclast; autoimmune disease; transplant rejection; osteoporosis; cancer; Alzheimer's disease; viral; infection; asthma; anaphylaxis; psoriasis; rheumatoid arthritis; Crohn's disease; multiple sclerosis; HIV; corticosteroid; immunosuppression; anti-inflammatory; immunosuppressive; osteopathic; cytotoxic; neuroprotective; anti-HIV; human; antiarteriosclerotic; virucide; antidiabetic; antiallergic; dermatological; antibacterial; antiparasitic; antirheumatic; antiarthritic; osteopathic; antitumor.

Homo sapiens.

MO200183547-A2.

08-NOV-2001.

02-MAY-2001; 2001WO-US40654.

02-MAY-2000; 2000US-201261P.

22-AUG-2000; 2000US-0643260.

(UYVA ) UNIV YALE.

[illegible]

XX		Synthetic.
XV		MO200183554-A2.
XX	PD	08-NOV-2001.
XX	PF	02-MAY-2001; 2001WO-US14346.
XX	PR	02-MAY-2000; 2000US-201261P.
XX	PR	22-AUG-2000; 2000US-0643260.
PA	(PRAE-) PRAECIS PHARM INC.	
XX	(UYTA ) UNIV YALE.	
PI	May MJ, Ghosh S, Findels MA, Phillips K;	
XX	WPI: 2002-121889/16.	
DR		
PT	Novel antiinflammatory compound comprising membrane translocation	
PT	domain fused to NEMO binding sequence, useful for blocking nuclear	
PT	factor kappaB activation, and for treating asthma, lung inflammation,	
PT	psoriasis	
XX		
PS	Claim 6; Page 61; 88pp; English.	
XX		
CC	The invention relates to an antiinflammatory compound (especially	
CC	AAH48628-AAH48643), comprising a membrane translocation domain	
CC	(AAH48620-AAH48637 or AAH48646-AAH48651) which comprises from 6-15	
CC	amino acid residues, fused to a NEMO binding sequence	
CC	(AAH48525-AAH48619). The antiinflammatory compounds have antasthmatic,	
CC	cycostatic, antipsoriatic, antipneumatic, antiarthritic, osteopathic,	
CC	antibacterial, immunosuppressive, dermatological, neuroprotective,	
CC	nootropic, antiatherosclerotic, virucide and anti-allergic activity. The	
CC	compounds act as selective inhibitors of cytokine-mediated NFkappaB	
CC	activation by blocking interaction of Ikappab kinase beta (IKKbeta) at	
CC	the NEMO binding domain that results in inhibition of IKKbeta kinase	
CC	activation and subsequent decreased phosphorylation of Ikappab. The	
CC	compounds are useful for treating inflammatory disorders, e.g. asthma,	
CC	lung inflammation or cancer, psoriasis, rheumatoid arthritis,	
CC	osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,	
CC	gastrointestinal diseases such as lupus, polyarthritis, scleroderma,	
CC	granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;	
CC	Alzheimer's disease; atherosclerosis; viral infections; and ataxia	
CC	telangiectasia. The compounds are also useful for treating	
CC	pro-inflammatory responses such as allergies, urticaria, anaphylaxis,	
CC	drug or food sensitivity, eczema, dermatitis, sunburn, aging and	
CC	arthritis.	
XX		
SQ	Sequence 6 AA;	
Query Match	100.0%; Score 40; DB 23; Length 6;	
Best Local Similarity	100.0%; Pred. NO. 7.Be+05;	
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 LDMSWL 6	
Dd	1 LDMSWL 6	
RESULT 3		
AAH48655		
ID	AAH48655 standard; Peptide; 6 AA.	
XX	AAH48655;	
AC		
DT	20-MAR-2002 (first entry)	
DE	NBD mutant peptide SEQ ID NO 2.	

XX Antinflammatory; antiasthmatic; cytostatic; antipsoriatic; noctropic;  
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;  
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;  
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;  
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;  
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
 KW autoimmune disorder; multiple sclerosis; transplant rejection;  
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.  
 XX Synthetic.  
 OS  
 XX WO200183554-A2.  
 XX  
 XX 08-NOV-2001.  
 XX  
 XX 02-MAY-2001; 2001WO-US14346.  
 XX  
 XX 02-MAY-2000; 2000US-201261P.  
 XX  
 XX 22-AUG-2000; 2000US-0643260.  
 XX  
 XX (PRAE-) PRACIS PHARM INC.  
 XX (UYVA ) UNIV YALE.  
 XX  
 XX May MJ, Ghosh S, Findels MA, Phillips K;  
 XX  
 XX WPI; 2002-121889/16.  
 XX  
 XX Novel antinflammatory compound comprising membrane translocation  
 PT domain fused to NEMO binding sequence, useful for blocking nuclear  
 PT factor kappaB activation, and for treating asthma, lung inflammation,  
 PT psoriasis  
 PT  
 XX Example 6; Page 47; 88pp; English.  
 PS  
 XX The invention relates to an antinflammatory compound (especially  
 CC AAM48628-AAM48645), comprising a membrane translocation domain  
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15  
 CC amino acid residues, fused to a NEMO binding sequence  
 CC (AAM48525-AAM48619). The antinflammatory compounds have antiasthmatic,  
 CC cytoskeletal, antipsoriatic, antirheumatic, antiarthritic, osteopathic,  
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,  
 CC noctropic, antiatherosclerotic, virucide and antiallergic activity. The  
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB  
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at  
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase  
 CC activation and subsequent decreased phosphorylation of IkappaB. The  
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,  
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,  
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,  
 CC burstitis; autoimmune diseases such as lupus, polyarthritis, scleroderma,  
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;  
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia  
 CC telangiectasia. The compounds are also useful for treating  
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,  
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and  
 CC arthritis.  
 CC  
 XX Sequence 6 AA:  
 SQ  
 XX  
 QY Query Match 100.0%; Score 40; DB 23; Length 6;  
 Db Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 1 LDMSWL 6  
 1 LDMSWL 6  
 RESULT 4  
 AAM48534  
 ID AAM48534 standard; Peptide; 7 AA.

XX AAM48534;  
 AC  
 XX 20-MAR-2002 (first entry)  
 DT  
 XX  
 XX  
 DE Anti-inflammatory peptide SEQ ID NO 37.  
 XX  
 XX Antinflammatory; antiasthmatic; cytostatic; antipsoriatic; noctropic;  
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;  
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;  
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;  
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;  
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
 KW autoimmune disorder; multiple sclerosis; transplant rejection;  
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.  
 XX Synthetic.  
 OS  
 XX WO200183554-A2.  
 XX  
 XX 08-NOV-2001.  
 XX  
 XX 02-MAY-2001; 2001WO-US14346.  
 XX  
 XX 02-MAY-2000; 2000US-201261P.  
 XX  
 XX 22-AUG-2000; 2000US-0643260.  
 XX  
 XX (PRAE-) PRACIS PHARM INC.  
 XX (UYVA ) UNIV YALE.  
 XX  
 XX May MJ, Ghosh S, Findels MA, Phillips K;  
 XX  
 XX WPI; 2002-121889/16.  
 XX  
 XX Novel antinflammatory compound comprising membrane translocation  
 PT domain fused to NEMO binding sequence, useful for blocking nuclear  
 PT factor kappaB activation, and for treating asthma, lung inflammation,  
 PT psoriasis  
 PT  
 XX Claim 6; Page 61; 88pp; English.  
 PS  
 XX The invention relates to an antinflammatory compound (especially  
 CC AAM48628-AAM48645), comprising a membrane translocation domain  
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15  
 CC amino acid residues, fused to a NEMO binding sequence  
 CC (AAM48525-AAM48619). The antinflammatory compounds have antiasthmatic,  
 CC cytoskeletal, antipsoriatic, antirheumatic, antiarthritic, osteopathic,  
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,  
 CC noctropic, antiatherosclerotic, virucide and antiallergic activity. The  
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB  
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at  
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase  
 CC activation and subsequent decreased phosphorylation of IkappaB. The  
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,  
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,  
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,  
 CC burstitis; autoimmune diseases such as lupus, polyarthritis, scleroderma,  
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;  
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia  
 CC telangiectasia. The compounds are also useful for treating  
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,  
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and  
 CC arthritis.  
 CC  
 XX Sequence 7 AA:  
 SQ  
 XX  
 QY Query Match 100.0%; Score 40; DB 23; Length 7;  
 Db Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 1 LDMSWL 6  
 1 LDMSWL 6

DB 1 LDMSWL 6

RESULT 5

AA048527

ID AA048527 standard; Peptide; 8 AA.

AC AA048527;

XX 20-MAR-2002 (first entry)

DE Anti-inflammatory peptide SEQ ID NO 30.

XX Anti-inflammatory; antisthmatic; cytosolic; antiproliferative; neurotrophic;

KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;

KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;

KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;

KW cytokine; NF-kappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;

KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;

KW autoimmune disorder; multiple sclerosis; transplant rejection;

KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;

KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.

XX Synthetic.

OS WO200183554-A2.

PN 08-NOV-2001.

PD 02-MAY-2001; 2001WO-US14346.

PF 02-MAY-2000; 2000US-201261P.

XX 22-AUG-2000; 2000US-0643260.

PR (PRAE-) PRAECIS PHARM INC.

PA (UYVA) UNIV YALE.

XX May MJ, Ghosh S, Findeis MA, Phillips K;

PI WPI: 2002-121889/16.

DR Novel antiinflammatory compound comprising membrane translocation

PT domain fused to NEMO binding sequence, useful for blocking nuclear

PT factor kappaB activation, and for treating asthma, lung inflammation,

PT psoriasis

XX Claim 6; Page 61; 88pp; English.

XX The invention relates to an antiinflammatory compound (especially

CC AA048628-AA048645), comprising a membrane translocation domain

CC (AA048620-AA048627 or AA048646-AA048651) which comprises from 6-15

CC amino acid residues, fused to a NEMO binding sequence

CC (AA048525-AA048619). The antiinflammatory compounds have antisthmatic,

CC cytosolic, antiproliferative, antirheumatic, antiarthritic, osteopathic,

CC antibacterial, immunosuppressive, dermatological, neuroprotective,

CC neurotrophic, antiatherosclerotic, virucide and antiallergic activity. The

CC compounds act as selective inhibitors of cytokine-mediated NF-kappaB

CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at

CC the NEMO binding domain that results in inhibition of IKKbeta kinase

CC activation and subsequent decreased phosphorylation of IkappaB. The

CC compounds are useful for treating inflammatory disorders, e.g. asthma,

CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,

CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,

CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,

CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;

CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia

CC telangiectasia. The compounds are also useful for treating

CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,

CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and

CC arthritis.

XX Sequence 8 AA;

Query Match 100.0%; Score 40; DB 23; Length 8;

Best Local Similarity 100.0%; Pred. No. 7.8e+05;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSWL 6

DB 3 LDMSWL 8

RESULT 6

AA048535

ID AA048535 standard; Peptide; 8 AA.

AC AA048535;

XX 20-MAR-2002 (first entry)

DE Anti-inflammatory peptide SEQ ID NO 38.

XX Anti-inflammatory; antisthmatic; cytosolic; antiproliferative; neurotrophic;

KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;

KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;

KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;

KW cytokine; NF-kappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;

KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;

KW autoimmune disorder; multiple sclerosis; transplant rejection;

KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;

KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.

XX Synthetic.

OS WO200183554-A2.

PN 08-NOV-2001.

PD 02-MAY-2001; 2001WO-US14346.

PF 02-MAY-2000; 2000US-201261P.

XX 22-AUG-2000; 2000US-0643260.

PR (PRAE-) PRAECIS PHARM INC.

PA (UYVA) UNIV YALE.

XX May MJ, Ghosh S, Findeis MA, Phillips K;

PI WPI: 2002-121889/16.

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PT domain fused to NEMO binding sequence, useful for blocking nuclear

PT factor kappaB activation, and for treating asthma, lung inflammation,

PT psoriasis

XX Claim 6; Page 61; 88pp; English.

XX The invention relates to an antiinflammatory compound (especially

CC AA048628-AA048645), comprising a membrane translocation domain

CC (AA048620-AA048627 or AA048646-AA048651) which comprises from 6-15

CC amino acid residues, fused to a NEMO binding sequence

CC (AA048525-AA048619). The antiinflammatory compounds have antisthmatic,

CC cytosolic, antiproliferative, antirheumatic, antiarthritic, osteopathic,

CC antibacterial, immunosuppressive, dermatological, neuroprotective,

CC neurotrophic, antiatherosclerotic, virucide and antiallergic activity. The

CC compounds act as selective inhibitors of cytokine-mediated NF-kappaB

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CC compounds are useful for treating inflammatory disorders, e.g. asthma,

CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,

CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,

CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,

CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;

CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia

CC telangiectasia. The compounds are also useful for treating

CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,  
CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and  
CC arthritis.

XX Sequence 8 AA;

Query Match 100.0%; Score 40; DB 23; Length 8;  
Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDMSWL 6  
DB 1 LDMSWL 6

RESULT 7  
AAW96182

ID AAW96182 standard; peptide: 9 AA.

AC AAW96182;

XX 27-APR-1999 (first entry)

DE IKK-alpha polypeptide with binding activity.

XX I-kappa-B kinase; IKK-alpha; gene expression; modulation;  
KW suppression; activation; tumour necrosis factor; TNF; Interleukin-1;  
KM IL-1; TNF receptor associated factor; TRAF.

OS Homo sapiens.

PN WO9901541-A1.

PD 14-JAN-1999.

XX 01-JUL-1998; 98WO-US13782.

XX 10-JUL-1997; 97US-0890854.

PR 01-JUL-1997; 97US-0887115.

XX (TUL- ) TULARIK INC.

PI Cao Z, Regnier C, Rothe M;

DR WPI; 1999-106044/09.

XX Newly isolated human kinase Ikappab kinase (IKK- $\alpha$ ) polypeptides -  
PT useful in screening for agents that modulate the interaction of an  
PT IKK polypeptide to a binding target and for modulating signal  
PT transduction involving Ikappab in a cell  
XX Disclosure; Page -: 32pp; English.

CC I-kappa-B kinase (AAW96182), deletion mutants of it retaining  
CC I-kappa-B kinase activity and I-kappa-B polypeptides (comprising a  
CC six residue domain of I-kappa-B containing one of Ser32 and Ser36,  
CC and a candidate agent) can be used to screen for agents that  
CC modulate the interaction of an IKK polypeptide to a binding target.  
CC The modulation of the kinase activity of IKK-alpha forms a method  
CC for modulating signal transduction involving I-kappa-B in a cell.  
CC The IKK-alpha polypeptides are useful for generating oligonucleotide  
CC primers and probes for use in the isolation of natural  
CC IKK-alpha-encoding nucleic acids. The nucleic acids are useful as  
CC translatable transcripts, hybridization probes, polymerase chain  
CC reaction (PCR) probes and primers. Their diagnostic applications  
CC include IKK-alpha hybridization probes for identifying wild-type and  
CC mutant IKK-alpha alleles in clinical and laboratory samples.  
CC Therapeutic application includes the use of IKK-alpha nucleic acids  
CC for modulating cellular expression or intracellular  
CC concentration/availability of active IKK-alpha.  
CC Catalytically inactive IKK-alpha mutants suppress NF-kappa-B  
CC activation induced by tissue necrosis factor (TNF), interleukin-1  
CC (IL-1) stimulation, TNF receptor-associated factor (TRAF) and

SEA ID NO: 2  
AC NO: AAW96182  
Database: A-Genbank-101002

CC NF-kappa-B-inducing kinase (NIK) overexpression. Polypeptides of  
CC IKK-alpha showing exemplary binding activity are described in  
CC AAW96182-996182. These peptides all comprise one of Cys30, Glu543,  
CC Leu604, Thr679, Ser680, Thr686 or Ser687 of the full length  
CC IKK-alpha described in AAW96157. Deletion mutants of the invention  
CC comprise at least one of these regions.  
CC N.B. The present sequence is not given in the present specification  
CC but is derived from the sequence given in AAW96157 as specified.

XX Sequence 9 AA;

Query Match 100.0%; Score 40; DB 20; Length 9;  
Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDMSWL 6  
DB 2 LDMSWL 7

RESULT 8  
AAW48526

ID AAW48526 standard; Peptide: 9 AA.

AC AAW48526;

XX 20-MAR-2002 (first entry)

DE Anti-inflammatory peptide SEQ ID NO 29.

XX Antinflammatory; antiasthmatic; cytosolic; antipsoriatic; noctropic;  
KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;  
KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;  
KW antiangiogenic; membrane translocation domain; NEMO binding domain; eczema;  
KW cytokine; NF-kappa-B; Ikappab kinase beta; IKKbeta; cancer; psoriasis;  
KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
KW autoimmune disorder; multiple sclerosis; transplant rejection;  
KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.

XX Synthetic.

XX WO200183554-A2.

XX 08-NOV-2001.

XX 02-MAY-2001; 2001WO-US14346.

XX 02-MAY-2000; 2000US-201261P.

XX 22-AUG-2000; 2000US-0643260.

XX (PRAE-) PRAECIS PHARM INC.

XX May MJ, Ghosh S, Findeis MA, Phillips K;

DR WPI; 2002-121889/16.

XX Novel antinflammatory compound comprising membrane translocation  
PT domain fused to NEMO binding sequence, useful for blocking nuclear  
PT factor kappaB activation, and for treating asthma, lung inflammation,  
PT psoriasis  
XX Claim 6; Page 61; 88pp; English.

XX The invention relates to an antinflammatory compound (especially  
CC AAW48628-AAW48645), comprising a membrane translocation domain  
CC (AAW48620-AAW48627 or AAW48646-AAW48651) which comprises from 6-15  
CC amino acid residues, fused to a NEMO binding sequence  
CC (AAW48525-AAW48619). The antinflammatory compounds have antiasthmatic,  
CC cytosolic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,  
CC antibacterial, immunosuppressive, dermatological, neuroprotective,  
CC noctropic, antiatherosclerotic, virucide and antiangiogenic activity. The

CC compounds act as selective inhibitors of cytokine-mediated NFkappaB activation by blocking interaction of Ikappab kinase beta (IKKbeta) at the NEMO binding domain that results in inhibition of IKKbeta kinase activation and subsequent decreased phosphorylation of Ikappab. The CC compounds are useful for treating inflammatory disorders, e.g. asthma, lung inflammation or cancer, psoriasis, rheumatoid arthritis, osteoarthritis, inflammatory bowel disease, sepsis, vasculitis, bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma, granulomatosis, multiple sclerosis; transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis; viral infections; and ataxia telangiectasia. The compounds are also useful for treating pro-inflammatory responses such as allergies, urticaria, anaphylaxis, drug or food sensitivity, eczema, dermatitis, sunburn, aging and arthritis.

SQ Sequence 9 AA;

Query Match 100.0%; Score 40; DB 23; Length 9;  
Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDMSWL 6  
|||||  
DB 1 LDMSWL 6

RESULT 9  
AAM48529 standard; Peptide; 9 AA.

AC AAM48529;  
XX 20-MAR-2002 (first entry)  
DT  
XX  
DE Anti-inflammatory peptide SEQ ID NO 32.

XX  
KW Antiinflammatory; antiasthmatic; cytostatic; antiproliferative; neurotropic;  
KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;  
KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;  
KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;  
KW cytokine; NFkappaB; Ikappab kinase beta; IKKbeta; cancer; psoriasis;  
KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
KW autoimmune disorder; multiple sclerosis; transplant rejection;  
KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.

OS Synthetic.  
XX  
PN WO200183554-A2.  
XX  
PD 08-NOV-2001.  
XX  
PF 02-MAY-2001; 2001WO-US14346.  
XX  
PR 02-MAY-2000; 2000US-201261P.  
PR 22-AUG-2000; 2000US-0643260.  
XX  
PA (PRAE-) PRAECIS PHARM INC.  
PA (UYVA) UNIV YALE.  
XX  
PI May MJ, Ghosh S, Flindels MA, Phillips K;  
XX  
XX WPI; 2002-121889/16.  
DR  
XX  
XX Novel antiinflammatory compound comprising membrane translocation  
PT domain fused to NEMO binding sequence, useful for blocking nuclear  
PT factor kappaB activation, and for treating asthma, lung inflammation,  
PT psoriasis  
XX  
PS Claim 6; Page 61; 88pp; English.  
XX  
CC The invention relates to an antiinflammatory compound (especially  
CC AAM48628-AAM48645), comprising a membrane translocation domain

CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15  
CC amino acid residues, fused to a NEMO binding sequence  
CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,  
CC cytostatic, antiproliferative, antirheumatic, antiarthritic, osteopathic,  
CC antibacterial, immunosuppressive, dermatological, neuroprotective,  
CC neurotropic, antiatherosclerotic, virucide and antiallergic activity. The  
CC compounds act as selective inhibitors of cytokine-mediated NFkappaB  
CC activation by blocking interaction of Ikappab kinase beta (IKKbeta) at  
CC the NEMO binding domain that results in inhibition of IKKbeta kinase  
CC activation and subsequent decreased phosphorylation of Ikappab. The  
CC compounds are useful for treating inflammatory disorders, e.g. asthma,  
CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,  
CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,  
CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,  
CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;  
CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia  
CC telangiectasia. The compounds are also useful for treating  
CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,  
CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and  
CC arthritis.

SQ Sequence 9 AA;

Query Match 100.0%; Score 40; DB 23; Length 9;  
Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDMSWL 6  
|||||  
DB 1 LDMSWL 6

RESULT 10  
AAM48532 standard; Peptide; 9 AA.

AC AAM48532;  
XX  
DT 20-MAR-2002 (first entry)  
XX  
DE Anti-inflammatory peptide SEQ ID NO 35.

XX  
KW Antiinflammatory; antiasthmatic; cytostatic; antiproliferative; neurotropic;  
KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;  
KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;  
KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;  
KW cytokine; NFkappaB; Ikappab kinase beta; IKKbeta; cancer; psoriasis;  
KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
KW autoimmune disorder; multiple sclerosis; transplant rejection;  
KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.

OS Synthetic.  
XX  
PN WO200183554-A2.  
XX  
PD 08-NOV-2001.  
XX  
PF 02-MAY-2001; 2001WO-US14346.  
XX  
PR 02-MAY-2000; 2000US-201261P.  
PR 22-AUG-2000; 2000US-0643260.  
XX  
PA (PRAE-) PRAECIS PHARM INC.  
PA (UYVA) UNIV YALE.  
XX  
PI May MJ, Ghosh S, Flindels MA, Phillips K;  
XX  
XX WPI; 2002-121889/16.  
DR  
XX  
XX Novel antiinflammatory compound comprising membrane translocation  
PT domain fused to NEMO binding sequence, useful for blocking nuclear  
PT factor kappaB activation, and for treating asthma, lung inflammation,  
PT



02-MAY-2000; 2000US-201261P.  
 22-AUG-2000; 2000US-0643260.  
 (UYVA ) UNIV YALE.  
 May MJ, Ghosh S;  
 WPI: 2002-179350/23.  
 Modulating NF-kappaB induction in a cell, useful for treating e.g.  
 inflammatory disorders, osteoporosis and cancer, comprises contacting a  
 cell with an anti-inflammatory compound comprising at least one NEMO  
 binding domain -  
 Example 4; Page -: 82pp; English.  
 The invention relates to modulating NF-kappaB (NF-KB) induction in a cell  
 comprising contacting a cell with an anti-inflammatory compound  
 (ABB08725-ABB08742) comprising at least one NEMO binding domain  
 (ABB77313). The compound has acts through selective inhibition of  
 cytokine-mediated NF-KB activation by blocking the interaction of NEMO  
 with IKKbeta at the NEMO binding domain. Blockage of IKKbeta-NEMO  
 interaction results in inhibition of IKKbeta kinase activation and  
 subsequent decreased phosphorylation of I-kappaB. The compound may also  
 act (directly or indirectly) by blocking the recruitment of leukocytes  
 into sites of acute and chronic inflammation, by down-regulating the  
 expression of E-selectin on leukocytes or by blocking osteoclast  
 differentiation. The compound is useful in treating NF-KB mediated  
 conditions, where the condition is an inflammatory disorder, an  
 autoimmune disease, transplant rejection, osteoporosis, cancer, an  
 Alzheimer's disease, atherosclerosis, a viral infection or ataxia  
 telangiectasia. The inflammatory disorder is asthma, allergies,  
 urticaria, anaphylaxis, cutaneous inflammation, sepsis, psoriasis,  
 rheumatoid arthritis, osteoarthritis, psoriatic arthritis, inflammatory  
 bowel disease, chronic obstructive pulmonary disease, vasculitis and  
 bursitis. The inflammatory disorder may also be dermatitis, eczema,  
 psoriasis, osteoarthritis, psoriatic arthritis, lupus and  
 spondylarthritis. Also for Crohn's disease, ulcerative colitis,  
 polyarthritis, scleroderma, Wegner's granulomatosis, temporal arteritis,  
 cryoglobulinemia or multiple sclerosis. For chronic viral infections  
 caused by Epstein-Barr, cytomegalovirus or herpes simplex. Other viral  
 diseases include HIV and influenza. The compound may also be useful for  
 treating anaphylaxis, drug and food sensitivity, contact dermatitis,  
 sunburn or aging. The compound may be used to replace corticosteroids in  
 any application in which corticosteroids are used, including  
 immunosuppression in transplants and cancer therapy. Also for identifying  
 anti-inflammatory compounds and for diagnosis of an inflammatory disorder.  
 The compound may be administered alone or in combination with other known  
 anti-inflammatory agents. The present sequence is that of the NEMO  
 binding domain of IKKbeta.  
 Note: The present sequence is not given in the specification but is  
 encoded by the polynucleotide given at GenBank Accession No. AR067807,  
 nucleotides 2203-2235.  
 Sequence 10 AA:  
 Query Match 100.0%; Score 40; DB 23; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 3.3;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LDMSWL 6  
 DB 3 LDMSWL 8  
 RESULT 13  
 ID AAM48528 standard; Peptide: 10 AA.  
 AC AAM48528;  
 XX  
 XX  
 DT 20-MAR-2002 (first entry)  
 XX

Anti-inflammatory peptide SEQ ID NO 31.  
 Anti-inflammatory; antiasthmatic; cyostatic; antipsoriatic; nootropic;  
 antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;  
 immunosuppressive; dermatological; neuroprotective; antithrombotic;  
 antiallergic; membrane translocation domain; NEMO binding domain; eczema;  
 cytokine; NF-kappaB; I-kappaB kinase beta; IKKbeta; cancer; psoriasis;  
 rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
 autoimmune disorder; multiple sclerosis; transplant rejection;  
 osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
 ataxia telangiectasia; allergy; anaphylaxis; arthritis.  
 Synthetic.  
 WO200183554-A2.  
 08-NOV-2001.  
 02-MAY-2001; 2001WO-US14346.  
 02-MAY-2000; 2000US-201261P.  
 22-AUG-2000; 2000US-0643260.  
 (PRAE-) PRAECIS PHARM INC.  
 (UYVA ) UNIV YALE.  
 May MJ, Ghosh S, Findeis MA, Phillips K;  
 WPI: 2002-121889/16.  
 Novel anti-inflammatory compound comprising membrane translocation  
 domain fused to NEMO binding sequence, useful for blocking nuclear  
 factor kappaB activation, and for treating asthma, lung inflammation,  
 psoriasis -  
 Claim 6; Page 61; 88pp; English.  
 The invention relates to an anti-inflammatory compound (especially  
 AAM48628-AAM48645), comprising a membrane translocation domain  
 (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15  
 amino acid residues, fused to a NEMO binding sequence  
 (AAM48525-AAM48619). The anti-inflammatory compounds have antiasthmatic,  
 cyostatic, antipsoriatic, antirheumatic, antiallergic, osteopathic,  
 antibacterial, immunosuppressive, dermatological, neuroprotective,  
 nootropic, antiatherosclerotic, virucide and antiallergic activity. The  
 compounds act as selective inhibitors of cytokine-mediated NF-kappaB  
 activation by blocking interaction of I-kappaB kinase beta (IKKbeta) at  
 the NEMO binding domain that results in inhibition of I-kappaB kinase  
 activation and subsequent decreased phosphorylation of I-kappaB. The  
 compounds are useful for treating inflammatory disorders, e.g. asthma,  
 lung inflammation or cancer, psoriasis, rheumatoid arthritis,  
 osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,  
 bursitis; autoimmune diseases such as lupus, polyarthritis, scleroderma,  
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;  
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia  
 CC telangiectasia. The compounds are also useful for treating  
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,  
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and  
 CC arthritis.  
 Sequence 10 AA:  
 Query Match 100.0%; Score 40; DB 23; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 3.3;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LDMSWL 6  
 DB 2 LDMSWL 7  
 RESULT 14  
 ID AAM48531

ID AAM48531 standard; Peptide: 10 AA.  
 XX  
 AC AAM48531;  
 XX  
 DT 20-MAR-2002 (first entry)  
 XX  
 DE Anti-inflammatory peptide SEQ ID NO 34.  
 XX  
 XX Anti-inflammatory; antiasthmatic; cyostatic; antipsoriatic; nootropic;  
 KW antiinflammatory; antiarthritic; osteopathic; antibacterial; virucide;  
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;  
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;  
 KW cytokine; NF-kappaB; IkappaB Kinase Delta; IKKbeta; cancer; psoriasis;  
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
 KW autoimmune disorder; multiple sclerosis; transplant rejection;  
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200183554-A2.  
 XX  
 PD 08-NOV-2001.  
 XX  
 PF 02-MAY-2001; 2001WO-US4346.  
 XX  
 PR 02-MAY-2000; 2000US-201261P.  
 XX  
 PR 22-AUG-2000; 2000US-0643260.  
 XX  
 PA (PRAE-) PRACIS PHARM INC.  
 XX  
 PA (UYTA ) UNIV YALE.  
 PI May MJ, Ghosh S, Findels MA, Phillips K;  
 XX  
 PI WPI; 2002-121889/16.  
 XX  
 DR Novel antiinflammatory compound comprising membrane translocation  
 PT domain fused to NEMO binding sequence, useful for blocking nuclear  
 PT factor kappaB activation, and for treating asthma, lung inflammation,  
 PT psoriasis  
 XX  
 PS Claim 6; Page 61; 88pp; English.  
 XX  
 CC The invention relates to an antiinflammatory compound (especially  
 CC AAM48628-AAM48645), comprising a membrane translocation domain  
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15  
 CC amino acid residues, fused to a NEMO binding sequence  
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,  
 CC cyostatic, antipsoriatic, antiinflammatory, antiarthritic, osteopathic,  
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,  
 CC nootropic, antiatherosclerotic, virucide and antiallergic activity. The  
 CC compounds act as selective inhibitors of cytokine-mediated NF-kappaB  
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at  
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase  
 CC activation and subsequent decreased phosphorylation of IkappaB. The  
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,  
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,  
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,  
 CC granulomatous autoimmune diseases such as lupus, polymyalgia, osteoderma,  
 CC Alzheimers disease, atherosclerosis; transplant rejection; osteoporosis;  
 CC telangiectasia. The compounds are also useful for treating  
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,  
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and  
 CC arthritis.  
 XX  
 SO Sequence 10 AA:  
 Query Match 100.0%; Score 40; DB 23; Length 10;  
 Best local Similarity 100.0%; Pred. NO. 3.3;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 3 LDMSWL 8  
 RESULT 15  
 ABB77311  
 ID ABB77311 standard; peptide: 11 AA.  
 XX  
 AC ABB77311;  
 XX  
 DT 14-JUN-2002 (first entry)  
 XX  
 DE Human NBD peptide (WT).  
 XX  
 KW IKKbeta; IKKalpha; NEMO; NEMO binding domain; NBD; NF-kappaB; NF-kB;  
 KW kinase activation; leukocyte; inflammation; E-selectin; osteoclast;  
 KW autoimmune disease; transplant rejection; osteoporosis; cancer;  
 KW Alzheimer's disease; viral infection; asthma; anaphylaxis; psoriasis;  
 KW rheumatoid arthritis; Crohn's disease; multiple sclerosis; HIV;  
 KW corticosteroid; immunosuppression; antiinflammatory; immunosuppressive;  
 KW osteopathic; cyostatic; nootropic; neuroprotective; anti-HIV; human;  
 KW antiarteriosclerotic; virucide; antiasthmatic; antiallergic;  
 KW dermatological; antibacterial; antipsoriatic; antirheumatic;  
 KW antiarthritic; osteopathic; antitumor.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200183547-A2.  
 XX  
 PD 08-NOV-2001.  
 XX  
 PF 02-MAY-2001; 2001WO-US40654.  
 XX  
 PR 02-MAY-2000; 2000US-201261P.  
 XX  
 PR 22-AUG-2000; 2000US-0643260.  
 XX  
 PA (UYTA ) UNIV YALE.  
 PI May MJ, Ghosh S;  
 XX  
 PI WPI; 2002-179350/23.  
 XX  
 DR Modulating NF-kappaB induction in a cell, useful for treating e.g.  
 PT inflammatory disorders, osteoporosis and cancer, comprises contacting a  
 PT cell with an anti-inflammatory compound comprising at least one NEMO  
 PT binding domain  
 XX  
 PS Disclosure: Fig 12; 82pp; English.  
 XX  
 CC The invention relates to modulating NF-kappaB (NF-kB) induction in a cell  
 CC comprises contacting a cell with an anti-inflammatory compound  
 CC (ABB08725-ABB08742) comprising at least one NEMO binding domain  
 CC (ABB77313). The compound has acts through selective inhibition of  
 CC cytokine-mediated NF-kB activation by blocking the interaction of NEMO  
 CC with IKKbeta at the NEMO binding domain. Blockage of IKKbeta-NEMO  
 CC interaction results in inhibition of IKKbeta kinase activation and  
 CC subsequent decreased phosphorylation of IkappaB. The compound may also  
 CC act (directly or indirectly) by blocking the recruitment of leukocytes  
 CC into sites of acute and chronic inflammation, by down-regulating the  
 CC expression of E-selectin on leukocytes or by blocking osteoclast  
 CC differentiation. The compound is useful in treating NF-kB mediated  
 CC conditions, where the condition is an inflammatory disorder, an  
 CC autoimmune disease, transplant rejection, osteoporosis, cancer,  
 CC Alzheimer's disease, atherosclerosis, a viral infection or ataxia  
 CC telangiectasia. The inflammatory disorder is asthma, allergies,  
 CC urticaria, anaphylaxis, cutaneous inflammation, sepsis, psoriasis,  
 CC rheumatoid arthritis, osteoarthritis, psoriatic arthritis, inflammatory  
 CC bowel disease, chronic obstructive pulmonary disease, vasculitis and  
 CC bursitis. The inflammatory disorder may also be dermatitis, eczema,  
 CC psoriasis, osteoarthritis, psoriatic arthritis, lupus and  
 CC spondylarthritis. Also for Crohn's disease, ulcerative colitis,  
 CC polymyalgia, scleroderma, Wegner's granulomatosis, temporal arteritis,  
 CC cryoglobulinemia or multiple sclerosis. for chronic viral infections

CC caused by Epstein-barr, cytomegalovirus or herpes simplex. Other viral  
 CC diseases include HIV and influenza. The compound may also be useful for  
 CC treating anaphylaxis, drug and food sensitivity, contact dermatitis,  
 CC sunburn or aging. The compound may be used to replace corticosteroids in  
 CC any application in which corticosteroids are used, including  
 CC immunosuppression in transplants and cancer therapy. Also for identifying  
 CC antiinflammatory compounds and for diagnosis of an inflammatory disorder.  
 CC The compound may be administered alone or in combination with other known  
 CC anti-inflammatory agents. The present sequence is that of an NBD peptide,  
 CC useful to the invention.  
 XX

SQ Sequence 11 AA;

QY Query Match

Best Local Similarity 100.0%; Score 40; DB 23; Length 11;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSWL 6

DB 4 LDMSWL 9

Search completed: May 30, 2003, 14:49:40  
 Job time : 19.7529 secs

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## OM protein - protein search, using sw model

Run on: May 30, 2003, 14:32:12 ; Search time 6.03947 Seconds  
(without alignments)  
29.231 Million cell updates/sec

Title: US-09-643-260-2

Perfect score: 40

Sequence: 1 LMSWL 6

Scoring table: BLOSUM62

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :  
1: Issued\_Patents\_AA:\*  
2: /cgn2\_6/prodata/1/lae/55\_COMB.pep:\*  
3: /cgn2\_6/prodata/1/lae/55\_COMB.pep:\*  
4: /cgn2\_6/prodata/1/lae/55\_COMB.pep:\*  
5: /cgn2\_6/prodata/1/lae/55\_COMB.pep:\*  
6: /cgn2\_6/prodata/1/lae/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	40	100.0	745	2 US-08-887-518-3	Sequence 3, Appl
2	40	100.0	745	2 US-09-023-321-3	Sequence 3, Appl
3	40	100.0	745	2 US-08-890-853-4	Sequence 4, Appl
4	40	100.0	745	2 US-09-032-475-3	Sequence 3, Appl
5	40	100.0	745	2 US-09-099-125A-4	Sequence 4, Appl
6	40	100.0	745	2 US-09-099-125A-4	Sequence 4, Appl
7	40	100.0	745	2 US-09-032-476-4	Sequence 4, Appl
8	40	100.0	745	2 US-08-890-854-4	Sequence 4, Appl
9	40	100.0	745	2 US-09-023-324-4	Sequence 4, Appl
10	40	100.0	745	2 US-09-168-629-2	Sequence 4, Appl
11	40	100.0	745	2 US-08-910-820-10	Sequence 2, Appl
12	40	100.0	745	2 US-08-810-131A-2	Sequence 10, Appl
13	40	100.0	756	2 US-08-887-518-4	Sequence 2, Appl
14	40	100.0	756	2 US-09-023-321-4	Sequence 4, Appl
15	40	100.0	756	2 US-08-890-853-2	Sequence 4, Appl
16	40	100.0	756	2 US-09-032-475-4	Sequence 2, Appl
17	40	100.0	756	2 US-09-099-125A-2	Sequence 4, Appl
18	40	100.0	756	2 US-09-099-125A-2	Sequence 2, Appl
19	40	100.0	756	2 US-09-032-476-2	Sequence 2, Appl
20	40	100.0	756	2 US-08-890-854-2	Sequence 2, Appl
21	40	100.0	756	2 US-09-023-324-2	Sequence 2, Appl
22	40	100.0	756	2 US-09-168-629-15	Sequence 15, Appl
23	40	100.0	756	2 US-08-910-820-9	Sequence 9, Appl
24	36	90.0	100	1 US-08-241-853-28	Sequence 28, Appl
25	36	90.0	100	1 US-08-241-853-29	Sequence 28, Appl
26	36	90.0	100	1 US-08-850-917-28	Sequence 28, Appl
27	36	90.0	100	2 US-08-850-917-29	Sequence 29, Appl

28	36	90.0	616	4 US-09-136-574A-47	Sequence 47, Appl
29	36	90.0	982	2 US-08-673-789-4	Sequence 4, Appl
30	36	90.0	983	1 US-08-162-809-16	Sequence 16, Appl
31	36	90.0	983	1 US-08-167-919A-10	Sequence 10, Appl
32	36	90.0	983	2 US-08-449-645A-21	Sequence 21, Appl
33	36	90.0	983	2 US-08-702-367A-21	Sequence 21, Appl
34	36	90.0	983	3 US-08-715-106-10	Sequence 10, Appl
35	36	90.0	983	5 PCT-US95-04681-21	Sequence 21, Appl
36	36	90.0	1426	4 US-09-136-574A-43	Sequence 43, Appl
37	36	90.0	1751	4 US-09-136-574A-44	Sequence 44, Appl
38	35	87.5	38	2 US-08-488-161-55	Sequence 55, Appl
39	35	87.5	38	3 US-09-273-685-55	Sequence 55, Appl
40	35	87.5	38	5 PCT-US95-11934-55	Sequence 55, Appl
41	35	87.5	439	4 US-09-172-952-14	Sequence 14, Appl
42	34	85.0	170	4 US-09-199-637A-339	Sequence 339, App
43	33	82.5	23	6 5368712-2	Patent No. 5368712
44	33	82.5	23	6 5516890-2	Patent No. 5516890
45	33	82.5	138	1 US-08-686-878A-33	Sequence 33, Appl

## ALIGNMENTS

RESULT 1  
US-08-887-518-3  
Sequence 3, Application US/08887518  
Patent No. 5843721  
GENERAL INFORMATION:  
APPLICANT: Rothe, Mike  
APPLICANT: Wu, Lin  
TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESS: SCIENCE & TECHNOLOGY LAW GROUP  
STREET: 368 BUSH STREET, SUITE 3200  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/887,518  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: OSMAN, RICHARD A  
REGISTRATION NUMBER: 36,627  
REFERENCE/DOCKET NUMBER: T97-008  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 343-4341  
TELEFAX: (415) 343-4342  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 745 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-887-518-3

Query Match 100.0%; Score 40; DB 2; Length 745;

Best Local Similarity 100.0%; Pred. No. 1.1e+02; Indels 0; Gaps 0;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSWL 6  
DB 738 LMSWL 743

RESULT 2  
US-09-023-321-3  
Sequence 3, Application US/09023321  
Patent No. 5844073  
GENERAL INFORMATION:  
APPLICANT: Roche, Mike  
TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
STREET: 268 BUSH STREET, SUITE 3200  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/023,321  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/887,518  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: OSMAN, RICHARD A  
REGISTRATION NUMBER: 36,627  
REFERENCE/DOCKET NUMBER: T97-008  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 343-4341  
TELEFAX: (415) 343-4342  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 745 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-023-321-3

Query Match 100.0%; Score 40; DB 2; Length 745;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDMSWL 6  
Db 738 LDMSWL 743

RESULT 3  
US-08-890-853-4  
Sequence 4, Application US/08890853  
Patent No. 5851812  
GENERAL INFORMATION:  
APPLICANT: Goeddel, David V.  
APPLICANT: Moronicz, John  
TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
STREET: 268 BUSH STREET, SUITE 3200  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/890,853  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: OSMAN, RICHARD A  
REGISTRATION NUMBER: 36,627  
REFERENCE/DOCKET NUMBER: T97-006-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 343-4341  
TELEFAX: (415) 343-4342  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 745 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-890-853-4

Query Match 100.0%; Score 40; DB 2; Length 745;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDMSWL 6  
Db 738 LDMSWL 743

RESULT 4  
US-09-032-475-3  
Sequence 3, Application US/09032475  
Patent No. 5854003  
GENERAL INFORMATION:  
APPLICANT: Roche, Mike  
TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
STREET: 268 BUSH STREET, SUITE 3200  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/032,475  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/887,518  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: OSMAN, RICHARD A  
REGISTRATION NUMBER: 36,627  
REFERENCE/DOCKET NUMBER: T97-008  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 343-4341  
TELEFAX: (415) 343-4342  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 745 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-032-475-3

Query Match 100.0%; Score 40; DB 2; Length 745;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDMSWL 6  
|||||  
DB 738 LDMSWL 743

RESULT 5  
US-09-099-125A-4  
Sequence 4, Application US/09099125A  
Patent No. 5916760  
GENERAL INFORMATION:  
APPLICANT: Goeddel, David V.  
ATTORNEY/AGENT INFORMATION:  
TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
STREET: 268 BUSH STREET, SUITE 3200  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/099,125A  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/890,853  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: OSMAN, RICHARD A  
REGISTRATION NUMBER: 36,627  
REFERENCE/DOCKET NUMBER: T97-006-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 343-4341  
TELEFAX: (415) 343-4342  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 745 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-099-125A-4  
Query Match 100.0%; Score 40; DB 2; Length 745;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 LDMSWL 6  
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DB 738 LDMSWL 743  
RESULT 6  
US-09-099-124A-4  
Sequence 4, Application US/09099124A  
Patent No. 5939302  
GENERAL INFORMATION:  
APPLICANT: Goeddel, David V.  
ATTORNEY/AGENT INFORMATION:  
TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:

ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
STREET: 268 BUSH STREET, SUITE 3200  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94104

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/099,124A  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/890,853  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: OSMAN, RICHARD A  
REGISTRATION NUMBER: 36,627  
REFERENCE/DOCKET NUMBER: T97-006-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 343-4341  
TELEFAX: (415) 343-4342  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 745 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-099-124A-4

Query Match 100.0%; Score 40; DB 2; Length 745;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDMSWL 6  
|||||  
DB 738 LDMSWL 743

RESULT 7  
US-09-032-476-4  
Sequence 4, Application US/09032476  
Patent No. 6235492  
GENERAL INFORMATION:  
APPLICANT: Rothe, Mike  
ATTORNEY/AGENT INFORMATION:  
TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
STREET: 268 BUSH STREET, SUITE 3200  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/032,476  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/890,854  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:

NAME: OSMAN, RICHARD A  
REGISTRATION NUMBER: 36,627  
REFERENCE/DOCKET NUMBER: T97-006-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 343-4341  
TELEFAX: (415) 343-4342  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 745 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-032-476-4

Query Match 100.0%; Score 40; DB 4; Length 745;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDMSWL 6  
DB 738 LDMSWL 743

RESULT 8  
US-08-890-854-4  
Sequence 4, Application US/08890854  
Patent No. 6235512  
GENERAL INFORMATION:  
APPLICANT: Rothe, Mike  
APPLICANT: Cao, Zhaodan  
APPLICANT: R gnier, Catherine  
TITLE OF INVENTION: IKK-1 Proteins, Nucleic Acids and Methods  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
STREET: 268 BUSH STREET, SUITE 3200  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/890,854  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: OSMAN, RICHARD A  
REGISTRATION NUMBER: 36,627  
REFERENCE/DOCKET NUMBER: T97-006-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 343-4341  
TELEFAX: (415) 343-4342  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 745 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-890-854-4

Query Match 100.0%; Score 40; DB 4; Length 745;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDMSWL 6  
DB 738 LDMSWL 743

RESULT 9  
US-09-023-324-4  
Sequence 4, Application US/09023324  
Patent No. 6235513  
GENERAL INFORMATION:  
APPLICANT: Rothe, Mike  
APPLICANT: Cao, Zhaodan  
APPLICANT: R gnier, Catherine  
TITLE OF INVENTION: IKK-1 Proteins, Nucleic Acids and Methods  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
STREET: 268 BUSH STREET, SUITE 3200  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/023,324  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/890,854  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: OSMAN, RICHARD A  
REGISTRATION NUMBER: 36,627  
REFERENCE/DOCKET NUMBER: T97-006-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 343-4341  
TELEFAX: (415) 343-4342  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 745 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-023-324-4

Query Match 100.0%; Score 40; DB 4; Length 745;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDMSWL 6  
DB 738 LDMSWL 743

RESULT 10  
US-09-168-629-2  
Sequence 2, Application US/09168629  
Patent No. 6242253  
GENERAL INFORMATION:  
APPLICANT: Karlin, Michael  
APPLICANT: Didonato, Joseph A.  
APPLICANT: Rothwarf, David M.  
APPLICANT: Hayakawa, Makio  
APPLICANT: Zandi, Dbrahm  
TITLE OF INVENTION: IKK kinase, Subunits Thereof, and Methods of Using Same  
FILE REFERENCE: P-UD 3295  
CURRENT APPLICATION NUMBER: US/09/168,629  
CURRENT FILING DATE: 1998-10-08  
EARLIER APPLICATION NUMBER: 60/061,470  
EARLIER FILING DATE: 1997-10-09  
NUMBER OF SEQ ID NOS: 20

SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 2  
LENGTH: 745  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-168-629-2

Query Match 100.0%; Score 40; DB 4; Length 745;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMWSL 6  
|||||  
DB 738 LDMWSL 743

RESULT 11  
US-08-910-820-10  
Sequence 10, Application US/08910820  
Patent No. 6258579

GENERAL INFORMATION:  
APPLICANT: Mercutio, Frank  
APPLICANT: Zhu, Hengyi  
APPLICANT: Barbosa, Miguel  
APPLICANT: Li, Gfan  
APPLICANT: Murray, Brian W.  
TITLE OF INVENTION: STIMULUS-INDUCIBLE PROTEIN KINASE  
TITLE OF INVENTION: COMPLEX AND METHODS OF USE THEREFOR  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SEED and BERRY LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98104

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/910, 820  
FILING DATE: 12-AUG-1997  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Maki, David J.  
REGISTRATION NUMBER: 31,392  
REFERENCE/DOCKET NUMBER: 860098.413C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 745 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear

US-08-910-820-10

Query Match 100.0%; Score 40; DB 4; Length 745;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMWSL 6  
|||||  
DB 738 LDMWSL 743

RESULT 12  
US-08-810-131A-2  
Sequence 2, Application US/08810131A  
Patent No. 6268194

GENERAL INFORMATION:

APPLICANT: Karin, Michael  
APPLICANT: Didonato, Joseph A.  
APPLICANT: Rothwarf, David M.  
APPLICANT: Hayakawa, Makio  
APPLICANT: Zandi, Ebrahim

TITLE OF INVENTION: 1-Kappa-B Kinase and Methods of Using  
TITLE OF INVENTION: Same  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Campbell & Flores LLP  
STREET: 4370 La Jolla Village Drive, Suite 700  
CITY: San Diego  
STATE: California  
COUNTRY: United States  
ZIP: 92122

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/810, 131A

FILING DATE: 25-FEB-1997

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Campbell, Cathryn A.

REGISTRATION NUMBER: 31,815

REFERENCE/DOCKET NUMBER: P-UD 2408

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 535-9001

TELEFAX: (619) 535-8949

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 745 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-810-131A-2

QY 1 LDMWSL 6  
|||||  
DB 738 LDMWSL 743

Query Match 100.0%; Score 40; DB 4; Length 745;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 13  
US-08-887-518-4  
Sequence 4, Application US/08887518  
Patent No. 5843721  
GENERAL INFORMATION:  
APPLICANT: Wu, Lin  
APPLICANT: Rotne, Mike  
TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
STREET: 268 BUSH STREET, SUITE 3200  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/887, 518  
FILING DATE:

CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: OSMAN, RICHARD A  
REGISTRATION NUMBER: 36,627  
REFERENCE/DOCKET NUMBER: T97-008  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 343-4341  
TELEFAX: (415) 343-4342  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 756 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-887-518-4

Query Match 100.0%; Score 40; DB 2; Length 756;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDMSWL 6  
|||||  
Db 737 LDMSWL 742

RESULT 14  
US-09-023-321-4  
Sequence 4, Application US/09023321  
Patent No. 5844073  
GENERAL INFORMATION:  
APPLICANT: Rothe, Mike  
APPLICANT: Wu, Lin  
TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
STREET: 268 BUSH STREET, SUITE 3200  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/023.321  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/887.518  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: OSMAN, RICHARD A  
REGISTRATION NUMBER: 36,627  
REFERENCE/DOCKET NUMBER: T97-008  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 343-4341  
TELEFAX: (415) 343-4342  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 756 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-023-321-4

Query Match 100.0%; Score 40; DB 2; Length 756;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDMSWL 6  
|||||  
Db 737 LDMSWL 742

RESULT 15  
US-08-890-853-2  
Sequence 2, Application US/08890853  
Patent No. 5851812  
GENERAL INFORMATION:  
APPLICANT: Goeddel, David V.  
APPLICANT: Woronicz, John  
TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
STREET: 268 BUSH STREET, SUITE 3200  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/890.853  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: OSMAN, RICHARD A  
REGISTRATION NUMBER: 36,627  
REFERENCE/DOCKET NUMBER: T97-006-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 343-4341  
TELEFAX: (415) 343-4342  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 756 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-890-853-2

Query Match 100.0%; Score 40; DB 2; Length 756;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDMSWL 6  
|||||  
Db 737 LDMSWL 742

Search completed: May 30, 2003, 14:41:22  
Job time : 15.0395 secs

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## OM protein - protein search, using sw model

Run on: May 30, 2003, 14:50:13 ; Search time 10.4605 Seconds  
(without alignments)  
58.060 Million cell updates/sec

Title: US-09-643-260-2  
Perfect score: 40  
Sequence: 1 LDMSWL 6

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 383519 seqs, 101223694 residues

Total number of hits satisfying chosen parameters: 383519

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

## Database :

Published Applications, AA:\*

- 1: /cgn2\_6/ptodata/1/pubppa/US08\_NEW\_PUB pep:\*
- 2: /cgn2\_6/ptodata/1/pubppa/PTCT\_NEW\_PUB pep:\*
- 3: /cgn2\_6/ptodata/1/pubppa/US06\_NEW\_PUB pep:\*
- 4: /cgn2\_6/ptodata/1/pubppa/US06\_PUBCOMB pep:\*
- 5: /cgn2\_6/ptodata/1/pubppa/US07\_NEW\_PUB pep:\*
- 6: /cgn2\_6/ptodata/1/pubppa/US07\_PUBCOMB pep:\*
- 7: /cgn2\_6/ptodata/1/pubppa/PTCTUS\_PUBCOMB pep:\*
- 8: /cgn2\_6/ptodata/1/pubppa/US08\_PUBCOMB pep:\*
- 9: /cgn2\_6/ptodata/1/pubppa/US09\_NEW\_PUB pep:\*
- 10: /cgn2\_6/ptodata/1/pubppa/US09\_PUBCOMB pep:\*
- 11: /cgn2\_6/ptodata/1/pubppa/US10\_NEW\_PUB pep:\*
- 12: /cgn2\_6/ptodata/1/pubppa/US10\_PUBCOMB pep:\*
- 13: /cgn2\_6/ptodata/1/pubppa/US60\_NEW\_PUB pep:\*
- 14: /cgn2\_6/ptodata/1/pubppa/US60\_PUBCOMB pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40	100.0	6	9	US-09-847-940B-2
2	40	100.0	6	9	US-09-847-946A-2
3	40	100.0	6	9	US-09-847-946A-33
4	40	100.0	7	9	US-09-847-946A-37
5	40	100.0	8	9	US-09-847-946A-30
6	40	100.0	8	9	US-09-847-946A-38
7	40	100.0	9	9	US-09-847-946A-29
8	40	100.0	9	9	US-09-847-946A-32
9	40	100.0	9	9	US-09-847-946A-35
10	40	100.0	9	9	US-09-847-946A-36
11	40	100.0	10	9	US-09-847-946A-31
12	40	100.0	10	9	US-09-847-946A-34
13	40	100.0	11	9	US-09-847-946A-28
14	40	100.0	11	9	US-09-847-946A-132
15	40	100.0	11	9	US-09-847-946A-140
16	40	100.0	13	9	US-09-847-946A-143
17	40	100.0	13	9	US-09-847-946A-144
18	40	100.0	13	9	US-09-847-946A-145
19	40	100.0	13	9	US-09-847-946A-148

20	40	100.0	17	9	US-09-847-946A-141	Sequence 141, App
21	40	100.0	17	9	US-09-847-946A-142	Sequence 142, App
22	40	100.0	17	9	US-09-847-946A-146	Sequence 146, App
23	40	100.0	17	9	US-09-847-946A-147	Sequence 147, App
24	40	100.0	18	9	US-09-847-946A-131	Sequence 131, App
25	40	100.0	18	9	US-09-847-946A-135	Sequence 135, App
26	40	100.0	18	9	US-09-847-946A-136	Sequence 136, App
27	40	100.0	22	9	US-09-847-946A-133	Sequence 133, App
28	40	100.0	22	9	US-09-847-946A-134	Sequence 134, App
29	40	100.0	22	9	US-09-847-946A-137	Sequence 137, App
30	40	100.0	22	9	US-09-847-946A-138	Sequence 138, App
31	40	100.0	22	9	US-09-847-946A-139	Sequence 139, App
32	40	100.0	28	9	US-09-847-940B-18	Sequence 18, App
33	40	100.0	28	9	US-09-847-940B-18	Sequence 18, App
34	40	100.0	222	10	US-09-771-161A-141	Sequence 141, App
35	40	100.0	745	9	US-09-844-988-10	Sequence 10, App
36	40	100.0	745	9	US-10-243-408-4	Sequence 4, App
37	40	100.0	745	9	US-10-059-585-35	Sequence 35, App
38	40	100.0	745	10	US-09-796-872-2	Sequence 2, App
39	40	100.0	745	10	US-09-844-908-10	Sequence 10, App
40	40	100.0	756	9	US-09-844-988-9	Sequence 9, App
41	40	100.0	756	9	US-10-243-408-2	Sequence 2, App
42	40	100.0	756	10	US-09-796-872-15	Sequence 15, App
43	40	100.0	756	10	US-09-771-161A-232	Sequence 232, App
44	40	100.0	756	10	US-09-844-908-9	Sequence 9, App
45	40	100.0	996	9	US-10-072-036-123	Sequence 123, App

## ALIGNMENTS

RESULT 1  
US-09-847-940B-2  
Sequence 2, Application US/09847940B  
Patent No. US20020156000A1  
GENERAL INFORMATION:  
APPLICANT: May, Michael J.  
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
FILE REFERENCE: PFI-117CP  
CURRENT APPLICATION NUMBER: US/09/847, 940B  
CURRENT FILING DATE: 2001-05-02  
PRIOR APPLICATION NUMBER: 09/643, 260  
PRIOR FILING DATE: 2000-08-22  
NUMBER OF SEQ ID NOS: 27  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 2  
LENGTH: 6  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: NBD mutants  
US-09-847-940B-2  
Query Match 100.0%; Score 40; DB 9; Length 6;  
Best Local Similarity 100.0%; Pred. No. 3.4e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 LDMSWL 6  
Db 1 LDMSWL 6  
RESULT 2  
US-09-847-946A-2  
Sequence 2, Application US/09847946A  
Publication No. US20030054999A1  
GENERAL INFORMATION:  
APPLICANT: May, Michael J  
APPLICANT: Ghosh, Sanhar  
APPLICANT: Flindels, Mark A  
APPLICANT: Phillips, Kathryn  
APPLICANT: Hannig, Gerhard

;; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
;; FILE REFERENCE: PPI-119  
;; CURRENT APPLICATION NUMBER: US/09/847,946A  
;; CURRENT FILING DATE: 2001-05-02  
;; PRIOR APPLICATION NUMBER: 60/201,261  
;; PRIOR FILING DATE: 2000-05-02  
;; PRIOR APPLICATION NUMBER: 09/643,260  
;; PRIOR FILING DATE: 2000-08-22  
;; NUMBER OF SEQ ID NOS: 160  
;; SOFTWARE: PatentIn Ver. 2.0  
;; SEQ ID NO 2  
;; LENGTH: 6  
;; TYPE: prt  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Description of Artificial Sequence:NBD peptide  
US-09-847-946A-2

Query Match 100.0%; Score 40; DB 9; Length 6;  
Best Local Similarity 100.0%; Pred. No. 3.4e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDMSWL 6  
Db 1 LDMSWL 6

RESULT 3  
US-09-847-946A-33  
;; Sequence 33, Application US/09847946A  
;; Publication No. US2003005499A1  
;; GENERAL INFORMATION:  
;; APPLICANT: May, Michael J  
;; APPLICANT: Ghosh, Sankar  
;; APPLICANT: Findels, Mark A  
;; APPLICANT: Phillips, Kathryn  
;; APPLICANT: Hannig, Gerhard  
;; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
;; FILE REFERENCE: PPI-119  
;; CURRENT APPLICATION NUMBER: US/09/847,946A  
;; CURRENT FILING DATE: 2001-05-02  
;; PRIOR APPLICATION NUMBER: 60/201,261  
;; PRIOR FILING DATE: 2000-05-02  
;; PRIOR APPLICATION NUMBER: 09/643,260  
;; PRIOR FILING DATE: 2000-08-22  
;; NUMBER OF SEQ ID NOS: 160  
;; SOFTWARE: PatentIn Ver. 2.0  
;; SEQ ID NO 33  
;; LENGTH: 6  
;; TYPE: prt  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding  
US-09-847-946A-33

Query Match 100.0%; Score 40; DB 9; Length 6;  
Best Local Similarity 100.0%; Pred. No. 3.4e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDMSWL 6  
Db 1 LDMSWL 6

RESULT 4  
US-09-847-946A-37  
;; Sequence 37, Application US/09847946A  
;; Publication No. US2003005499A1  
;; GENERAL INFORMATION:  
;; APPLICANT: May, Michael J  
;; APPLICANT: Ghosh, Sankar  
;; APPLICANT: Findels, Mark A

;; APPLICANT: Phillips, Kathryn  
;; APPLICANT: Hannig, Gerhard  
;; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
;; FILE REFERENCE: PPI-119  
;; CURRENT APPLICATION NUMBER: US/09/847,946A  
;; CURRENT FILING DATE: 2001-05-02  
;; PRIOR APPLICATION NUMBER: 60/201,261  
;; PRIOR FILING DATE: 2000-05-02  
;; PRIOR APPLICATION NUMBER: 09/643,260  
;; PRIOR FILING DATE: 2000-08-22  
;; NUMBER OF SEQ ID NOS: 160  
;; SOFTWARE: PatentIn Ver. 2.0  
;; SEQ ID NO 37  
;; LENGTH: 7  
;; TYPE: prt  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding  
US-09-847-946A-37

Query Match 100.0%; Score 40; DB 9; Length 7;  
Best Local Similarity 100.0%; Pred. No. 3.4e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDMSWL 6  
Db 1 LDMSWL 6

RESULT 5  
US-09-847-946A-30  
;; Sequence 30, Application US/09847946A  
;; Publication No. US2003005499A1  
;; GENERAL INFORMATION:  
;; APPLICANT: May, Michael J  
;; APPLICANT: Ghosh, Sankar  
;; APPLICANT: Findels, Mark A  
;; APPLICANT: Phillips, Kathryn  
;; APPLICANT: Hannig, Gerhard  
;; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
;; FILE REFERENCE: PPI-119  
;; CURRENT APPLICATION NUMBER: US/09/847,946A  
;; CURRENT FILING DATE: 2001-05-02  
;; PRIOR APPLICATION NUMBER: 60/201,261  
;; PRIOR FILING DATE: 2000-05-02  
;; PRIOR APPLICATION NUMBER: 09/643,260  
;; PRIOR FILING DATE: 2000-08-22  
;; NUMBER OF SEQ ID NOS: 160  
;; SOFTWARE: PatentIn Ver. 2.0  
;; SEQ ID NO 30  
;; LENGTH: 8  
;; TYPE: prt  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding  
US-09-847-946A-30

Query Match 100.0%; Score 40; DB 9; Length 8;  
Best Local Similarity 100.0%; Pred. No. 3.4e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDMSWL 6  
Db 3 LDMSWL 8

RESULT 6  
US-09-847-946A-38  
;; Sequence 38, Application US/09847946A  
;; Publication No. US2003005499A1  
;; GENERAL INFORMATION:

APPLICANT: May, Michael J  
APPLICANT: Ghosh, Sankar  
APPLICANT: Findels, Mark A  
APPLICANT: Phillips, Kathryn  
APPLICANT: Hannig, Gerhard  
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
FILE REFERENCE: PFI-119  
CURRENT APPLICATION NUMBER: US/09/847,946A  
CURRENT FILING DATE: 2001-05-02  
PRIOR APPLICATION NUMBER: 60/201,261  
PRIOR FILING DATE: 2000-05-02  
PRIOR APPLICATION NUMBER: 09/643,260  
PRIOR FILING DATE: 2000-08-22  
NUMBER OF SEQ ID NOS: 160  
SOFTWARE: Patentln Ver. 2.0  
SEQ ID NO 38  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:NEMO binding  
US-09-847-946A-38

Query Match 100.0%; Score 40; DB 9; Length 8;  
Best Local Similarity 100.0%; Pred. No. 3.4e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDMSWL 6  
DB 1 LDMSWL 6

RESULT 7  
US-09-847-946A-29  
Sequence 29, Application US/09847946A  
Publication No. US20030054999A1  
GENERAL INFORMATION:  
APPLICANT: May, Michael J  
APPLICANT: Ghosh, Sankar  
APPLICANT: Findels, Mark A  
APPLICANT: Phillips, Kathryn  
APPLICANT: Hannig, Gerhard  
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
FILE REFERENCE: PFI-119  
CURRENT APPLICATION NUMBER: US/09/847,946A  
CURRENT FILING DATE: 2001-05-02  
PRIOR APPLICATION NUMBER: 60/201,261  
PRIOR FILING DATE: 2000-05-02  
PRIOR APPLICATION NUMBER: 09/643,260  
PRIOR FILING DATE: 2000-08-22  
NUMBER OF SEQ ID NOS: 160  
SOFTWARE: Patentln Ver. 2.0  
SEQ ID NO 29  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:NEMO binding  
US-09-847-946A-29

Query Match 100.0%; Score 40; DB 9; Length 9;  
Best Local Similarity 100.0%; Pred. No. 3.4e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDMSWL 6  
DB 1 LDMSWL 6

RESULT 8  
US-09-847-946A-32

Sequence 32, Application US/09847946A  
Publication No. US20030054999A1  
GENERAL INFORMATION:  
APPLICANT: May, Michael J  
APPLICANT: Ghosh, Sankar  
APPLICANT: Findels, Mark A  
APPLICANT: Phillips, Kathryn  
APPLICANT: Hannig, Gerhard  
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
FILE REFERENCE: PFI-119  
CURRENT APPLICATION NUMBER: US/09/847,946A  
CURRENT FILING DATE: 2001-05-02  
PRIOR APPLICATION NUMBER: 60/201,261  
PRIOR FILING DATE: 2000-05-02  
PRIOR APPLICATION NUMBER: 09/643,260  
PRIOR FILING DATE: 2000-08-22  
NUMBER OF SEQ ID NOS: 160  
SOFTWARE: Patentln Ver. 2.0  
SEQ ID NO 32  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:NEMO binding  
US-09-847-946A-32

Query Match 100.0%; Score 40; DB 9; Length 9;  
Best Local Similarity 100.0%; Pred. No. 3.4e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDMSWL 6  
DB 1 LDMSWL 6

RESULT 9  
US-09-847-946A-35  
Sequence 35, Application US/09847946A  
Publication No. US20030054999A1  
GENERAL INFORMATION:  
APPLICANT: May, Michael J  
APPLICANT: Ghosh, Sankar  
APPLICANT: Findels, Mark A  
APPLICANT: Phillips, Kathryn  
APPLICANT: Hannig, Gerhard  
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
FILE REFERENCE: PFI-119  
CURRENT APPLICATION NUMBER: US/09/847,946A  
CURRENT FILING DATE: 2001-05-02  
PRIOR APPLICATION NUMBER: 60/201,261  
PRIOR FILING DATE: 2000-05-02  
PRIOR APPLICATION NUMBER: 09/643,260  
PRIOR FILING DATE: 2000-08-22  
NUMBER OF SEQ ID NOS: 160  
SOFTWARE: Patentln Ver. 2.0  
SEQ ID NO 35  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:NEMO binding  
US-09-847-946A-35

Query Match 100.0%; Score 40; DB 9; Length 9;  
Best Local Similarity 100.0%; Pred. No. 3.4e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDMSWL 6  
DB 3 LDMSWL 8

RESULT 10  
US-09-847-946A-36

; Sequence 36, Application US/09847946A  
; Publication No. US20030054999A1

; GENERAL INFORMATION:

; APPLICANT: May, Michael J

; APPLICANT: Ghosh, Sankar

; APPLICANT: Findels, Mark A

; APPLICANT: Phillips, Kathryn

; APPLICANT: Hannig, Gerhard

; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF

; FILE REFERENCE: PPI-119

; CURRENT APPLICATION NUMBER: US/09/847,946A

; CURRENT FILING DATE: 2001-05-02

; PRIOR APPLICATION NUMBER: 60/201,261

; PRIOR FILING DATE: 2000-05-02

; PRIOR APPLICATION NUMBER: 09/643,260

; PRIOR FILING DATE: 2000-08-22

; NUMBER OF SEQ ID NOS: 160

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 36

; LENGTH: 9

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE: OTHER INFORMATION: Description of Artificial Sequence:NEMO binding

; OTHER INFORMATION: sequence

US-09-847-946A-36

Query Match

Best Local Similarity 100.0%; Score 40; DB 9; Length 9;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDMSWL 6

DB 2 LDMSWL 7

RESULT 11

US-09-847-946A-31

; Sequence 31, Application US/09847946A

; Publication No. US20030054999A1

; GENERAL INFORMATION:

; APPLICANT: May, Michael J

; APPLICANT: Ghosh, Sankar

; APPLICANT: Findels, Mark A

; APPLICANT: Phillips, Kathryn

; APPLICANT: Hannig, Gerhard

; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF

; FILE REFERENCE: PPI-119

; CURRENT APPLICATION NUMBER: US/09/847,946A

; CURRENT FILING DATE: 2001-05-02

; PRIOR APPLICATION NUMBER: 60/201,261

; PRIOR FILING DATE: 2000-05-02

; PRIOR APPLICATION NUMBER: 09/643,260

; PRIOR FILING DATE: 2000-08-22

; NUMBER OF SEQ ID NOS: 160

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 31

; LENGTH: 10

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE: OTHER INFORMATION: Description of Artificial Sequence:NEMO binding

; OTHER INFORMATION: sequence

US-09-847-946A-31

Query Match

Best Local Similarity 100.0%; Score 40; DB 9; Length 10;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDMSWL 6

DB 2 LDMSWL 7

RESULT 12  
US-09-847-946A-34

; Sequence 34, Application US/09847946A  
; Publication No. US20030054999A1

; GENERAL INFORMATION:

; APPLICANT: May, Michael J

; APPLICANT: Ghosh, Sankar

; APPLICANT: Findels, Mark A

; APPLICANT: Phillips, Kathryn

; APPLICANT: Hannig, Gerhard

; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF

; FILE REFERENCE: PPI-119

; CURRENT APPLICATION NUMBER: US/09/847,946A

; CURRENT FILING DATE: 2001-05-02

; PRIOR APPLICATION NUMBER: 60/201,261

; PRIOR FILING DATE: 2000-05-02

; PRIOR APPLICATION NUMBER: 09/643,260

; PRIOR FILING DATE: 2000-08-22

; NUMBER OF SEQ ID NOS: 160

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 34

; LENGTH: 10

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE: OTHER INFORMATION: Description of Artificial Sequence:NEMO binding

; OTHER INFORMATION: sequence

US-09-847-946A-34

Query Match

Best Local Similarity 100.0%; Score 40; DB 9; Length 10;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDMSWL 6

DB 3 LDMSWL 8

RESULT 13  
US-09-847-946A-28

; Sequence 28, Application US/09847946A  
; Publication No. US20030054999A1

; GENERAL INFORMATION:

; APPLICANT: May, Michael J

; APPLICANT: Ghosh, Sankar

; APPLICANT: Findels, Mark A

; APPLICANT: Phillips, Kathryn

; APPLICANT: Hannig, Gerhard

; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF

; FILE REFERENCE: PPI-119

; CURRENT APPLICATION NUMBER: US/09/847,946A

; CURRENT FILING DATE: 2001-05-02

; PRIOR APPLICATION NUMBER: 60/201,261

; PRIOR FILING DATE: 2000-05-02

; PRIOR APPLICATION NUMBER: 09/643,260

; PRIOR FILING DATE: 2000-08-22

; NUMBER OF SEQ ID NOS: 160

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 28

; LENGTH: 11

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE: OTHER INFORMATION: Description of Artificial Sequence:NEMO binding

; OTHER INFORMATION: sequence

US-09-847-946A-28

Query Match

Best Local Similarity 100.0%; Score 40; DB 9; Length 11;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDMSWL 6

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LDMSWL 6  
|||||  
Db 3 LDMSWL 8

## RESULT 14

US-09-847-946A-132  
; Sequence 132, Application US/09847946A  
; Publication No. US20030054999A1  
; GENERAL INFORMATION:  
; APPLICANT: May, Michael J  
; APPLICANT: Ghosh, Sankar  
; APPLICANT: Fingels, Mark A  
; APPLICANT: Phillips, Kathryn  
; APPLICANT: Hannig, Gerhard  
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
; FILE REFERENCE: PFI-119  
; CURRENT APPLICATION NUMBER: US/09/847,946A  
; CURRENT FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: 60/201,261  
; PRIOR FILING DATE: 2000-05-02  
; PRIOR APPLICATION NUMBER: 09/643,260  
; PRIOR FILING DATE: 2000-08-22  
; NUMBER OF SEQ ID NOS: 160  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 132  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial  
; OTHER INFORMATION: Sequence:anti-inflammatory compound  
US-09-847-946A-132

Query Match 100.0%; Score 40; DB 9; Length 11;  
Best Local Similarity 100.0%; Pred. No. 4.3;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSWL 6  
|||||  
Db 3 LDMSWL 8

## RESULT 15

US-09-847-946A-140  
; Sequence 140, Application US/09847946A  
; Publication No. US20030054999A1  
; GENERAL INFORMATION:  
; APPLICANT: May, Michael J  
; APPLICANT: Ghosh, Sankar  
; APPLICANT: Fingels, Mark A  
; APPLICANT: Phillips, Kathryn  
; APPLICANT: Hannig, Gerhard  
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
; FILE REFERENCE: PFI-119  
; CURRENT APPLICATION NUMBER: US/09/847,946A  
; CURRENT FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: 60/201,261  
; PRIOR FILING DATE: 2000-05-02  
; PRIOR APPLICATION NUMBER: 09/643,260  
; PRIOR FILING DATE: 2000-08-22  
; NUMBER OF SEQ ID NOS: 160  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 140  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial  
; OTHER INFORMATION: Sequence:anti-inflammatory compound  
US-09-847-946A-140

Query Match 100.0%; Score 40; DB 9; Length 11;  
Best Local Similarity 100.0%; Pred. No. 4.3;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LDMSWL 6  
|||||  
Db 3 LDMSWL 8

Search completed: May 30, 2003, 15:53:14  
Job time : 11.4605 secs



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OM protein - protein search, using sw model

Run on: May 30, 2003, 14:32:12 ; Search time 6.03947 Seconds  
(without alignments)  
29.231 Million cell updates/sec

Title: US-09-643-260-3

Perfect score: 26

Sequence: 1 LDASAL 6

Scoring table: BLOSUM62  
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Searched: 262574 seqs, 29422922 residues

262574

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: /cgn2\_6/ptodata/1/1aa/5A.COMB.pep:\*  
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3: /cgn2\_6/ptodata/1/1aa/6A.COMB.pep:\*  
4: /cgn2\_6/ptodata/1/1aa/6B.COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/PCrus.COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/Backfilest.pep:\*

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	26	100.0	1313	4	US-08-989-299-9
2	24	92.3	20	9	US-09-140-149-9
3	24	92.3	40	4	US-09-480-993-18
4	24	92.3	83	1	US-08-370-225-16
5	24	92.3	83	1	US-08-461-859-16
6	24	92.3	83	5	PCT-US93-10069-16
7	24	92.3	274	1	US-08-318-947A-20
8	24	92.3	274	2	US-08-795-303-20
9	24	92.3	298	2	US-08-874-347-25
10	24	92.3	298	2	US-08-969-106-2
11	24	92.3	298	4	US-09-093-522-25
12	24	92.3	298	4	US-09-457-040B-29
13	24	92.3	298	4	US-09-411-628-13
14	24	92.3	359	4	US-09-098-219B-2
15	24	92.3	405	1	US-08-370-193A-9
16	24	92.3	723	4	US-09-434-408-2
17	24	92.3	2618	4	US-09-413-814-28
18	23	88.5	44	4	US-08-905-223-345
19	23	88.5	65	5	US-08-227-536-6
20	23	88.5	65	5	PCT-US95-04682-6
21	23	88.5	201	1	US-08-444-083-8
22	23	88.5	201	1	US-08-286-304-8
23	23	88.5	201	1	US-08-442-745-8
24	23	88.5	201	1	US-08-443-129-8
25	23	88.5	201	1	US-08-443-952-8
26	23	88.5	201	1	US-08-443-130-8
27	23	88.5	201	1	US-08-792-019B-11

28	23	88.5	201	3	US-09-106-182-4	Sequence 4, Appli
29	23	88.5	201	3	US-08-988-819-11	Sequence 11, Appli
30	23	88.5	201	3	US-08-898-911-8	Sequence 8, Appli
31	23	88.5	201	4	US-09-016-534-11	Sequence 11, Appli
32	23	88.5	201	5	PCT-US95-04467-8	Sequence 2, Appli
33	23	88.5	626	4	US-09-019-385-2	Sequence 2, Appli
34	23	88.5	905	4	US-09-754-250-4	Sequence 4, Appli
35	23	88.5	920	4	US-09-754-250-2	Sequence 4, Appli
36	23	88.5	921	1	US-08-297-644-39	Sequence 39, Appli
37	23	88.5	921	1	US-08-297-644-39	Sequence 39, Appli
38	23	88.5	921	1	US-08-297-510-39	Sequence 39, Appli
39	23	88.5	921	1	US-08-479-532-39	Sequence 39, Appli
40	23	88.5	921	1	US-08-455-526-39	Sequence 39, Appli
41	23	88.5	921	1	US-08-455-525-39	Sequence 39, Appli
42	23	88.5	921	3	US-09-139-491-39	Sequence 39, Appli
43	23	88.5	921	4	US-09-754-250-5	Sequence 5, Appli
44	23	88.5	921	5	PCT-US92-03222-39	Sequence 39, Appli
45	23	88.5	941	1	US-07-872-644-45	Sequence 45, Appli

#### ALIGNMENTS

RESULT 1  
US-08-989-299-9  
Sequence 9, Application US/08989299  
Patent No. 6194556  
GENERAL INFORMATION:  
APPLICANT: Acton, Susan L.  
TITLE OF INVENTION: ANGIOGENIN CONVERTING ENZYME HOMOLOG  
TITLE OF INVENTION: AND THERAPEUTIC AND DIAGNOSTIC USES THEREFOR  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESS: FOLEY HONG & ELLIOT LLP  
STREET: One Post Office Square  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109-2170  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/989,299  
FILING DATE: 11-DEC-1997  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Arnold E., Beth  
REGISTRATION NUMBER: 35,430  
REFERENCE/DOCKET NUMBER: MTA-025.01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-832-7000  
FAX: 617-832-7000  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1313 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-989-299-9

Query Match 100.0%; Score 26; DB 4; Length 1313;  
Best Local Similarity 100.0%; Pred. No. 3.1e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASAL 6  
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DB 600 LDASAL 605

## RESULT 2

US-09-140-149-9  
; Sequence 9, Application US/09140149  
; Patent No. 6117680  
; GENERAL INFORMATION:  
; APPLICANT: Natesan, Sridaran  
; APPLICANT: Gilman, Michael Z  
; TITLE OF INVENTION: No. 6117680el Compositions and Methods for Regulation of  
; FILE REFERENCE: 363C  
; CURRENT APPLICATION NUMBER: US/09/140,149  
; CURRENT FILING DATE: 1998-08-26  
; EARLIER APPLICATION NUMBER: 08/918,401  
; EARLIER FILING DATE: 1997-08-26  
; EARLIER APPLICATION NUMBER: 08/920,610  
; EARLIER FILING DATE: 1997-08-27  
; EARLIER APPLICATION NUMBER: 09/126,009  
; EARLIER FILING DATE: 1998-07-23  
; EARLIER APPLICATION NUMBER: PCT/US97/15219  
; EARLIER FILING DATE: 1997-08-27  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: Patentln Ver. 2.0  
; SEQ ID NO 9  
; LENGTH: 20  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:synthetic  
; US-09-140-149-9

Query Match 92.3%; Score 24; DB 3; Length 20;  
Best Local Similarity 83.3%; Pred. No. 8.3;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDASAL 6  
:|||||

DB 11 MDASAL 16

## RESULT 3

US-09-480-993-18  
; Sequence 18, Application US/09480993  
; Patent No. 6383790  
; GENERAL INFORMATION:  
; APPLICANT: Shokat, Kevin M.  
; TITLE OF INVENTION: High Affinity Kinase Inhibitors for Target Validation  
; FILE REFERENCE: 51538-5001-US  
; CURRENT APPLICATION NUMBER: US/09/480,993  
; CURRENT FILING DATE: 2000-01-11  
; EARLIER APPLICATION NUMBER: US 60/115,340  
; EARLIER FILING DATE: 1999-01-11  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: Patentln Ver. 2.1  
; SEQ ID NO 18  
; LENGTH: 40  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: Cdk2, cyclin-dependent kinase  
; US-09-480-993-18

Query Match 92.3%; Score 24; DB 4; Length 40;  
Best Local Similarity 83.3%; Pred. No. 18;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDASAL 6  
:|||||

DB 33 MDASAL 38

## RESULT 4

US-08-370-225-16  
; Sequence 16, Application US/08370225  
; Patent No. 5580736  
; GENERAL INFORMATION:  
; APPLICANT: Brent, Roger  
; APPLICANT: Gyuris, Jeno  
; APPLICANT: Golemis, Erica  
; TITLE OF INVENTION: Interaction Trap System for Isolating  
; NUMBER OF SEQUENCES: 33  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: U.S.A.  
; ZIP: 02110-2804  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 MB  
; COMPUTER: IBM PS/2 Model 50z or 55sx  
; OPERATING SYSTEM: MS-DOS (Version 5.0)  
; SOFTWARE: Wordperfect (Version 5.1)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/370,225  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/969,038  
; FILING DATE: 10/30/92  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Clark, Paul T.  
; REGISTRATION NUMBER: 30,162  
; REFERENCE/DOCKET NUMBER: 00786/143001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 542-5070  
; TELEFAX: (617) 542-8906  
; TELEX: 200154  
; INFORMATION FOR SEQ ID NO: 16:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 83  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; US-08-370-225-16

Query Match 92.3%; Score 24; DB 1; Length 83;  
Best Local Similarity 83.3%; Pred. No. 42;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDASAL 6  
:|||||

DB 18 MDASAL 23

## RESULT 5

US-08-461-859-16  
; Sequence 16, Application US/08461859  
; Patent No. 5786169  
; GENERAL INFORMATION:  
; APPLICANT: Brent, Roger  
; APPLICANT: Gyuris, Jeno  
; APPLICANT: Golemis, Erica  
; TITLE OF INVENTION: Interaction Trap System for Isolating  
; NUMBER OF SEQUENCES: 35  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson P.C.  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: U.S.A.  
; ZIP: 02110-2804

Query Match 92.3%; Score 24; DB 4; Length 40;  
Best Local Similarity 83.3%; Pred. No. 18;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
COMPUTER: IBM PS/2 Model 502 or 55SX  
OPERATING SYSTEM: MS-DOS (Version 5.0)  
SOFTWARE: WordPerfect (Version 5.1)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/461,859  
FILING DATE: June 5, 1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/370,225  
FILING DATE: January 9, 1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/969,038  
FILING DATE: October 30, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Lech, Karen F.  
REGISTRATION NUMBER: 35,238  
REFERENCE/DOCKET NUMBER: 00786/143002  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 542-5070  
TELEFAX: (617) 542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 83  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
US-08-461-859-16

Query Match 92.3%; Score 24; DB 1; Length 83;  
Best Local Similarity 83.3%; Pred. No. 42;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASAL 6  
DB 18 MDASAL 23

RESULT 6  
PCT-US93-10069-16  
GENERAL INFORMATION:  
APPLICANT: Brent, Roger  
APPLICANT: Gyuris, Jenio  
APPLICANT: Golemis, Erica  
TITLE OF INVENTION: Interaction Trap System for Isolating  
NUMBER OF SEQUENCES: 33  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: U.S.A.  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
COMPUTER: IBM PS/2 Model 502 or 55SX  
OPERATING SYSTEM: MS-DOS (Version 5.0)  
SOFTWARE: WordPerfect (Version 5.1)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/10069  
FILING DATE: 20-OCT-1993  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/969,038  
FILING DATE: 10/30/92  
ATTORNEY/AGENT INFORMATION:  
NAME: Clark, Paul T.  
REGISTRATION NUMBER: 30,162  
REFERENCE/DOCKET NUMBER: 00786/143001

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 542-5070  
TELEFAX: (617) 542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 83  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
PCT-US93-10069-16

Query Match 92.3%; Score 24; DB 5; Length 83;  
Best Local Similarity 83.3%; Pred. No. 42;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASAL 6  
DB 18 MDASAL 23

RESULT 7  
US-08-318-947A-20  
Sequence 20, Application US/08318947A  
Patent No. 5798245  
GENERAL INFORMATION:  
APPLICANT: Anderson, Paul J.  
APPLICANT: Tian, Qingsheng  
TITLE OF INVENTION: TTA-1 BINDING PROTEINS AND ISOLATED  
TITLE OF INVENTION: COMPLEMENTARY DNA ENCODING THE SAME  
NUMBER OF SEQUENCES: 21  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sughrue, Mion, Zinn, Macpeak & Seas  
STREET: 2100 Pennsylvania Avenue, NW Suite 800  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/318,947A  
FILING DATE: 06-OCT-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/133,530  
FILING DATE: 07-OCT-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Mack, Susan J.  
REGISTRATION NUMBER: 30,951  
REFERENCE/DOCKET NUMBER: A6462  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)293-7060  
TELEFAX: (202)293-2920  
TELEX: 6491103  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 274 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-318-947A-20

Query Match 92.3%; Score 24; DB 1; Length 274;  
Best Local Similarity 83.3%; Pred. No. 1,66+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASAL 6  
DB 91 MDASAL 96

RESULT 8  
US-08-795-303-20  
; Sequence 20, Application US/08795303  
; Patent No. 5948656  
; GENERAL INFORMATION:  
; APPLICANT: Anderson, Paul J.  
; APPLICANT: Tian, Qingsheng  
; TITLE OF INVENTION: TIA-1 BINDING PROTEINS AND ISOLATED  
; TITLE OF INVENTION: COMPLEMENTARY DNA ENCODING THE SAME  
; NUMBER OF SEQUENCES: 21  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sughrue, Mion, Zinn, Macpeak & Seas  
; STREET: 2100 Pennsylvania Avenue, NW Suite 800  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20037  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentln Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/795,303  
; FILING DATE: 04-FEB-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/318,947  
; FILING DATE: 06-OCT-1994  
; APPLICATION NUMBER: 08/133,530  
; FILING DATE: 07-OCT-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mack, Susan J.  
; REGISTRATION NUMBER: 30,951  
; REFERENCE/DOCKET NUMBER: A6462  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)293-7060  
; TELEFAX: (202)293-2920  
; TELEX: 6491103  
; INFORMATION FOR SEQ ID NO: 20:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 274 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-795-303-20  
Query Match 92.3%; Score 24; DB 2; Length 274;  
Best Local Similarity 83.3%; Pred. No. 1.6e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDASAL 6  
:|||||  
DB 91 MDASAL 96

RESULT 9  
US-08-874-347-25  
; Sequence 25, Application US/08874347  
; Patent No. 5863741  
; GENERAL INFORMATION:  
; APPLICANT: Limper, Andrew H.  
; APPLICANT: Isof, Edward B.  
; APPLICANT: Thomas, Charles F.  
; APPLICANT: Gustafson, Michael P.  
; TITLE OF INVENTION: CDC2 PROTEIN KINASE FROM PNEUMOCYSTIS  
; TITLE OF INVENTION: CARINI1  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson P.C., P.A.  
; STREET: 60 South Sixth Street, Suite 3300

CITY: Minneapolis  
STATE: MN  
COUNTRY: USA  
ZIP: 55402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/874,347  
; FILING DATE: 13-JUN-1997  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ellinger, Mark S.  
; REGISTRATION NUMBER: 34,812  
; REFERENCE/DOCKET NUMBER: 07039/055001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 612-335-5070  
; TELEFAX: 612-288-9696  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 25:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 298 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-874-347-25  
Query Match 92.3%; Score 24; DB 2; Length 298;  
Best Local Similarity 83.3%; Pred. No. 1.8e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDASAL 6  
:|||||  
DB 91 MDASAL 96

RESULT 10  
US-08-969-106-2  
; Sequence 2, Application US/08969106  
; Patent No. 5986055  
; GENERAL INFORMATION:  
; APPLICANT: Yang, M.  
; APPLICANT: Mandabalan, K.  
; APPLICANT: Schulz, V.  
; TITLE OF INVENTION: CDK2 INTERACTIONS  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds LLP  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/969,106  
; FILING DATE: 13-NOV-1997  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mistrock, S. Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 7934-057  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-790-9090  
; TELEFAX: 212-869-9741  
; TELEX: 66141 PENNIE

;; INFORMATION FOR SEQ ID NO: 2;  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 298 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS:  
;; TOPOLOGY: unknown  
;; MOLECULE TYPE: protein  
US-08-969-106-2

Query Match 92.3%; Score 24; DB 2; Length 298;  
Best Local Similarity 83.3%; Pred. No. 1.8e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDASAL 6  
:|||||  
Db 91 MDASAL 96

RESULT 11  
US-09-093-522-25  
; Sequence 25, Application US/09093522  
; Patent No. 6015700  
; GENERAL INFORMATION:

;; APPLICANT: Limper, Andrew H.  
;; APPLICANT: Lee, Edward B.  
;; APPLICANT: Thomas, Charles F.  
;; APPLICANT: Gustafson, Michael P.  
;; TITLE OF INVENTION: CDC2 PROTEIN KINASE FROM PNEUMOCYSTIS  
;; TITLE OF INVENTION: CARINI  
;; NUMBER OF SEQUENCES: 26  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Fish & Richardson P.C., P.A.  
;; STREET: 60 South Sixth Street, Suite 3300  
;; CITY: Minneapolis  
;; STATE: MN  
;; COUNTRY: USA  
;; ZIP: 55402

;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Diskette  
;; COMPUTER: IBM Compatible  
;; OPERATING SYSTEM: DOS  
;; SOFTWARE: FastSeq for Windows Version 2.0  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/09/093,522  
;; FILING DATE: 08-JUN-1998  
;; CLASSIFICATION:  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 08/874,347  
;; FILING DATE: 13-JUN-1997

;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Ellinger, Mark S.  
;; REGISTRATION NUMBER: 34,812  
;; REFERENCE/DOCKET NUMBER: 07039/055002  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 612-335-5070  
;; TELEFAX: 612-288-9696  
;; TELEX:  
;; INFORMATION FOR SEQ ID NO: 25:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 298 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
US-09-093-522-25

Query Match 92.3%; Score 24; DB 3; Length 298;  
Best Local Similarity 83.3%; Pred. No. 1.8e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDASAL 6  
:|||||  
Db 91 MDASAL 96

RESULT 12  
US-09-457-040B-29  
; Sequence 29, Application US/09457040B  
; Patent No. 6387641  
; GENERAL INFORMATION:

;; APPLICANT: Vertex Pharmaceuticals Incorporated  
;; APPLICANT: Bellon, Steve  
;; TITLE OF INVENTION: Crystallized p38 Complexes  
;; FILE REFERENCE: VPI/98-14  
;; CURRENT APPLICATION NUMBER: US/09/457,040B  
;; CURRENT FILING DATE: 1999-12-08  
;; NUMBER OF SEQ ID NOS: 41  
;; SOFTWARE: PatentIn version 3.0  
;; SEQ ID NO 29  
;; LENGTH: 298  
;; TYPE: PRT  
;; ORGANISM: Human

US-09-457-040B-29

Query Match 92.3%; Score 24; DB 4; Length 298;  
Best Local Similarity 83.3%; Pred. No. 1.8e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDASAL 6  
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Db 91 MDASAL 96

RESULT 13  
US-09-411-628-13  
; Sequence 13, Application US/09411628  
; Patent No. 6428994  
; GENERAL INFORMATION:

;; APPLICANT: University of Southern California  
;; TITLE OF INVENTION: CDNA, GENOMIC, AND PREDICTED PROTEIN  
;; FILE REFERENCE: 13761-707  
;; CURRENT APPLICATION NUMBER: US/09/411,628  
;; CURRENT FILING DATE: 1999-10-01  
;; EARLIER APPLICATION NUMBER: US 60/102,906  
;; EARLIER FILING DATE: 1998-10-02  
;; NUMBER OF SEQ ID NOS: 16  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 13  
;; LENGTH: 298  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
;; FEATURE:  
;; NAME/KEY: VARIANT  
;; LOCATION: (1)...(298)  
;; OTHER INFORMATION: Xaa = Any Amino Acid  
US-09-411-628-13

Query Match 92.3%; Score 24; DB 4; Length 298;  
Best Local Similarity 83.3%; Pred. No. 1.8e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDASAL 6  
:|||||  
Db 91 MDASAL 96

RESULT 14  
US-09-098-219B-2  
; Sequence 2, Application US/09098219B  
; Patent No. 6441277  
; GENERAL INFORMATION:

;; APPLICANT: Barry, Gerard  
;; APPLICANT: Cheikh, No. 6441277dline  
;; APPLICANT: Kishore, Ganesh  
;; TITLE OF INVENTION: Expression of Fructose 1,6 Biphosphate

TITLE OF INVENTION: Aldolase in Transgenic Plants  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold White & Durkee  
STREET: P.O. Box 4433  
CITY: Houston  
STATE: TX  
COUNTRY: US  
ZIP: 77210-4433  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/098,219B  
FILING DATE:  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/049,995  
FILING DATE: 17-JUN-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Kammerer, Patricia A.  
REGISTRATION NUMBER: 29,775  
REFERENCE/DOCKET NUMBER: MOBT:086  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 713-787-1400  
TELEFAX: 713-787-1440  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 359 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
US-09-098-219B-2

Query Match 92.3%; Score 24; DB 4; Length 359;  
Best Local Similarity 83.3%; Pred. No. 2.2e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASAL 6  
Db 191 MDASAL 196

RESULT 15  
US-08-370-193A-9  
Sequence 9, Application US/08370193A  
Patent No. 5573945  
GENERAL INFORMATION:  
APPLICANT: ONO, EIJI  
APPLICANT: TSUJIMOTO, NOBUHARU  
APPLICANT: MATSUI, KAZUHIKO  
APPLICANT: KURAHASHI, KAZUHIKO  
TITLE OF INVENTION: MUTANT AND METHOD FOR PRODUCING  
TITLE OF INVENTION: L-GLUTAMIC ACID BY FERMENTATION  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,  
P.C.  
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400  
CITY: ARLINGTON  
STATE: VA  
COUNTRY: USA  
ZIP: 22202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/370,193A  
FILING DATE: 09-JAN-1995

CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: OBLON, NORMAN F.  
REGISTRATION NUMBER: 24,618  
REFERENCE/DOCKET NUMBER: 10-714-0  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-413-3000  
TELEFAX: 703-413-2220  
TELEX: 248855 OPAT UR  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 405 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-370-193A-9

Query Match 92.3%; Score 24; DB 1; Length 405;  
Best Local Similarity 83.3%; Pred. No. 2.6e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASAL 6  
Db 127 LDASAL 132

Search completed: May 30, 2003, 14:41:23  
Job time: 7.03947 secs



XX 02-MAY-2001; 2001MO-US40654.  
 PF XX  
 XX 02-MAY-2000; 2000US-201261P.  
 PR 22-AUG-2000; 2000US-0643260.  
 XX  
 XX (UYVA ) UNIV YALE.  
 PI May MJ, Ghosh S;  
 DR WPI: 2002-179350/23.  
 XX  
 PT Modulating NF-kappaB induction in a cell, useful for treating e.g.  
 PT inflammatory disorders, osteoporosis and cancer, comprises contacting a  
 PT cell with an anti-inflammatory compound comprising at least one NEMO  
 PT binding domain -  
 PS Claim 23; Page 44; 82pp; English.  
 XX  
 CC The invention relates to modulating NF-kappaB (NF-kB) induction in a cell  
 CC comprising contacting a cell with an anti-inflammatory compound  
 CC (AB08725-AB08742) comprising at least one NEMO binding domain  
 CC (AB077313). The compound has acts through selective inhibition of  
 CC cytokine-mediated NF-kB activation by blocking the interaction of NEMO  
 CC with Ikkbeta at the NEMO binding domain. Blockage of Ikkbeta-NEMO  
 CC interaction results in inhibition of Ikkbeta kinase activation and  
 CC subsequent decreased phosphorylation of Ikkappa. The compound may also  
 CC act (directly or indirectly) by blocking the recruitment of leukocytes  
 CC into sites of acute and chronic inflammation, by down-regulating the  
 CC expression of E-selectin on leukocytes or by blocking osteoclast  
 CC differentiation. The compound is useful in treating NF-kB mediated  
 CC conditions, where the condition is an inflammatory disorder, an  
 CC autoimmune disease, transplant rejection, osteoporosis, cancer,  
 CC Alzheimer's disease, atherosclerosis, a viral infection or ataxia  
 CC telangiectasia. The inflammatory disorder is asthma, allergies,  
 CC urticaria, anaphylaxis, cutaneous inflammation, sepsis, psoriasis,  
 CC rheumatoid arthritis, osteoarthritis, psoriatic arthritis, inflammatory  
 CC bowel disease, chronic obstructive pulmonary disease, vasculitis and  
 CC buritis. The inflammatory disorder may also be dermatitis, eczema,  
 CC psoriasis, osteoarthritis, psoriatic arthritis, lupus and  
 CC sporadic arthritis. Also for Crohn's disease, ulcerative colitis,  
 CC polymyalgia, scleroderma, Wegner's granulomatosis, temporal arteritis,  
 CC cryoglobulinemia and multiple sclerosis. For chronic viral infections  
 CC caused by Epstein-Barr, cytomegalovirus or herpes simplex. Other viral  
 CC diseases include HIV and influenza. The compound may also be useful for  
 CC treating anaphylaxis, drug and food sensitivity, contact dermatitis,  
 CC sunburn or aging. The compound may be used to replace corticosteroids in  
 CC any application in which corticosteroids are used, including  
 CC immunosuppression in transplants and cancer therapy. Also for identifying  
 CC anti-inflammatory compounds and for diagnosis of an inflammatory disorder.  
 CC The compound may be administered alone or in combination with other known  
 CC anti-inflammatory agents. The present sequence is that of a mutated NEMO  
 CC binding domain of Ikkbeta.  
 XX  
 SQ Sequence 6 AA;  
 OY  
 DB 1 LDASAL 6  
 1 LDASAL 6  
 |||||  
 Query Match 100.0%; Score 26; DB 23; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DE NBD mutant peptide SEQ ID NO 3.  
 XX  
 XX Antiinflammatory; antiasthmatic; cytosolic; antipsoriatic; nootropic;  
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virocidic;  
 KW immunosuppressive; dermatologic; neuroprotective; antiatherosclerotic;  
 KW anti-allergic; membrane translocation domain; NEMO binding domain; eczema;  
 KW cytokine; NFkappaB; Ikkappa kinase beta; Ikkbeta; cancer; psoriasis;  
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
 KW autoimmune disorder; multiple sclerosis; transplant rejection;  
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200183554-A2.  
 XX  
 PD 08-NOV-2001.  
 XX  
 PF 02-MAY-2001; 2001MO-US14346.  
 XX  
 XX 02-MAY-2000; 2000US-201261P.  
 PR 22-AUG-2000; 2000US-0643260.  
 XX  
 PA (PRAE-) PRAECS PHARM INC.  
 PA (UYVA ) UNIV YALE.  
 PI May MJ, Ghosh S, Flindeis MA, Phillips K;  
 DR WPI: 2002-121889/16.  
 XX  
 PT Novel antiinflammatory compound comprising membrane translocation  
 PT domain fused to NEMO binding sequence, useful for blocking nuclear  
 PT factor kappaB activation, and for treating asthma, lung inflammation,  
 PT psoriasis -  
 PS Example 6; Page 47; 88pp; English.  
 XX  
 CC The invention relates to an antiinflammatory compound (especially  
 CC AAM48628-AAM48645), comprising a membrane translocation domain  
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15  
 CC amino acid residues, fused to a NEMO binding sequence  
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,  
 CC cytosolic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,  
 CC antibacterial, immunosuppressive, dermatologic, neuroprotective,  
 CC nootropic, antiatherosclerotic, virocidic and anti-allergic activity. The  
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB  
 CC activation by blocking interaction of Ikkappa kinase beta (Ikkbeta) at  
 CC the NEMO binding domain that results in inhibition of Ikkbeta kinase  
 CC activation and subsequent decreased phosphorylation of Ikkappa. The  
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,  
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,  
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,  
 CC buritis; autoimmune diseases such as lupus, polymyalgia, scleroderma,  
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;  
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia  
 CC telangiectasia. The compounds are also useful for treating  
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,  
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and  
 CC arthritis.  
 XX  
 SQ Sequence 6 AA;  
 OY  
 DB 1 LDASAL 6  
 1 LDASAL 6  
 |||||  
 Query Match 100.0%; Score 26; DB 23; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 3  
 ABB08741

ID ABB08741 standard; peptide: 28 AA.  
 XX ABB08741;  
 AC  
 XX  
 XX 14-JUN-2002 (first entry)  
 DE  
 XX Mutated IKKbeta NEMO binding domain peptide SEQ ID NO 19.  
 XX  
 XX IKKbeat; IKKalpha; NEMO; NEMO binding domain; NBD; NF-kappaB; NF-kB;  
 KW kinase activation; leukocyte; inflammation; E-selectin; osteoclast;  
 KW autoimmune disease; transplant rejection; osteoporosis; cancer;  
 KW Alzheimer's disease; viral; infection; asthma; anaphylaxis; psoriasis;  
 KW rheumatoid arthritis; Crohn's disease; multiple sclerosis; HIV;  
 KW corticosteroid; immunosuppression; anti-inflammatory; immunosuppressive;  
 KW osteopathic; cytoskeletal; neoplastic; neuroprotective; anti-HIV; human;  
 KW antiarteriosclerotic; virucide; antistatic; antiallergic;  
 KW dematological; antibacterial; antiparasitic; antirheumatic;  
 KW antiarthritic; osteopathic; antitumor; mutant; mutein.  
 XX  
 XX Homo sapiens.  
 OS Synthetic.  
 XX  
 XX Key  
 FH Misc-difference 22 Location/Qualifiers  
 FT Misc-difference 24 /note= "Wildtype Trp substituted by Ala"  
 FT Misc-difference 24 /note= "Wildtype Trp substituted by Ala"  
 XX  
 XX W0200183547-A2.  
 PN  
 XX  
 XX 08-NOV-2001.  
 PD  
 XX  
 XX 02-MAY-2001; 2001WO-US40654.  
 PE  
 XX  
 XX 02-MAY-2000; 2000US-201261P.  
 PR 22-AUG-2000; 2000US-0643260.  
 PA  
 XX (UYTA ) UNIV YALE.  
 PA  
 XX May MJ, Ghosh S;  
 PI  
 XX WPI: 2002-179350/23.  
 DR  
 XX  
 XX Modulating NF-kappaB induction in a cell, useful for treating e.g.  
 PT inflammatory disorders, osteoporosis and cancer, comprises contacting a  
 PT cell with an anti-inflammatory compound comprising at least one NEMO  
 PT binding domain  
 XX  
 XX Claim 23; Fig 5; 82pp; English.  
 PS  
 XX The invention relates to modulating NF-kappaB (NF-kB) induction in a cell  
 CC comprises contacting a cell with an anti-inflammatory compound  
 CC (ABB08725-ABB08742) comprising at least one NEMO binding domain  
 CC (BB7313). The compound has acts through selective inhibition of  
 CC cytokine-mediated NF-kB activation by blocking the interaction of NEMO  
 CC with IKKbeta at the NEMO binding domain. Blockage of IKKbeta-NEMO  
 CC interaction results in inhibition of IKKbeta kinase activation and  
 CC subsequent decreased phosphorylation of Ikbppab. The compound may also  
 CC act (directly or indirectly) by blocking the recruitment of leukocytes  
 CC into sites of acute and chronic inflammation, by down-regulating the  
 CC expression of E-selectin on leukocytes or by blocking osteoclast  
 CC differentiation. The compound is useful in treating NF-kB mediated  
 CC conditions, where the condition is an inflammatory disorder, an  
 CC autoimmune disease, transplant rejection, osteoporosis, cancer,  
 CC Alzheimer's disease, atherosclerosis, a viral infection or ataxia  
 CC telangiectasia. The inflammatory disorder is asthma, allergies,  
 CC urticaria, anaphylaxis, cutaneous inflammation, sepsis, psoriasis,  
 CC rheumatoid arthritis, osteoarthritis, psoriatic arthritis, inflammatory  
 CC bowel disease, chronic obstructive pulmonary disease, vasculitis and  
 CC bursitis. The inflammatory disorder may also be dermatitis, eczema,  
 CC psoriasis, osteoarthritis, psoriatic arthritis, lupus and  
 CC spondylarthritis. Also for Crohn's disease, ulcerative colitis,  
 CC polymyalgia, scleroderma, Wegner's granulomatosis, temporal arteritis,

CC cryoglobulinaemia or multiple sclerosis. For chronic viral infections  
 CC caused by Epstein-barr, cytomegalovirus or herpes simplex. Other viral  
 CC diseases include HIV and influenza. The compound may also be useful for  
 CC treating anaphylaxis, drug and food sensitivity, contact dermatitis,  
 CC sunburn or aging. The compound may be used to replace corticosteroids in  
 CC any application in which corticosteroids are used, including  
 CC immunosuppression in transplants and cancer therapy. Also for identifying  
 CC anti-inflammatory compounds and for diagnosis of an inflammatory disorder.  
 CC The compound may be administered alone or in combination with other known  
 CC anti-inflammatory agents. The present sequence is that of a mutated NEMO  
 CC binding domain of IKKbeta.  
 XX  
 XX Sequence 28 AA:  
 SQ  
 Query Match 100.0%; Score 26; DB 23; Length 28;  
 Best Local Similarity 100.0%; Pred. No. 16;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 IDASAL 6  
 DB 20 IDASAL 25  
 RESULT 4  
 AAM48524  
 ID AAM48524 standard; Peptide: 28 AA.  
 AC  
 XX AAM48524;  
 XX  
 XX 20-MAR-2002 (first entry)  
 DT  
 XX  
 XX NBD peptide SEQ ID NO 19.  
 DE  
 XX  
 XX Anti-inflammatory; antisthmatic; cytoskeletal; antiparasitic; neoplastic;  
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;  
 KW immunosuppressive; dermatological; neuroprotective; antithrombotic;  
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;  
 KW cytokine; NF-kappaB; Ikbppab kinase beta; IKKbeta; cancer; psoriasis;  
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
 KW autoimmune disorder; multiple sclerosis; transplant rejection;  
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.  
 XX  
 XX Synthetic.  
 OS  
 XX  
 XX W0200183554-A2.  
 PN  
 XX  
 XX 08-NOV-2001.  
 PD  
 XX  
 XX 02-MAY-2001; 2001WO-US14346.  
 PE  
 XX  
 XX 02-MAY-2000; 2000US-201261P.  
 PR 22-AUG-2000; 2000US-0643260.  
 PA  
 XX (PRAE ) PRAECIS PHARM INC.  
 PA  
 XX (UYTA ) UNIV YALE.  
 PI  
 XX May MJ, Ghosh S, Findels MA, Phillips K;  
 DR WPI: 2002-121889/16.  
 XX  
 XX Novel anti-inflammatory compound comprising membrane translocation  
 PT domain fused to NEMO binding sequence, useful for blocking nuclear  
 PT factor kappaB activation, and for treating asthma, lung inflammation,  
 PT psoriasis  
 XX  
 XX Example 5; Fig 5; 88pp; English.  
 PS  
 XX The invention relates to an anti-inflammatory compound (especially  
 CC AAM48628-AAM48645), comprising a membrane translocation domain  
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15  
 CC amino acid residues, fused to a NEMO binding sequence  
 CC (AAM48525-AAM48619). The anti-inflammatory compounds have antisthmatic,

Query Match	Best Local Similarity	100.0%;	Score 26;	DB 23;	Length 28;
Matches	6;	Conservative	0;	Mismatches	0;
				Indels	0;
				Gaps	0;
QY	1 LDASAL 6				
DB	20 LDASAL 25				
RESULT 5	AAV04950				
ID	AAV04950 standard; Protein; 84 AA.				
XX	AAV04950;				
AC					
XX					
DT	06-JUL-1999 ((first entry)				
XX					
DE	Mycobacterium species protein sequence 41D.				
XX					
XX	Secreted protein; Mycobacterium; primer; PCR; amplification; probe;				
KM	hybridisation; detection; vaccine; immunisation; infection.				
XX					
OS	Mycobacterium sp.				
XX					
PN	W09909186-A2.				
FD					
XX	25-FEB-1999.				
XX					
PF	14-AUG-1998; 98WO-FR01813.				
XX					
PR	11-SEP-1997; 97FR-0011325.				
PR	14-AUG-1997; 97FR-0010404.				
XX					
PA	(INSP ) INST PASTEUR.				
PI					
XX					
PI	Glequel B, Lim EM, Pellicio V, Portnoi D, Coguet de la Salmoniere Y,				
XX	Guigneno A;				
DR	WPI: 1999-181045/15.				
XX	N-PSDB; AAX34203.				
PT					
PT	Mycobacterial DNA vectors containing reporter constructs - for				
PT	identifying coding or promoter sequences involved in				
XX	infection-associated protein expression				
XX					
PS	Claim 32; Fig 41D; 309pp; French.				
XX					
CC	Sequences AAV04742-V05000 and AAV07201-V07204 represent secreted				
CC	proteins from various Mycobacterium species microorganisms. The				
CC	encoding nucleotide sequences can be used as primers and probes for				
CC	methods for detecting and identifying mycobacteria, especially belonging				
CC	to the M. tuberculosis complex. The encoded proteins can be used in				
CC	vaccines for immunisation against a bacterial or viral infection.				

[illegible]

XX 06-JUL-1999 (first entry)  
XX Mycobacterium species protein sequence 41F.  
DE Mycobacterium species protein sequence 41F.  
XX Secreted protein; Mycobacterium; primer; PCR; amplification; probe;  
KW hybridisation; detection; vaccine; immunisation; infection.  
XX Mycobacterium sp.  
OS MO9909186-A2.  
XX 25-FEB-1999.  
XX 14-AUG-1998; 98WO-FR01813.  
XX 11-SEP-1997; 97FR-0011325.  
PR 14-AUG-1997; 97FR-0010404.  
XX (INSP ) INST PASTEUR.  
PA Gicquel B, Lim EM, Pelicic V, Portnoi D, Coquet de la Salmoniere Y;  
PI Guigneno A;  
XX WPI, 1999-181045/15.  
DR N-PSDB; AAX34204.  
XX Mycobacterial DNA vectors containing reporter constructs - for  
PT identifying coding or promoter sequences involved in  
PT infection-associated protein expression  
XX Claim 32; Fig 41F; 309pp; French.  
XX Sequences AAY04742-Y05000 and AAY07201-Y07204 represent secreted  
CC proteins from various Mycobacterium species microorganisms. The  
CC encoding nucleotide sequences can be used as primers and probes for  
CC methods for detecting and identifying mycobacteria, especially belonging  
CC to the M. tuberculosis complex. The encoded proteins can be used in  
CC vaccines for immunisation against a bacterial or viral infection.  
XX Sequence 102 AA;  
SQ

Query Match 100.0%; Score 26; DB 20; Length 102;  
Best Local Similarity 100.0%; Pred. NO. 68;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDASAL 6  
Db 26 LDASAL 31

RESULT 8  
AAG3536  
ID AAG3536 standard; Protein; 102 AA.  
XX  
AC AAG3536;  
XX  
DT 18-OCT-2000 (first entry)  
XX  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 43425.  
XX  
KW Protein identification; signal transduction pathway; metabolic pathway;  
KW hybridisation assay; genetic mapping; gene expression control; promoter;  
KW termination sequence.  
XX  
OS Arabidopsis thaliana.  
XX  
PN EPI033405-A2.  
XX  
PD 06-SEP-2000.  
XX  
PF 25-FEB-2000; 2000EP-0301439.  
XX

PR 25-FEB-1999; 99US-0121825.  
PR 05-MAR-1999; 99US-0123180.  
PR 09-MAR-1999; 99US-0123548.  
PR 23-MAR-1999; 99US-0125788.  
PR 25-MAR-1999; 99US-0126264.  
PR 29-MAR-1999; 99US-0126785.  
PR 01-APR-1999; 99US-0127462.  
PR 06-APR-1999; 99US-0128234.  
PR 08-APR-1999; 99US-0128714.  
PR 16-APR-1999; 99US-0129845.  
PR 19-APR-1999; 99US-0130077.  
PR 21-APR-1999; 99US-0130449.  
PR 23-APR-1999; 99US-0130510.  
PR 28-APR-1999; 99US-0130891.  
PR 30-APR-1999; 99US-0131449.  
PR 30-APR-1999; 99US-0132407.  
PR 04-MAY-1999; 99US-0132484.  
PR 05-MAY-1999; 99US-0132485.  
PR 06-MAY-1999; 99US-0132486.  
PR 07-MAY-1999; 99US-0132487.  
PR 11-MAY-1999; 99US-0134256.  
PR 14-MAY-1999; 99US-0134218.  
PR 14-MAY-1999; 99US-0134219.  
PR 14-MAY-1999; 99US-0134221.  
PR 14-MAY-1999; 99US-0134370.  
PR 18-MAY-1999; 99US-0134768.  
PR 19-MAY-1999; 99US-0134941.  
PR 20-MAY-1999; 99US-0135124.  
PR 21-MAY-1999; 99US-0135353.  
PR 24-MAY-1999; 99US-0135629.  
PR 25-MAY-1999; 99US-0136021.  
PR 27-MAY-1999; 99US-0136392.  
PR 28-MAY-1999; 99US-0136782.  
PR 01-JUN-1999; 99US-0137222.  
PR 03-JUN-1999; 99US-0137528.  
PR 04-JUN-1999; 99US-0137502.  
PR 07-JUN-1999; 99US-0137724.  
PR 08-JUN-1999; 99US-0138094.  
PR 10-JUN-1999; 99US-0138540.  
PR 10-JUN-1999; 99US-0138847.  
PR 14-JUN-1999; 99US-0138119.  
PR 16-JUN-1999; 99US-0139452.  
PR 16-JUN-1999; 99US-0139453.  
PR 17-JUN-1999; 99US-0139492.  
PR 18-JUN-1999; 99US-0139454.  
PR 18-JUN-1999; 99US-0139455.  
PR 18-JUN-1999; 99US-0139456.  
PR 18-JUN-1999; 99US-0139457.  
PR 18-JUN-1999; 99US-0139458.  
PR 18-JUN-1999; 99US-0139459.  
PR 18-JUN-1999; 99US-0139460.  
PR 18-JUN-1999; 99US-0139461.  
PR 18-JUN-1999; 99US-0139462.  
PR 18-JUN-1999; 99US-0139463.  
PR 18-JUN-1999; 99US-0139750.  
PR 18-JUN-1999; 99US-0139763.  
PR 21-JUN-1999; 99US-0139817.  
PR 22-JUN-1999; 99US-0139899.  
PR 23-JUN-1999; 99US-0140353.  
PR 23-JUN-1999; 99US-0140354.  
PR 24-JUN-1999; 99US-0140695.  
PR 28-JUN-1999; 99US-0140823.  
PR 29-JUN-1999; 99US-0140991.  
PR 30-JUN-1999; 99US-0141287.  
PR 01-JUL-1999; 99US-0141842.  
PR 01-JUL-1999; 99US-0142154.  
PR 02-JUL-1999; 99US-0142055.  
PR 06-JUL-1999; 99US-0142390.  
PR 08-JUL-1999; 99US-0142803.  
PR 09-JUL-1999; 99US-0142920.  
PR 12-JUL-1999; 99US-0142977.

PR 13-JUL-1999; 99US-0143542.  
 PR 14-JUL-1999; 99US-0143624.  
 PR 15-JUL-1999; 99US-0144005.  
 PR 16-JUL-1999; 99US-0144085.  
 PR 16-JUL-1999; 99US-0144086.  
 PR 19-JUL-1999; 99US-0144325.  
 PR 19-JUL-1999; 99US-0144331.  
 PR 19-JUL-1999; 99US-0144332.  
 PR 19-JUL-1999; 99US-0144333.  
 PR 19-JUL-1999; 99US-0144334.  
 PR 19-JUL-1999; 99US-0144335.  
 PR 20-JUL-1999; 99US-0144352.  
 PR 20-JUL-1999; 99US-0144632.  
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AA001907;

06-NOV-2001 (first entry)

Human polypeptide SEQ ID NO 15799.

Human; cytokine; cell proliferation; gene therapy;

vaccine; peptide therapy; stem cell growth factor; haematopoiesis;

tissue growth factor; immunomodulatory; cancer; leukaemia;

nervous system disorders; arthritis; inflammation.

OS Homo sapiens.

PN WO200164835-A2.

PD 07-SEP-2001.

PF 26-FEB-2001; 2001WO-US04927.

PR 28-FEB-2000; 2000US-0515126.

PR 18-MAY-2000; 2000US-0577409.  
 XX (HYSE-) HYSQ INC.  
 PA Tang YT, Liu C, Dmanac RT;  
 PI

XX WPI: 2001-514838/56.  
DR N-PSDB; AAI81838.  
XX Isolated nucleic acids and polypeptides, useful for preventing  
PT diagnosing and treating e.g. leukaemia, inflammation and immune  
PT disorders -  
XX  
XX Claim 20; SEQ ID NO 15799; 1399pp + Sequence listing; English.  
PS  
CC The invention relates to human polynucleotides (AAI79941-AAI93841) and  
CC the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to  
CC cytokine, cell proliferation or cell differentiation or which may induce  
CC production of other cytokines in other cell populations. The  
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or  
CC peptide therapy. The polypeptides have various cytokine-like activities,  
CC e.g. stem cell growth factor activity, haematopoiesis regulating  
CC activity, tissue growth factor activity, immunomodulatory activity and  
CC activin/inhibin activity and may be useful in the diagnosis and/or  
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and  
CC inflammation.  
CC Note: The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences.  
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KW hybridisation assay; genetic mapping; gene expression control; promoter;
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#### RESULT 12

ID AAG90584 standard; Protein; 240 AA.

AC AAG90584;

DT 26-SEP-2001 (first entry)

DE C glutamicum protein fragment SEQ ID NO: 4338.

KW Coryneform bacterium; amino acid synthesis; vitamin; saccharide;  
KW organic acid synthesis.

OS Corynebacterium glutamicum.

PN EPI108790-A2.

PD 20-JUN-2001.

PF 18-DEC-2000; 2000EP-0127688.

PR 16-DEC-1999; 99JP-0377484.

PR 07-APR-2000; 2000JP-0159162.

PR 03-AUG-2000; 2000JP-0280988.

PA (KYOW) KYOWA HAKKO KOGYO KK.

PI Nakagawa S, Mizoguchi H, Ando S, Hayashi M, Ochiai K, Yokoi H;  
PI Tateishi N, Senoh A, Ikeda M, Ozaki A.

DR WPI: 2001-376931/40.

DR N-PSDB; AAH65803.

PT Novel polynucleotides derived from Coryneform bacteria, for identifying  
PT mutation point of a gene, measuring expression of a gene, analysing  
PT expression profile or pattern of a gene and identifying homologous gene

PI Claim 17; SEQ ID NO: 4338; 246bp + Sequence Listing; English.

CC The present invention provides a number of nucleotide and protein  
CC sequences from the Coryneform bacterium Corynebacterium glutamicum. These  
CC are useful for identifying the mutation point of a gene derived from a  
CC mutant of coryneform bacterium, measuring expression amount and  
CC analysing the expression profile or expression pattern of a gene derived  
CC from coryneform bacterium, and identifying a homologue of a gene derived  
CC from coryneform bacterium. Coryneform bacteria are useful for producing  
CC amino acids, nucleic acids, vitamins, saccharides and organic acids,  
CC particularly L-lysine. The present sequence is a protein described  
CC in the exemplification of the invention.  
CC Note: The sequence data for this patent did not form part of the printed

CC specification, but was obtained in electronic format directly from the  
CC European Patent Office.  
CC  
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DB 70 LDASAL 75

#### RESULT 13

ID AAG51025 standard; Protein; 271 AA.

AC AAG51025;

DT 18-OCT-2000 (first entry)

DE Arabidopsis thaliana protein fragment SEQ ID NO: 64719.

KW Protein identification; signal transduction pathway; metabolic pathway;  
KW hybridisation assay; genetic mapping; gene expression control; promoter;  
KW termination sequence.

OS Arabidopsis thaliana.

PN EPI1033405-A2.

PD 06-SEP-2000.

PF 25-FEB-2000; 2000EP-0301439.

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PR 05-MAR-1999; 99US-0123180.

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   pharmaceutical.
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OS Drosophila melanogaster.
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PN W0200171042-A2.
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PA (PEKE ) PE CORP NY.
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PI Venter JC, Adams M, Li PWD, Myers EW;
DR WPI; 2001-656860/75.
DR N-PSDB; ABL14957.
XX
XX New isolated nucleic acid detection reagent for detecting 1000 or more
   genes from Drosophila and for elucidating cell signalling and cell-cell
   interactions -
PS Disclosure; SEQ ID NO 39354; 21pp + Sequence Listing; English.
XX
XX The invention relates to an isolated nucleic acid detection reagent
   capable of detecting 1000 or more genes from Drosophila. The invention is
   useful in developmental biology and in elucidating cell signalling and
   cell-cell interactions in higher eukaryotes for the development of
   insecticides, therapeutics and pharmaceutical drugs. The invention
   discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
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XX The sequence data for this patent did not form part of the printed
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GenCore version 5.1.6  
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5	30	90.9	261	10	US-09-765-205-14
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8	30	90.9	935	9	US-10-077-751-1
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25	28	84.8	353	9	US-10-092-256-33	Sequence 33, App1
26	28	84.8	356	9	US-09-738-626-6651	Sequence 6651, Ap
27	28	84.8	380	10	US-09-764-864-1195	Sequence 1195, Ap
28	28	84.8	504	9	US-10-114-893-67	Sequence 67, App1
29	28	84.8	529	10	US-09-815-242-10473	Sequence 10473, A
30	27	81.8	6	9	US-09-847-940B-11	Sequence 11, App1
31	27	81.8	6	9	US-09-847-940B-12	Sequence 12, App1
32	27	81.8	6	9	US-09-847-946A-11	Sequence 11, App1
33	27	81.8	6	9	US-09-847-946A-12	Sequence 12, App1
34	27	81.8	6	9	US-09-847-946A-12	Sequence 12, App1
35	27	81.8	6	9	US-09-847-946A-12	Sequence 12, App1
36	27	81.8	6	9	US-09-847-946A-12	Sequence 12, App1
37	27	81.8	7	9	US-09-847-946A-88	Sequence 88, App1
38	27	81.8	7	9	US-09-847-946A-99	Sequence 99, App1
39	27	81.8	8	9	US-09-847-946A-81	Sequence 81, App1
40	27	81.8	8	9	US-09-847-946A-89	Sequence 89, App1
41	27	81.8	8	9	US-09-847-946A-92	Sequence 92, App1
42	27	81.8	8	9	US-09-847-946A-100	Sequence 100, App
43	27	81.8	9	9	US-09-847-946A-80	Sequence 80, App1
44	27	81.8	9	9	US-09-847-946A-83	Sequence 83, App1
45	27	81.8	9	9	US-09-847-946A-86	Sequence 86, App1

#### ALIGNMENTS

RESULT 1  
US-09-847-940B-10  
Sequence 10, Application US/09847940B  
Patent No. US2002015600A1  
GENERAL INFORMATION:  
APPLICANT: May, Michael J.  
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
FILE REFERENCE: PRI-117CP  
CURRENT APPLICATION NUMBER: US/09/847, 940B  
CURRENT FILING DATE: 2001-05-02  
PRIOR APPLICATION NUMBER: 09/643, 260  
PRIOR FILING DATE: 2000-08-22  
NUMBER OF SEQ ID NOS: 27  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 10  
LENGTH: 6  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: NBD mutants  
US-09-847-940B-10

Query Match: 100.0%; Score 33; DB 9; Length 6;  
Best Local Similarity 100.0%; Pred. No. 3.4e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6  
DB 1 LDASWL 6

RESULT 2  
US-09-847-946A-10  
Sequence 10, Application US/09847946A  
Publication No. US20030054999A1  
GENERAL INFORMATION:  
APPLICANT: May, Michael J  
APPLICANT: Ghosh, Sankar  
APPLICANT: Pindels, Mark A  
APPLICANT: Phillips, Kathryn  
APPLICANT: Hannig, Gerhard

```

; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PFI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: NBD peptide
US-09-847-946A-10

Query Match
Best Local Similarity 100.0%; Score 33; DB 9; Length 6;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDASWL 6
DB 1 LDASWL 6

RESULT 3
US-09-738-626-6278
; Sequence 6278, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHITAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAOKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 6278
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-6278

Query Match
Best Local Similarity 100.0%; Score 33; DB 9; Length 105;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDASWL 6
DB 48 LDASWL 53

RESULT 4
US-10-169-048-2
; Sequence 2, Application US/10169048
; Publication No. US20030072769A1

; GENERAL INFORMATION:
; APPLICANT: Clarke, Edna Elizabeth
; APPLICANT: Zhou, Liqing
; APPLICANT: Shea, Jacqueline Elizabeth
; APPLICANT: Feldman, Robert Graham
; APPLICANT: Holden, David William
; TITLE OF INVENTION: Streptococcus Pyogenes Virulence Genes and Proteins And Their
; FILE REFERENCE: GJE-97
; CURRENT APPLICATION NUMBER: US/10/169,048
; CURRENT FILING DATE: 2002-06-24
; PRIOR APPLICATION NUMBER: PCT/GB00/04997
; PRIOR FILING DATE: 2000-12-22
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-10-169-048-2

Query Match
Best Local Similarity 90.9%; Score 30; DB 9; Length 221;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDASWL 6
DB 36 LDASWL 41

RESULT 5
US-09-765-205-14
; Sequence 14, Application US/09765205
; Patent No. US20020034800A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Li
; TITLE OF INVENTION: BONE MARROW SECRETED PROTEINS AND POLYNUCLEOTIDES
; FILE REFERENCE: 1456.004/200130.449
; CURRENT APPLICATION NUMBER: US/09/765,205
; CURRENT FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: US/09/212,440
; PRIOR FILING DATE: 1998-12-16
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 261
; TYPE: PRT
; ORGANISM: human
US-09-765-205-14

Query Match
Best Local Similarity 90.9%; Score 30; DB 10; Length 261;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDASWL 6
DB 161 LDASWL 166

RESULT 6
US-09-738-626-6970
; Sequence 6970, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHITAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAOKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
```

```

; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: Patentln ver. 3.0
; SEQ ID NO 6970
; LENGTH: 919
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
; US-09-738-626-6970

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Query Match      90.9%; Score 30; DB 9; Length 919;
Best Local Similarity 83.3%; Pred. No. 1.2e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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OY      1 LDASWL 6
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Db      105 LDASWL 110

```

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RESULT 7
US-10-078-107-1
; Sequence 1, Application US/10078107
; Publication No. US20020182688A1
; GENERAL INFORMATION:
; APPLICANT: IZUI, HIROSHI
; APPLICANT: HARA, YOSHIHIKO
; APPLICANT: SATO, MASAKAZU
; APPLICANT: AKIYOSHI, NAOKI
; TITLE OF INVENTION: METHOD FOR PRODUCING L-GLUTAMIC ACID
; FILE REFERENCE: 219846050
; CURRENT APPLICATION NUMBER: US/10/078,107
; CURRENT FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: JP 2001-044134
; PRIOR FILING DATE: 2001-02-20
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentln version 3.1
; SEQ ID NO 1
; LENGTH: 935
; TYPE: PRT
; ORGANISM: Enterobacter agglomerans
; US-10-078-107-1

```

```

Query Match      90.9%; Score 30; DB 9; Length 935;
Best Local Similarity 83.3%; Pred. No. 1.2e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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OY      1 LDASWL 6
        ||:||||
Db      10 LDASWL 15

```

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RESULT 8
US-10-077-751-1
; Sequence 1, Application US/10077751
; Publication No. US20020192772A1
; GENERAL INFORMATION:
; APPLICANT: SATO, MASAKAZU
; APPLICANT: AKIYOSHI, NAOKI
; TITLE OF INVENTION: METHOD FOR PRODUCING L-GLUTAMIC ACID
; FILE REFERENCE: 219849050
; CURRENT APPLICATION NUMBER: US/10/077,751
; CURRENT FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: JP 2001-044135
; PRIOR FILING DATE: 2001-02-20
; NUMBER OF SEQ ID NOS: 8

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; SOFTWARE: Patentln version 3.1
; SEQ ID NO 1
; LENGTH: 935
; TYPE: PRT
; ORGANISM: Enterobacter agglomerans
; US-10-077-751-1

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```

Query Match      90.9%; Score 30; DB 9; Length 935;
Best Local Similarity 83.3%; Pred. No. 1.2e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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OY      1 LDASWL 6
        ||:||||
Db      10 LDASWL 15

```

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RESULT 9
US-09-784-208-3
; Sequence 3, Application US/09784208
; Patent No. US20010019836A1
; GENERAL INFORMATION:
; APPLICANT: IZUI, HIROSHI
; APPLICANT: ONO, Eiji
; APPLICANT: MATSUI, Kazuhiko
; APPLICANT: MORIYA, Mika
; APPLICANT: ITO, Hisao
; APPLICANT: HARA, Yoshihiko
; TITLE OF INVENTION: L-GLUTAMIC ACID-PRODUCING BACTERIUM AND METHOD FOR
; FILE REFERENCE: 0010-0989-0
; CURRENT APPLICATION NUMBER: US/09/784,208
; CURRENT FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: 09/271,438
; PRIOR FILING DATE: 1999-03-18
; PRIOR APPLICATION NUMBER: JP 10-69068
; PRIOR FILING DATE: 1998-03-18
; PRIOR APPLICATION NUMBER: JP 10-297129
; PRIOR FILING DATE: 1998-10-19
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 3
; LENGTH: 935
; TYPE: PRT
; ORGANISM: Enterobacter agglomerans
; US-09-784-208-3

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```

Query Match      90.9%; Score 30; DB 10; Length 935;
Best Local Similarity 83.3%; Pred. No. 1.2e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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OY      1 LDASWL 6
        ||:||||
Db      10 LDASWL 15

```

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RESULT 10
US-09-854-133-123
; Sequence 123, Application US/09854133
; Publication No. US20020183499A1
; GENERAL INFORMATION:
; APPLICANT: Lodes, Michael J.
; APPLICANT: Mohamath, Raodoh
; APPLICANT: Henderson, Robert A.
; APPLICANT: Benson, Darin R.
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
; FILE REFERENCE: 210121.475C10
; CURRENT APPLICATION NUMBER: US/09/854,133
; CURRENT FILING DATE: 2001-05-11
; NUMBER OF SEQ ID NOS: 735
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 123

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LENGTH: 136  
TYPE: PRT  
ORGANISM: Homo sapien  
US-09-854-133-123

Query Match  
Best Local Similarity 100.0%; Score 29; DB 9; Length 136;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDASW 5  
DB 32 LDASW 36

RESULT 11  
US-09-738-973-123  
Sequence 123, Application US/09738973  
Patent No. US20020110563A1  
GENERAL INFORMATION:  
APPLICANT: Reed, Steven G.  
APPLICANT: Henderson, Robert A.  
APPLICANT: Lodes, Michael J.  
APPLICANT: Fling, Steven P.  
APPLICANT: Mohamath, Raodoh  
APPLICANT: Algate, Paul A.  
APPLICANT: Secrist, Heather  
APPLICANT: Indirlas, Carol Joseph  
APPLICANT: Benson, Darin R.  
APPLICANT: Elliot, Mark  
APPLICANT: Mannion, Jane  
APPLICANT: Kalos, Michael D.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR  
FILE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER  
FILE REFERENCE: 210121.475C9  
CURRENT APPLICATION NUMBER: US/09/738,973  
CURRENT FILING DATE: 2000-12-14  
NUMBER OF SEQ ID NOS: 587  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 123  
LENGTH: 136  
TYPE: PRT  
ORGANISM: Homo sapien  
US-09-738-973-123

Query Match  
Best Local Similarity 100.0%; Score 29; DB 10; Length 136;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDASW 5  
DB 32 LDASW 36

RESULT 12  
US-09-981-353-90  
Sequence 90, Application US/09981353  
Patent No. US20020160382A1  
GENERAL INFORMATION:  
APPLICANT: Lasek, Amy W.  
APPLICANT: Jones, David A.  
TITLE OF INVENTION: GENES EXPRESSED IN COLON CANCER  
FILE REFERENCE: PA-0038 US  
CURRENT APPLICATION NUMBER: US/09/981,353  
CURRENT FILING DATE: 2001-10-11  
NUMBER OF SEQ ID NOS: 194  
SOFTWARE: PERL Program  
SEQ ID NO 90  
LENGTH: 297  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc.feature  
OTHER INFORMATION: Incyte ID NO. US20020160382A1 1281620C01

US-09-981-353-90

Query Match  
Best Local Similarity 100.0%; Score 29; DB 9; Length 297;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDASW 5  
DB 32 LDASW 36

RESULT 13  
US-09-815-242-12482  
Sequence 12482, Application US/09815242  
Patent No. US20020061569A1  
GENERAL INFORMATION:  
APPLICANT: Haselbeck, Robert  
APPLICANT: Ohlsen, Karl L.  
APPLICANT: Zyskind, Judith W.  
APPLICANT: Wall, Daniel  
APPLICANT: Trawick, John D.  
APPLICANT: Carr, Grant J.  
APPLICANT: Yamamoto, Robert T.  
APPLICANT: Xu, H. Howard  
TITLE OF INVENTION: Identification of Essential Genes in  
FILE OF INVENTION: Prokaryotes  
FILE REFERENCE: ELITRA.011A  
CURRENT APPLICATION NUMBER: US/09/815,242  
CURRENT FILING DATE: 2001-03-21  
PRIOR APPLICATION NUMBER: 60/191,078  
PRIOR FILING DATE: 2000-03-21  
PRIOR APPLICATION NUMBER: 60/206,848  
PRIOR FILING DATE: 2000-05-23  
PRIOR APPLICATION NUMBER: 60/207,727  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: 60/242,578  
PRIOR FILING DATE: 2000-10-23  
PRIOR APPLICATION NUMBER: 60/253,625  
PRIOR FILING DATE: 2000-11-27  
PRIOR APPLICATION NUMBER: 60/257,931  
PRIOR FILING DATE: 2000-12-22  
PRIOR APPLICATION NUMBER: 60/269,308  
PRIOR FILING DATE: 2001-02-16  
NUMBER OF SEQ ID NOS: 14110  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 12482  
LENGTH: 305  
TYPE: PRT  
ORGANISM: Staphylococcus aureus  
US-09-815-242-12482

Query Match  
Best Local Similarity 100.0%; Score 29; DB 10; Length 305;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 DASWL 6  
DB 177 DASWL 181

RESULT 14  
US-09-738-626-6011  
Sequence 6011, Application US/09738626  
Publication No. US20020197605A1  
GENERAL INFORMATION:  
APPLICANT: NAKAGAWA, SATOSHI  
APPLICANT: MIZOGUCHI, HIROSHI  
APPLICANT: ANDO, SEIKO  
APPLICANT: HAYASHI, MIKIRO  
APPLICANT: OCHIAI, KEIKO  
APPLICANT: YOKOI, HARUHIKO  
APPLICANT: TATEISHI, NAOKO  
APPLICANT: SENOH, AKIHIRO

APPLICANT: IKEDA, MASATO  
APPLICANT: OZAKI, AKIO  
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES  
FILE REFERENCE: 249-125  
CURRENT APPLICATION NUMBER: US/09/738,626  
CURRENT FILING DATE: 2000-12-18  
PRIOR APPLICATION NUMBER: JP 99/377484  
PRIOR FILING DATE: 1999-12-16  
PRIOR APPLICATION NUMBER: JP 00/159162  
PRIOR FILING DATE: 2000-04-07  
PRIOR APPLICATION NUMBER: JP 00/280988  
PRIOR FILING DATE: 2000-08-03  
NUMBER OF SEQ ID NOS: 7059  
SOFTWARE: PatentIn ver. 3.0  
SEQ ID NO 6011  
LENGTH: 314  
TYPE: PRT  
ORGANISM: Corynebacterium glutamicum  
US-09-738-626-6011

Query Match 87.9%; Score 29; DB 9; Length 314;  
Best Local Similarity 100.0%; Pred. No. 6.5e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDASW 5  
Db 105 LDASW 109

RESULT 15  
US-09-815-242-5327  
Sequence 5327, Application US/09815242  
Patent No. US2002061569A1  
GENERAL INFORMATION:  
APPLICANT: Haselbeck, Robert  
APPLICANT: Ohlsen, Karl L.  
APPLICANT: Zyskind, Judith W.  
APPLICANT: Wall, Daniel  
APPLICANT: Trawick, John D.  
APPLICANT: Carr, Grant J.  
APPLICANT: Yamamoto, Robert T.  
APPLICANT: Xu, H. Howard  
TITLE OF INVENTION: Identification of Essential Genes in  
TITLE OF INVENTION: Prokaryotes  
FILE REFERENCE: ELITRA.011A  
CURRENT APPLICATION NUMBER: US/09/815,242  
CURRENT FILING DATE: 2001-03-21  
PRIOR APPLICATION NUMBER: 60/191,078  
PRIOR FILING DATE: 2000-03-21  
PRIOR APPLICATION NUMBER: 60/206,848  
PRIOR FILING DATE: 2000-05-23  
PRIOR APPLICATION NUMBER: 60/207,727  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: 60/242,578  
PRIOR FILING DATE: 2000-10-23  
PRIOR APPLICATION NUMBER: 60/253,625  
PRIOR FILING DATE: 2000-11-27  
PRIOR APPLICATION NUMBER: 60/257,931  
PRIOR FILING DATE: 2000-12-22  
PRIOR APPLICATION NUMBER: 60/269,308  
PRIOR FILING DATE: 2001-02-16  
NUMBER OF SEQ ID NOS: 14110  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 5327  
LENGTH: 322  
TYPE: PRT  
ORGANISM: Staphylococcus aureus  
FEATURE:  
NAME/KEY: VARIANT  
LOCATION: (1)...(322)  
OTHER INFORMATION: Xaa - Any Amino Acid  
US-09-815-242-5327

Query Match 87.9%; Score 29; DB 10; Length 322;  
Best Local Similarity 100.0%; Pred. No. 6.6e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 DASWL 6  
Db 194 DASWL 198

Search completed: May 30, 2003, 15:53:18  
Job time : 11.4605 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 30, 2003, 14:32:11 ; Search time 14.7632 Seconds  
(without alignments)  
83.741 Million cell updates/sec

Title: US-09-643-260-10  
Perfect score: 33  
Sequence: 1 LDASWL 6

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues  
Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-Processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

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2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phase:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertbrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
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4	31	93.9	535 17	Q27987
5	31	93.9	763 10	Q95025
6	30	90.9	187 2	Q9JRL5
7	30	90.9	187 2	Q9JRL0
8	30	90.9	187 2	Q9JRL9
9	30	90.9	187 2	Q9JRL8
10	30	90.9	187 2	Q9JRL7
11	30	90.9	221 16	Q9A120
12	30	90.9	225 17	Q8TR10
13	30	90.9	245 2	Q68096
14	30	90.9	261 4	Q9P012
15	30	90.9	261 1	Q9GK13
16	30	90.9	290 2	Q9R03

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18	30	90.9	290 2	Q9F238	Q9f238 xanthomonas
19	30	90.9	290 2	Q51899	Q51899 xanthomonas
20	30	90.9	307 11	Q9CXJ5	Q9cxj5 mus musculus
21	30	90.9	316 16	Q98IR6	Q98ir6 rhizobium
22	30	90.9	317 4	Q9BRA3	Q9bra3 homo sapien
23	30	90.9	332 2	Q9RA30	Q9ra30 vibrio mar
24	30	90.9	344 11	Q8R306	Q8r306 mus musculi
25	30	90.9	442 10	Q95K32	Q95k32 arabidopsis
26	30	90.9	461 10	Q9M0J8	Q9m0j8 arabidopsis
27	30	90.9	688 9	Q9FZR2	Q9fzr2 mycoplasma
28	30	90.9	810 16	Q8ZKN4	Q8zkn4 salmonella
29	30	90.9	810 16	Q8Z226	Q8z226 salmonella
30	30	90.9	906 16	Q8YXK2	Q8yxk2 anabaena sp
31	30	90.9	919 2	Q93MH3	Q93mh3 corynebacte
32	30	90.9	997 2	Q68533	Q68533 pseudomonas
33	29	87.9	69 10	Q43289	Q43289 arabidopsis
34	29	87.9	150 16	Q9H7X9	Q9h7x9 pseudomonas
35	29	87.9	151 5	Q77003	Q77003 biophthalari
36	29	87.9	156 4	Q96G14	Q96g14 homo sapien
37	29	87.9	162 8	Q94Z49	Q94z49 neolepidape
38	29	87.9	162 8	Q94Z27	Q94z27 profundiver
39	29	87.9	192 10	Q9FTQ9	Q9ftq9 oryza meyer
40	29	87.9	220 2	Q68537	Q68537 bordetella
41	29	87.9	243 16	Q913F8	Q913f8 pseudomonas
42	29	87.9	246 2	Q52408	Q52408 pseudomonas
43	29	87.9	252 16	Q9KCS0	Q9kcs0 bacillus ha
44	29	87.9	255 16	Q9RZP2	Q9rzp2 delnoccocus
45	29	87.9	256 10	Q95JZ0	Q95jz0 arabidopsis

## ALIGNMENTS

### RESULT 1

Q968Y8 PRELIMINARY; PRT; 518 AA.  
ID Q968Y8  
AC Q968Y8;  
DT 01-DEC-2001 (TREMURel. 19, Created)  
DI 01-DEC-2001 (TREMURel. 19, Last sequence update)  
DT 01-JUN-2002 (TREMURel. 21, Last annotation update)  
DE Hypothetical protein T28B4.1b.  
GN T28B4.1b.  
OS Caenorhabditis elegans.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;  
OC Rhabditidae; Pelodicerinae; Caenorhabditis.  
OX NCBI\_TaxID-6239;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-BRISTOL N2;  
RX MEDLINE-99069613; PubMed-9851916;  
RA None;  
RT "Genome sequence of the nematode C. elegans: a platform for  
investigating biology. The C. elegans Sequencing Consortium.";  
RL Science 282:2012-2018(1998).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN-BRISTOL N2;  
RA "The sequence of C. elegans cosmid T28B4.";  
RT Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN-BRISTOL N2;  
RA Waterston R.;  
DR Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF026206; AAK39308.1;  
DR InterPro; IPR001810; F-box.  
DR Pfam; PF00646; F-box; 1.  
DR PROSITE; PSS0181; FBOX; 1.  
SQ SEQUENCE 518 AA; 60125 MW; ABA30CG11618EDP4 CRC64;  
Query Match 100.0%; Score 33; DB 5; Length 518;

Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 IDASWL 6  
|||||  
DB 323 IDASWL 328

## RESULT 2

O968Y7 PRELIMINARY; PRT; 535 AA.

AC O968Y7.  
DT 01-DEC-2001 (TREMBLrel. 19, Created)  
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
DE T28B4.1a protein.  
GN T28B4.1a.  
OS Caenorhabditis elegans.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
OC Rhabditidae; Peloderinae; Caenorhabditis.  
OX NCBI\_TaxID=6239;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-BRISTOL N2;  
RX MEDLINE=99069613; PubMed=9851916;

RA None;  
RT "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium.";  
RL Science 282:2012-2018 (1998).

RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN-BRISTOL N2;  
RA Wilson R., Greco T., Sansone J.;  
RT "The sequence of C. elegans cosmid T28B4.";  
RL submitted (OCT-1997) to the EMBL/Genbank/DBJ databases.

RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN-BRISTOL N2;  
RA Waterston R.;  
RL Submitted (APR-2001) to the EMBL/Genbank/DBJ databases.  
DR EMBL: AF026206; AAK39309.1;  
DR InterPro: IPR001810; F-box.  
DR Pfam: PF00646; F-box; 1.  
DR PROSITE: PS50181; FBOX; 1.  
SQ SEQUENCE 535 AA; 62357 MW; CFEA8794E186C104 CRC64;

Query Match 100.0%; Score 33; DB 5; Length 535;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 IDASWL 6  
|||||  
DB 340 IDASWL 345

## RESULT 3

O82AJ4 PRELIMINARY; PRT; 308 AA.

AC O82AJ4.  
DT 01-MAR-2002 (TREMBLrel. 20, Created)  
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)  
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
DE High-affinity branched-chain amino acid transport system, permease protein.  
GN LIVH OR YPO3807.  
OS Yersinia pestis.  
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
OC Yersinia.  
OX NCBI\_TaxID=632;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-CO-92 / BIOVAR ORIENTALIS;  
RX MEDLINE=21470413; PubMed=11586360;

RA Parkhill J., Wren B.W., Thomson N.R., Tibball R.W., Holden M.T.G.,  
RA Prentice M.B., Sebalina M., James K.D., Churcher C., Mungall K.L.,  
RA Baker S., Basham D., Bentley S.D., Brooks K., Cerdano-Tarraga A.M.,  
RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,  
RA Felwell T., Hamlin N., Holroyd S., Jagsels K., Karlyshev A.V.,  
RA Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,  
RA Simmonds M., Skellton J., Stevens K., Whitehead S., Barrall B.G.;  
RT "Genome sequence of Yersinia pestis, the causative agent of plague.";  
RL Nature 413:523-527 (2001).  
DR EMBL: AJ14159; CAC93274.1;  
DR InterPro: IPR001851; Bac\_lmmem\_transp.  
DR Pfam: PF02653; BPD\_transp\_2; 1.  
KW Complete Proteome.  
SQ SEQUENCE 308 AA; 33042 MW; 9C25277B553063A7 CRC64;

Query Match 93.9%; Score 31; DB 16; Length 308;  
Best Local Similarity 83.3%; Pred. No. 2.4e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 IDASWL 6  
|||||  
DB 66 IDASWL 71

## RESULT 4

O27987 PRELIMINARY; PRT; 535 AA.

AC O27987.  
DT 01-JAN-1998 (TREMBLrel. 05, Created)  
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)  
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
DE Cytochrome oxidase, subunit I (CYDA-2).  
GN AF2297.  
OS Archaeoglobus fulgidus.  
OC Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;  
OC Archaeoglobaceae; Archaeoglobus.  
OX NCBI\_TaxID=2234;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-VC-16 / DSM 4304 / ATCC 49558;  
RX MEDLINE=98049343; PubMed=9389475;

RA Kleink H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,  
RA Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,  
RA Richardson D.L., Kervavage A.R., Graham D.E., Kyrtides N.C.,  
RA Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,  
RA Kirschner E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,  
RA Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodok A., Zhou L.,  
RA Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,  
RA Cotton M.D., Spriggs T., Artlich P., Kaine B.P., Sykes S.M.,  
RA Sadow F.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,  
RA Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,  
RA Venter J.C.;  
RT "The complete genome sequence of the hyperthermophilic, sulphate-  
reducing archaeon Archaeoglobus fulgidus.";  
RL Nature 390:364-370 (1997).  
DR EMBL: AE000946; AAB88960.1;  
DR InterPro: IPR002585; Bac\_dpg\_cox.  
DR InterPro: IPR000515; BPD\_transp.  
DR Pfam: PF01654; Bac\_dpg\_cox; 1.  
DR PROSITE: PS00402; BPD\_TRANSF\_INN\_MEMBER; UNKNOWN\_1.  
KW Hypothetical protein; Complete proteome.  
SQ SEQUENCE 535 AA; 57605 MW; 68C821D58A11EE96 CRC64;

Query Match 93.9%; Score 31; DB 17; Length 535;  
Best Local Similarity 83.3%; Pred. No. 4.3e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 IDASWL 6  
|||||  
DB 8 IDASWL 13

RESULT 5  
Q9SUZ5 PRELIMINARY; PRT; 763 AA.  
AC Q9SUZ5;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)  
DE Hypothetical 85.2 kDa protein.  
GN F4F15.210.  
OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eucosids II; Brassicales; Brassicaceae; Arabidopsids.  
OX NCBI\_TaxID=3702;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Alceraz J.P., Clabault G., Cottet A., Mache R., Mewes H.W., Lemcke K.,  
RA Mayer K.F.X., Quelet F., Salanoubat M.;  
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RA EU Arabidopsis sequencing project;  
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AL049711; CAB41330.1; -  
DR InterPro; IPR001965; Znf\_PHD.  
DR SMART; SM00249; PHD; 2.  
DR SMART; SM00184; RING; 1.  
KW Hypothetical protein.  
SQ SEQUENCE 763 AA; 85199 MW; 92BB47843D5314F9 CRC64;  
Query Match 93.9%; Score 31; DB 10; Length 763;  
Best Local Similarity 83.3%; Pred. No. 6.3e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LDASWL 6  
DB 613 IDASWI 618  
RESULT 6  
Q9JRL5 PRELIMINARY; PRT; 187 AA.  
AC Q9JRL5;  
DT 01-OCT-2000 (TREMBLrel. 15, Created)  
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
DE Metallo-beta-lactamase 511 (Fragment).  
GN MBL511 OR MBL5.  
OS Xanthomonas maltophilia (Pseudomonas maltophilia) (Stenotrophomonas  
OS maltophilia).  
OC Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;  
OC Stenotrophomonas.  
OX NCBI\_TaxID=40324;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA STRAIN-511, AND 37;  
RA Walker R.A., Higgins P., Payne D.J., Ames S.G.;  
RT "A biochemical and molecular assessment of the heterogeneity of the  
RT metallo-beta-lactamases from clinical Stenotrophomonas maltophilia  
RT isolates."  
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AJ289086; CAB94705.1; -  
DR HSSP; A52700; ISMT.  
DR InterPro; IPR001018; Beta\_lactamase\_B.  
DR InterPro; IPR001279; Blactamase-like.  
DR Pfam; PF00753; lactamase\_B; 1.  
DR SMART; SM00495; ChlBD3; 1.  
DR PROSITE; PS00743; BETA\_LACTAMASE\_B\_1; 1.  
FT NON\_TER 1  
FT NON\_TER 187

SQ SEQUENCE 187 AA; 19811 MW; 7A2B11372028E5FE CRC64;  
Query Match 90.9%; Score 30; DB 2; Length 187;  
Best Local Similarity 83.3%; Pred. No. 2.2e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LDASWL 6  
DB 12 VDASWL 17  
RESULT 7  
Q9JRM0 PRELIMINARY; PRT; 187 AA.  
AC Q9JRM0;  
DT 01-OCT-2000 (TREMBLrel. 15, Created)  
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)  
DE Metallo-beta-lactamase 1 (Fragment).  
GN MBL1.  
OS Xanthomonas maltophilia (Pseudomonas maltophilia) (Stenotrophomonas  
OS maltophilia).  
OC Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;  
OC Stenotrophomonas.  
OX NCBI\_TaxID=40324;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA STRAIN-GEL;  
RA Walker R.A., Higgins P., Payne D.J., Ames S.G.;  
RT "A biochemical and molecular assessment of the heterogeneity of the  
RT metallo-beta-lactamases from clinical Stenotrophomonas maltophilia  
RT isolates."  
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AJ289081; CAB94700.1; -  
DR HSSP; P52700; ISMT.  
DR InterPro; IPR001018; Beta\_lactamase\_B.  
DR InterPro; IPR001279; Blactamase-like.  
DR Pfam; PF00753; lactamase\_B; 1.  
DR PROSITE; PS00743; BETA\_LACTAMASE\_B\_1; 1.  
FT NON\_TER 1  
FT NON\_TER 187  
SQ SEQUENCE 187 AA; 19901 MW; 72B8515412892A08 CRC64;  
Query Match 90.9%; Score 30; DB 2; Length 187;  
Best Local Similarity 83.3%; Pred. No. 2.2e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LDASWL 6  
DB 12 VDASWL 17  
RESULT 8  
Q9JRL9 PRELIMINARY; PRT; 187 AA.  
AC Q9JRL9;  
DT 01-OCT-2000 (TREMBLrel. 15, Created)  
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)  
DE Metallo-beta-lactamase 2 (Fragment).  
GN MBL2.  
OS Xanthomonas maltophilia (Pseudomonas maltophilia) (Stenotrophomonas  
OS maltophilia).  
OC Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;  
OC Stenotrophomonas.  
OX NCBI\_TaxID=40324;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA STRAIN-0062;  
RA Walker R.A., Higgins P., Payne D.J., Ames S.G.;  
RT "A biochemical and molecular assessment of the heterogeneity of the  
RT metallo-beta-lactamases from clinical Stenotrophomonas maltophilia  
RT isolates."  
FT NON\_TER 1

Submitted (May-2000) to the EMBL/Genbank/DBJ databases.

DR EMBL: AJ289082; CAB94701.1; -.

DR HSSP: P52700; 1SML.

DR InterPro: IPR001018; Beta\_lactamase\_B.

DR InterPro: IPR001279; Blactamase-like.

DR Pfam: PF00753; lactamase\_B.1.

DR PROSITE: PS00743; BETA\_LACTAMASE\_B\_1; 1.

FT NON\_TER 1

FT NON\_TER 187

SQ SEQUENCE 187 AA; 19960 MW; 877D49E4B4C898F4 CRC64;

Query Match 90.9%; Score 30; DB 2; Length 187;  
Best Local Similarity 83.3%; Pred. No. 2.2e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDASWL 6  
DB 12 VDASWL 17

RESULT 9

O9JRL8 PRELIMINARY; PRT; 187 AA.

AC O9JRL8;

DT 01-OCT-2000 (TREMBLrel. 15, Created)

DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)

DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)

DE Metallo-beta-lactamase 3 (Fragment).

GN MBL3.

OS Xanthomonas maltophilia (Stenotrophomonas maltophilia).

CC Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;

OC Stenotrophomonas.

OX NCBI\_TaxID=40324;

RP SEQUENCE FROM N.A.

RC STRAIN=U152;

RA Walker R.A., Higgins P., Payne D.J., Ames S.G.;  
"A biochemical and molecular assessment of the heterogeneity of the metallo-beta-lactamases from clinical Stenotrophomonas maltophilia isolates."

RT Submitted (May-2000) to the EMBL/Genbank/DBJ databases.

RL EMBL: AJ289083; CAB94702.1; -.

DR HSSP: P52700; 1SML.

DR InterPro: IPR001018; Beta\_lactamase\_B.

DR InterPro: IPR001279; Blactamase-like.

DR Pfam: PF00753; lactamase\_B.1.

DR PROSITE: PS00743; BETA\_LACTAMASE\_B\_1; 1.

FT NON\_TER 1

FT NON\_TER 187

SQ SEQUENCE 187 AA; 19931 MW; F07D49E4B4C88043 CRC64;

Query Match 90.9%; Score 30; DB 2; Length 187;  
Best Local Similarity 83.3%; Pred. No. 2.2e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDASWL 6  
DB 12 VDASWL 17

RESULT 10

O9JRL7 PRELIMINARY; PRT; 187 AA.

AC O9JRL7;

DT 01-OCT-2000 (TREMBLrel. 15, Created)

DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)

DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)

DE Metallo-beta-lactamase 4 (Fragment).

GN MBL4.

OS Xanthomonas maltophilia (Stenotrophomonas maltophilia).

CC Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;

Stenotrophomonas.

OX NCBI\_TaxID=40324;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=J2323;

RA Walker R.A., Higgins P., Payne D.J., Ames S.G.;  
"A biochemical and molecular assessment of the heterogeneity of the metallo-beta-lactamases from clinical Stenotrophomonas maltophilia isolates."

RT Submitted (May-2000) to the EMBL/Genbank/DBJ databases.

RL EMBL: AJ289084; CAB94703.1; -.

DR HSSP: P52700; 1SML.

DR InterPro: IPR001018; Beta\_lactamase\_B.

DR InterPro: IPR001279; Blactamase-like.

DR Pfam: PF00753; lactamase\_B.1.

DR PROSITE: PS00743; BETA\_LACTAMASE\_B\_1; 1.

FT NON\_TER 1

FT NON\_TER 187

SQ SEQUENCE 187 AA; 19900 MW; D3C749E4B60C3F18 CRC64;

Query Match 90.9%; Score 30; DB 2; Length 187;  
Best Local Similarity 83.3%; Pred. No. 2.2e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDASWL 6  
DB 12 VDASWL 17

RESULT 11

O9A120 PRELIMINARY; PRT; 221 AA.

AC O9A120;

DT 01-JUN-2001 (TREMBLrel. 17, Created)

DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)

DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)

DE Putative NAD(P)H-flavin oxidoreductase.

GN SPY0512.

OS Streptococcus pyogenes.

CC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;

OC Streptococcaceae; Streptococcus.

OX NCBI\_TaxID=1314;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=SF370 / ATCC 700294 / SEROTYPE M1;

RX MEDLINE=21192684; PubMed=11296296;

RA Ferretti J.J., McShan W.M., Ajdic D.J., Savic G., Lyon K.,  
Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,  
Qian Y., Jia H.G., Najjar F.Z., Ren Q., Zhu H., Song L., White J.,  
Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;  
"Complete genome sequence of an M1 strain of Streptococcus pyogenes."

RT Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).

DR EMBL: AE006509; AKR3511.1; -.

DR InterPro: IPR000415; Nitroreductase.

DR Pfam: PF00881; Nitroreductase; 1.

KW Complete Proteome.

SQ SEQUENCE 221 AA; 25283 MW; 724C14E54FC72CB5 CRC64;

Query Match 90.9%; Score 30; DB 16; Length 221;  
Best Local Similarity 83.3%; Pred. No. 2.7e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDASWL 6  
DB 36 LDAWL 41

RESULT 12

O8TR10 PRELIMINARY; PRT; 225 AA.

ID O8TR10

AC O8TR10;

DT 01-JUN-2002 (TREMBLrel. 21, Created)

DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)

DT 01-JUN-2002 (TREMblrel. 21, last annotation update)  
 GN Hypothetical protein MA1374.  
 DN MA1374.  
 OS Methanosarcina acetivorans.  
 OC Archaea; Euryarchaeota; Methanococci; Methanosarcinales;  
 CC Methanosarcinaceae; Methanosarcina.  
 OX NCBI\_Taxid=2214;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C2A / ATCC 35395 / DSM 2834;  
 RX MEDLINE=21929760; PubMed=11932238;  
 RA Galagan J.E., Nusbaum C., Roy A., Endrizzi M.G., MacDonald P.,  
 RA Fitzhugh W., Calvo S., Engels R., Smirnov S., Alnoor D., Brown A.,  
 RA Allen N., Naylor J., Stange-Thomann N., DeRellano K., Johnson R.,  
 RA Linton L., McEwan P., McKernan K., Talamas J., Turrell A., Ye W.,  
 RA Zimmer A., Barber R.D., Cann I., Graham D.E., Grahame D.A., Guss A.M.,  
 RA Hedderich R., Ingram-Smith C., Kuetner H.C., Krzycki J.A.,  
 RA Leigh J.A., Li W., Liu J., Makhopadhyay B., Reeve J.N., Smith K.,  
 RA Springer T.A., Umayam L.A., White O., White R.H., de Macario E.C.,  
 RA Perry J.G., Jarrell K.E., Jing H., Macario A.J.L., Paulsen I.,  
 RA Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E.,  
 RA Metcalf W.W., Birren B.;  
 RT "The genome of Methanosarcina acetivorans reveals extensive metabolic  
 RT and physiological diversity.";  
 RL Genome Res. 12:532-543(2002).  
 DR EMBL: AE010807; AA04790.1; -;  
 KW Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 225 AA; 25146 MW; A57346D1D6FB9D1 CRC64;

Query Match 90.9%; Score 30; DB 17; Length 225;  
 Best Local Similarity 83.3%; Pred. No. 2.7e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDASWL 6  
 Db 149 LDSSWL 154

RESULT 13  
 ID 068096 PRELIMINARY; PRT; 245 AA.  
 AC 068096;  
 DT 01-AUG-1998 (TREMblrel. 07, Created)  
 DT 01-AUG-1998 (TREMblrel. 07, Last sequence update)  
 DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)  
 DE S-adenosyl-1-methionine-precursor-2 methyltransferase (EC  
 DE 2.1.1.1).  
 OS Rhodospirillum rubrum (Rhodospirillum rubrum).  
 OC Bacteria; Proteobacteria; alpha subdivision; Rhodospirillum group;  
 CC Rhodospirillum.  
 OX NCBI\_Taxid=1061;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=SB1003;  
 RX MEDLINE=97404404; PubMed=9256491;  
 RA Vitek C., Paces V., Maltsev N., Paces J., Haselkorn R., Fongstein M.;  
 RT "Sequence of a 189-kb segment of the chromosome of Rhodospirillum  
 RT capsulatus SB1003.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 94:9384-9388(1997).  
 DR EMBL: AF010496; AAC16186.1; -;  
 DR InterPro: IPR000878; Cor/Por\_Mettransf.  
 DR InterPro: IPR003043; Uropor\_Mettransf.  
 DR Pfam: PF005590; TP\_methylase; 1.  
 DR PROSITE: PS00840; SUMT\_2; 1.  
 KW Methyltransferase; Transferase.  
 SQ SEQUENCE 245 AA; 26942 MW; AEF48C5B6CCF CRC64;

Query Match 90.9%; Score 30; DB 2; Length 245;  
 Best Local Similarity 83.3%; Pred. No. 3e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 LDASWL 6  
 Db 111111

Db 197 LDASWL 202

RESULT 14  
 ID 09P012 PRELIMINARY; PRT; 261 AA.  
 AC 09P012;  
 DT 01-OCT-2000 (TREMblrel. 15, Created)  
 DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)  
 DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)  
 DE 30 kDa protein (Hypothetical 30.0 kDa protein).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 OX NCBI\_Taxid=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=ADRENAL GLAND;  
 RA Gu Y., Huang C., Wu T., Peng Y., Ren S., Gu W., Jiang C., Li Y.,  
 RA Han Z., Wang Y., Chen Z., Fu G.;  
 RT "A novel gene expressed in the human adrenal gland.";  
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=BRAIN;  
 RA Strausberg R.;  
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF157321; AA67487.1; -;  
 DR EMBL: BC022807; AA422807.1; -;  
 KW Hypothetical protein  
 SQ SEQUENCE 261 AA; 29952 MW; 0FB279E54D6C1FCC CRC64;

Query Match 90.9%; Score 30; DB 4; Length 261;  
 Best Local Similarity 83.3%; Pred. No. 3.2e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDASWL 6  
 Db 161 LDASWL 166

RESULT 15  
 ID 099K13 PRELIMINARY; PRT; 261 AA.  
 AC 099K13;  
 DT 01-JUN-2001 (TREMblrel. 17, Created)  
 DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)  
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)  
 DE Hypothetical 30.0 kDa protein.  
 OS Mus musculus (Mouse).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_Taxid=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Strausberg R.;  
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: BC004641; AA04641.1; -;  
 KW Hypothetical protein.  
 SQ SEQUENCE 261 AA; 29980 MW; 0FA0CE154D6C1FCC CRC64;

Query Match 90.9%; Score 30; DB 11; Length 261;  
 Best Local Similarity 83.3%; Pred. No. 3.2e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDASWL 6  
 Db 161 LDASWL 166

Search completed: May 30, 2003, 14:38:57  
 Job time: 16.7632 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 30, 2003, 14:32:12 ; Search time 6.5921 Seconds  
(without alignments)  
87.500 Million cell updates/sec

Title: US-09-643-260-10

Perfect score: 33

Sequence: 1 LDASWL 6

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :  
1: PIR1:\*  
2: PIR2:\*  
3: PIR3:\*  
4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	33	100.0	419	2 T32441	hypothetical prote
2	31	93.9	308	2 AF0463	high-affinity bran
3	31	93.9	535	2 A69537	cytochrome oxidase
4	31	93.9	763	2 T49089	hypothetical prote
5	30	90.9	245	2 T03533	probable precursor
6	30	90.9	290	2 T48880	beta-lactamase (Ec
7	30	90.9	290	2 S45349	Li metallo-beta-la
8	30	90.9	332	2 T44437	aminodeoxychorism
9	30	90.9	442	2 T04815	hypothetical prote
10	30	90.9	461	2 D85312	probable homeodoma
11	30	90.9	810	2 AH0337	diffusional aspar
12	30	90.9	906	2 AG1957	hypothetical prote
13	30	90.9	919	1 QYFKG	phosphoenolpyruvat
14	29	87.9	150	2 C82994	conserved hypochet
15	29	87.9	177	1 B41377	cytochrome c-L pre
16	29	87.9	243	2 G83450	hypothetical prote
17	29	87.9	252	2 C83837	hypothetical prote
18	29	87.9	255	2 F73626	probable 3-alpha-h
19	29	87.9	256	2 F84612	hypothetical prote
20	29	87.9	264	2 D84504	probable VSF-1-lik
21	29	87.9	269	2 A75397	probable signal pe
22	29	87.9	274	2 E83444	probable transcrip
23	29	87.9	277	2 T29979	hypothetical prote
24	29	87.9	278	2 H82759	cell division prot
25	29	87.9	282	2 E70890	hypothetical prote
26	29	87.9	286	2 A48399	probable oxidoredu
27	29	87.9	286	2 A85739	probable dehydrat
28	29	87.9	286	2 H90879	probable dehydrat
29	29	87.9	289	1 A37209	thiosulfate sulfur

30	29	87.9	295	2 S15081	thiosulfate sulfur
31	29	87.9	296	1 ROHU	thiosulfate sulfur
32	29	87.9	296	2 AH2327	hypothetical prote
33	29	87.9	297	1 ROBO	thiosulfate sulfur
34	29	87.9	297	2 JC4398	thiosulfate sulfur
35	29	87.9	297	2 JC5286	thiosulfate sulfur
36	29	87.9	301	2 G83182	hypothetical prote
37	29	87.9	316	2 F89791	peptidoglycan hydr
38	29	87.9	318	2 T52653	thiosulfate sulfur
39	29	87.9	326	2 B99790	hypothetical prote
40	29	87.9	329	2 A86300	hypothetical prote
41	29	87.9	333	2 F70578	probable transpos
42	29	87.9	339	2 S15305	ribg protein - Sal
43	29	87.9	359	2 AH0766	CDPglucose 4,6-deh
44	29	87.9	360	2 T26037	hypothetical prote
45	29	87.9	360	2 S32695	Mnt-2 protein - Ca

#### ALIGNMENTS

RESULT 1  
T32441  
hypothetical protein T28B4.1 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 29-Oct-1999. #sequence\_revision 29-Oct-1999 #text\_change 18-Feb-2000  
C:Accession: T32441  
R:Wilson, R.; Greco, T.; Sansone, J.  
submitted to the EMBL Data Library, September 1997  
A:Description: The sequence of C. elegans cosmid T28B4.  
A:Reference number: Z21168  
A:Accession: T32441  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-419 <NT>  
A:Cross-references: EMBL:AR026206; PIDN:RA871262.1; GSPDB:GN00028; CESP:T28B4.1  
A:Experimental source: strain Bristol N2; clone T28B4  
C:Genetics:  
A:Gene: CESP:T28B4.1  
A:Map position: X  
A:Introns: 47/3; 68/3; 102/3; 153/1; 207/1; 296/1

Query Match  
Best Local Similarity 100.0%; Score 33; DB 2; Length 419;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6  
DB 340 LDASWL 345

RESULT 2  
AF0463  
high-affinity branched-chain amino acid transport system, permease protein llvH [limp  
C:Species: Yersinia pestis  
C:Date: 02-Nov-2001 #sequence\_revision 02-Nov-2001 #text\_change 09-Nov-2001  
C:Accession: AF0463  
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Tittball, R.W.; Holden, M.T.G.; Prentice, M  
demo-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G  
ll, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barril  
Nature 413: 523-527, 2001  
A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.  
A:Reference number: AB0001; MUID:21470413; PMID:11586360  
A:Accession: AF0463  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-308 <NR>  
A:Cross-references: GB:AL590842; PIDN:CAC93274.1; PID:G15981721; GSPDB:GN00175  
C:Genetics:  
A:Gene: llvH  
C:Superfamily: leucine transport protein llvH

Query Match 93.9%; Score 31; DB 2; Length 308;

Best Local Similarity 83.3%; Pred. No. 92;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LDASWL 6  
DB 66 IDASWL 71

## RESULT 3

A69537  
cytochrome oxidase, subunit I (cydA-2) homolog - *Archaeoglobus fulgidus*  
C:Species: *Archaeoglobus fulgidus*  
C:Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 17-Mar-2000  
C:Accession: A69537  
R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson  
; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.;  
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weisman, J.F.; McDonald, L.  
Nature 380, 364-370, 1997  
A:Authors: Overbeek, R.; Cotton, M.D.; Spriggs, T.; Artlisch, P.; Kaine, B.P.; Sykes, S.  
Smith, H.O.; Woese, C.R.; Venter, J.C.  
A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo  
A:Reference number: A69250; MUID:98049343; PMID:9389475  
A:Accession: A69537  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-535 <KLE>  
A:Cross-references: GB:AE000946; GB:AE000782; NID:g2689269; PIDN:AA888960.1; PID:g264822  
C:Superfamily: cytochrome d complex terminal oxidase chain I

Query Match  
Best Local Similarity 93.9%; Score 31; DB 2; Length 535;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6  
DB 8 IDASWL 13

## RESULT 4

T49089  
hypothetical protein F4F15.210 - *Arabidopsis thaliana*  
C:Species: *Arabidopsis thaliana* (mouse-ear cress)  
C:Date: 02-Jun-2000 #sequence\_revision 02-Jun-2000 #text\_change 02-Jun-2000  
C:Accession: T49089  
R:Alvarez, J.P.; Clabault, G.; Cottet, A.; Mache, R.; Mewes, H.W.; Rudd, S.; Lemcke, K.;  
submitted to the Protein Sequence Database, April 2000  
A:Reference number: Z25015  
A:Accession: T49089  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-763 <ALC>  
A:Cross-references: EMBL:AL049711; GSPDB:GN00061; ATSP:F4F15.210  
A:Experimental source: cultivar Columbia; BAC clone F4F15  
C:Genetics:  
A:Gene: ATSP:F4F15.210  
A:Map position: 3  
A:Introns: 11/2; 124/3; 183/1; 199/3; 230/3; 274/1; 297/3; 325/2; 351/3; 478/1; 641/2; 6

Query Match  
Best Local Similarity 93.9%; Score 31; DB 2; Length 763;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6  
DB 613 IDASWL 618

## RESULT 5

T03533  
probable precorrin-2 methyltransferase (EC 2.1.1.-) - *Rhodobacter capsulatus*  
C:Species: *Rhodobacter capsulatus*  
C:Date: 24-Mar-1999 #sequence\_revision 24-Mar-1999 #text\_change 18-Feb-2000  
C:Accession: T03533

R:Vlcek, C.; Paces, V.; Maltsev, N.; Paces, J.; Haselkorn, R.; Fongstein, M.  
Proc. Natl. Acad. Sci. U.S.A. 94, 9384-9388, 1997  
A:Title: Sequence of a 189-kb segment of the chromosome of *Rhodobacter capsulatus* SBI  
A:Reference number: Z14955; MUID:97404404; PMID:9256491

A:Accession: T03533  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-245 <VIC>  
A:Cross-references: EMBL:AF010496; NID:g3128256; PIDN:AAAC16186.1; PID:g3128334  
C:Genetics:  
A:Map position: 1  
C:Superfamily: precorrin-3 methylase  
C:Keywords: methyltransferase

Query Match  
Best Local Similarity 90.9%; Score 30; DB 2; Length 245;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6  
DB 197 IDASWL 202

## RESULT 6

T48880  
beta-lactamase (EC 3.5.2.6) L-1 precursor [validated] - *Pseudomonas maltophilia*  
N:Alternate names: L-1 metallo-beta-lactamase  
C:Species: *Pseudomonas maltophilia*  
C:Date: 02-Jun-2000 #sequence\_revision 02-Jun-2000 #text\_change 02-Jun-2000  
C:Accession: T48880  
R:Sanschagrin, F.; Dufresne, J.; Levesque, R.C.  
Antimicrob. Agents Chemother. 42, 1245-1248, 1998  
A:Title: Molecular heterogeneity of the L-1 metallo-beta-lactamase family from *Stenot*  
A:Reference number: Z24841; MUID:98253990; PMID:9593158  
A:Accession: T48880  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-290 <SAN>  
A:Cross-references: EMBL:AF010282; PIDN:AAAC21590.1  
A:Experimental source: strain GNI2873  
C:Genetics:  
A:Gene: blas  
A:Function:  
A:Description: catalyzes the hydrolysis of an amide bond in the beta-lactam ring of t  
C:Keywords: antibiotic resistance; hydrolase  
F:1-33/Domain: signal sequence #status predicted <SIG>  
F:34-290/Product: L-1 metallo-beta-lactamase #status predicted <MAT>

Query Match  
Best Local Similarity 90.9%; Score 30; DB 2; Length 290;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6  
DB 34 IDASWL 39

## RESULT 7

S45349  
L1 metallo-beta-lactamase - *Xanthomonas maltophilia*  
C:Species: *Xanthomonas maltophilia*  
C:Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 01-Aug-1997  
C:Accession: S45349  
R:Walsh, T.R.; Hall, L.; Assinder, S.J.; Nichols, W.W.; Cartwright, S.J.; McGowan, A.  
Biochim. Biophys. Acta 1218, 199-201, 1994  
A:Title: Sequence analysis of the L1 metallo-beta-lactamase from *Xanthomonas maltophi*  
A:Reference number: S45349; MUID:94289479; PMID:8018721  
A:Accession: S45349  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-290 <MAL>

Query Match  
90.9%; Score 30; DB 2; Length 290;

Best Local Similarity 93.3%; Pred. No. 1.4e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDASWL 6  
Db 34 VDASWL 39

## RESULT 8

T44437

aminoacylchroismate lyase homolog [imported] - Moritella marina

C:Species: Moritella marina

C>Date: 21-Jan-2000 #sequence\_revision 21-Jan-2000 #text\_change 18-Feb-2000

C:Accession: T44437

R:Morita, N.; Ueno, A.; Tanaka, M.; Ohgita, S.; Hoshino, T.; Kawasaki, K.; Yumoto, I.;

Biotechnol. Lett. 21, 641-646, 1999

A:Title: Cloning and sequencing of clustered genes involved in fatty acid biosynthesis

A:Reference number: 222768

A:Accession: T44437

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-332 <MOR>

A:Cross-references: EMBL:AB021978; PIDN:BA05259.1

A:Experimental source: ATCC 15381

C:Genetics:

A:Note: pABC

C:Superfamily: yceg protein

OY 1 LDASWL 6  
Db 187 LDAAML 192

## RESULT 9

T04815

hypothetical protein F10M23.260 - Arabidopsis thaliana (fragment)

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 11-Jun-1999

C:Accession: T04815

R:Bayan, M.; Lechary, A.; Chetdor, F.; Krivitzky, M.; Kreis, M.; Hohnsels, J.; Mewes, H.

Submitted to the Protein Sequence Database, February 1999

A:Reference number: Z15385

A:Accession: T04815

A:Molecule type: DNA

A:Residues: 1-442 <BEV>

A:Cross-references: EMBL:AL035440

A:Experimental source: cultivar Columbia; BAC clone F10M23

C:Genetics:

A:Map position: 4

A:Introns: 140/3; 165/3; 236/1; 358/3

A:Note: F10M23.260

OY 1 LDASWL 6  
Db 128 VDASWL 133

## RESULT 10

D85312

probable homeodomain protein [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 16-Feb-2001

C:Accession: D85312

R:anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring

A:Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.

A:Reference number: A85001; MUID:20083488; PMID:10617198

A:Accession: D85312

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-461 <STO>

A:Cross-references: GB:NC\_001268; NID:g7269545; PIDN:CAF79547.1; GSPDB:GN00140

C:Genetics:

A:Gene: AT4g26920

A:Map position: 4

OY 1 LDASWL 6  
Db 128 VDASWL 133

## RESULT 11

AH0937

bifunctional aspartokinase II/homoserine dehydrogenase II can I write [imported] - Sal.

C:Species: Salmonella enterica subsp. enterica serovar Typh

A:Note: This species has also been called Salmonella typh

C>Date: 09-Nov-2001 #sequence\_revision 09-Nov-2001 #text\_change 27-Nov-2001

C:Accession: AH0937

R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Church

th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farr

S.; Mout, S.; O'Garra, P.

Nature 413, 848-852, 2001

A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens,

A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica se

A:Reference number: AB0502; PMID:11677608

A:Accession: AH0937

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-810 <PAR>

A:Cross-references: GB:AL513382; PIDN:CAD09522.1; PID:g16504639; GSPDB:GN00176

C:Genetics:

A:Gene: SRY3768

C:Superfamily: thra bifunctional enzyme; aspartate kinase homology; homoserine dehydr

OY 1 LDASWL 6  
Db 146 LDAAML 151

## RESULT 12

AG1957

hypothetical protein all1210 [imported] - Nostoc sp. (strain PCC 7120)

C:Species: Nostoc sp.

A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120

C>Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 30-Jun-2002

C:Accession: AG1957

R:Keneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Irigu

Nakazaki, N.; Shimo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata

DNA Res. 8, 205-213, 2001

A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium

A:Reference number: AB1807; MUID:21595285; PMID:11759840

A:Accession: AG1957

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-906 <KUR>

A:Cross-references: GB:BA000019; PIDN:BA073167.1; PID:g17130557; GSPDB:GN00179

A:Experimental source: strain PCC 7120

C:Genetics:

A:Gene: all1210

Query Match 90.9%; Score 30; DB 2; Length 906;  
 Best Local Similarity 83.3%; Pred. No. 4.4e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 DASWL 6  
 |||||  
 DB 225 LDSSWL 230

## RESULT 13

QYFKG

phosphoenolpyruvate carboxylase (EC 4.1.1.31) - *Corynebacterium glutamicum*C:Species: *Corynebacterium glutamicum*

C:Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 18-Jun-1999

C:Accession: S05512; JS0183

R:Keywords: B.J.; Follett, M.T.; Griot, M.U.; Sinskey, A.J.

Mol. Gen. Genet. 218, 330-339, 1989

A:Title: The phosphoenolpyruvate carboxylase gene of *Corynebacterium glutamicum*: molecu

A:Reference number: S05511; M01D:89384460; PMID:2779518

A:Accession: S05512

A:Molecule type: DNA

A:Residues: 1-919 &lt;EIK&gt;

A:Cross-references: GB:X14234; NID:948688; PIDN:CAA32450.1; PID:948689

A:Note: the authors translated the codon ATT for residue 387 as Glu, AAA for residue 553

R:O'Regan, M.; Thierbach, G.; Bachmann, B.; Villerval, D.; Lepage, P.; Viret, J.F.; Lemou

Gene 77, 237-251, 1989

A:Title: Cloning and nucleotide sequence of the phosphoenolpyruvate carboxylase-coding g

A:Reference number: JS0183; M01D:89326141; PMID:2666264

A:Accession: JS0183

A:Molecule type: DNA

A:Residues: 1-606; 'KT', 609-799, 'FT', 802-914, 'L', 916-919 &lt;ORE&gt;

A:Cross-references: GB:M25819; NID:9144984; PIDN:AAA83537.1; PID:9144985

A:Experimental source: ATCC 13032

A:Note: residues 2-15 were confirmed by protein sequencing

C:Comment: This enzyme catalyzes the carboxylation (by carbon dioxide) of phosphoenolpyr

C:Genetics: The activity of this protein is not stimulated by acetyl-CoA in the absence o

A:Gene: ppc

C:Superfamily: phosphoenolpyruvate carboxylase

C:Keywords: allosteric regulation; carbon dioxide fixation; carbon-carbon lyase; carboxy

F:2-919/Product: phosphoenolpyruvate carboxylase [status predicted &lt;MNT&gt;

F:611-624/Region: substrate binding [status predicted]

Query Match 90.9%; Score 30; DB 1; Length 919;

Best Local Similarity 83.3%; Pred. No. 4.4e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDASWL 6

|||:|

DB 105 LDATWL 110

RESULT 14

C82994

conserved hypothetical protein PA5211 [imported] - *Pseudomonas aeruginosa* (strain PA01)C:Species: *Pseudomonas aeruginosa*

C:Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 31-Dec-2000

C:Accession: C82994

R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; B

adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lam,

; Lory, S.; Olson, M.V.

A:Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic patho

A:Reference number: AB2950; M01D:20437337; PMID:10984043

A:Accession: C82994

A:Status: Preliminary

A:Molecule type: DNA

A:Residues: 1-150 &lt;STO&gt;

A:Cross-references: GB:AE004934; GB:AE004091; NID:99951515; PIDN:AA08596.1; GSPDB:GN001

C:Genetics:

A:Experimental source: strain PA01

A:Gene: PA5211

Query Match 87.9%; Score 29; DB 2; Length 150;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 DASWL 6  
 |||||  
 DB 117 DASWL 121

## RESULT 15

B41377

cytochrome c-L precursor [validated] - *Paracoccus denitrificans*

N:Alternate names: cytochrome c5511; cytochrome c552; moxg protein

C:Species: *Paracoccus denitrificans*

C:Date: 28-May-1992 #sequence\_revision 02-Jul-1996 #text\_change 15-Sep-2000

C:Accession: B41377

R:Van Spanning, R.J.M.; Mansell, C.W.; De Boer, T.; Hazelaar, M.J.; Anazawa, H.; Herm

J. Bacteriol. 173, 6948-6961, 1991

A:Title: Isolation and characterization of the moxg, moxg, moxg, and moxg genes of Pa

A:Reference number: A41377; M01D:92041581; PMID:1657871

A:Accession: B41377

A:Molecule type: DNA

A:Residues: 1-177 &lt;VAN&gt;

A:Cross-references: GB:M57684; NID:9150589; PIDN:AA25583.1; PID:9150591

R:Chen, L.; Durely, R.C.E.; Matthews, F.S.; Davidson, V.L.

Science 264, 86-90, 1994

A:Title: Structure of an electron transfer complex: methylamine dehydrogenase, amicya

A:Reference number: A57985; M01D:94188715; PMID:8140419

A:Contents: annotation; X-ray crystallography, 2.4 angstroms, residues 23-117

R:Chen, L.; Matthews, F.S.

submitted to the Brookhaven Protein Data Bank, October 1993

A:Reference number: A52094; PDB:2MTA

A:Contents: annotation; X-ray crystallography, 2.4 angstroms, residues 23-169

C:Genetics:

A:Gene: moxg

C:Complex: associates in a heterotetramer with methylamine dehydrogenase large and sm

C:Function:

A:Description: electron acceptor for methanol dehydrogenase; can also accept an elect

A:Pathway: methanol oxidation; methylamine oxidation

C:Superfamily: cytochrome c-L; cytochrome c6 homology

C:Keywords: chromoprotein; electron transfer; heme; heterotetramer; iron; metalloprot

F:1-22/Domains: signal sequence [status predicted &lt;SIG&gt;

F:23-177/Product: cytochrome c-L [status experimental &lt;MNT&gt;

F:69-142/Domains: cytochrome c6 homology &lt;CT6&gt;

F:79,82/Binding site: heme (Cys) (covalent) [status experimental

F:83,123/Binding site: heme iron (His, Met) (axial ligands) [status experimental

Query Match 87.9%; Score 29; DB 1; Length 177;

Best Local Similarity 100.0%; Pred. No. 1.3e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 DASWL 6

|||:|

DB 152 DASWL 156

Search completed: May 30, 2003, 14:52:52

Job time : 8.5921 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 30, 2003, 14:32:12 ; Search time 6.5921 Seconds  
(without alignments)  
87.500 Million cell updates/sec

Title: US-09-643-260-11

Perfect score: 35

Sequence: 1 LDFSWL 6

Scoring table: BLOSUM62  
Gapop 10.0 , Gapect 0.5

Searched: 283224 segs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR.73:\*  
2: PIR2:\*  
3: PIR3:\*  
4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	35	100.0	331	2 A70663	probable PPE prote
2	35	100.0	414	2 T44513	hypothetical prote
3	33	94.3	61	2 D82732	hypothetical prote
4	33	94.3	144	2 A10698	probable pathogen
5	33	94.3	253	2 D71975	hypothetical prote
6	33	94.3	253	2 B64532	hypothetical prote
7	33	94.3	518	2 A81865	conserved hypotet
8	33	94.3	518	2 C81077	conserved hypotet
9	33	94.3	868	2 S65186	NIP80 protein - ye
10	33	94.3	1214	2 T21915	hypothetical prote
11	32	91.4	208	1 F69462	hypothetical prote
12	32	91.4	371	2 T04971	hypothetical prote
13	32	91.4	449	2 F83328	probable sodium/ac
14	32	91.4	467	2 E95850	probable amino aci
15	32	91.4	490	2 G59535	probable membrane
16	31	88.6	121	2 S64036	probable membrane
17	31	88.6	150	2 S74754	hypothetical prote
18	31	88.6	159	2 F82836	hypothetical prote
19	31	88.6	199	2 F30439	hypothetical prote
20	31	88.6	224	2 F70570	probable pdkn prot
21	31	88.6	236	1 TVMSA1	transferring prote
22	31	88.6	236	1 L53744	gene bcl-2 protein
23	31	88.6	236	2 JC7383	B-cell lymphoma 2
24	31	88.6	239	1 TVHDA1	transferring prote
25	31	88.6	247	2 C96594	unknown protein, 7
26	31	88.6	253	2 S65170	hypothetical prote
27	31	88.6	262	2 G72694	hypothetical prote
28	31	88.6	296	2 T31582	hypothetical prote
29	31	88.6	331	2 B95880	conserved hypotet

30	31	88.6	338	2 A82890	hypothetical prote
31	31	88.6	387	2 D88968	protein T7/B7.3 [1
32	31	88.6	401	2 T44831	probable emlihan r
33	31	88.6	440	2 B71153	hypothetical prote
34	31	88.6	461	2 B83601	probable transport
35	31	88.6	467	2 AE1892	hypothetical prote
36	31	88.6	472	2 B75501	glycogen synthase
37	31	88.6	484	2 T33504	hypothetical prote
38	31	88.6	495	2 H70391	cysteine-tRNA lig
39	31	88.6	516	2 AC1892	hypothetical prote
40	31	88.6	544	2 T45498	hypothetical prote
41	31	88.6	611	2 G83177	probable sodium/hy
42	31	88.6	612	2 S62930	hypothetical prote
43	31	88.6	612	2 S62956	hypothetical prote
44	31	88.6	641	2 F97573	hypothetical prote
45	31	88.6	641	2 AG2794	hypothetical prote

## ALIGNMENTS

### RESULT 1

A70663

probable PPE protein - Mycobacterium tuberculosis (strain H37RV)

C:Species: Mycobacterium tuberculosis

C:Date: 17-Jul-1998 #sequence.revision 17-Jul-1998 #text\_change 22-Oct-1999

C:Accession: A70663

R:Cole, S.T.; Broesch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon

R:Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd,

Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.

Nature 393, 537-544, 1998

A:Authors: Squires, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete geno

A:Reference number: A70500; MUID:98295987; PMID:9634230

A:Accession: A70663

A>Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-391 <COL>

A:Cross-references: GB:Z83860; GB:AL123456; NID:93261681; PIDN:CA806149.1; PID:e29075

A:Experimental source: strain H37RV

C:Genetics:

A:Gene: PPE

Query Match 100.0%; Score 35; DB 2; Length 391;

Best Local Similarity 100.0%; Pred. No. 20;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDFSWL 6

Db 3 LDFSWL 8

### RESULT 2

T44513

hypothetical protein 5P [imported] - Plesiomonas shigelloides

C:Species: Plesiomonas shigelloides

C:Date: 21-Jan-2000 #sequence.revision 21-Jan-2000 #text\_change 21-Jan-2000

C:Accession: T44513

R:Chida, T.; Okamura, N.; Yoshida, Y.; Ohnari, K.; Arakawa, E.; Watanabe, H.

submitted to the EMBL Data Library, April 1999

A:Description: Complete DNA sequence of the O-antigen (rtb) gene cluster in Plesiomon

A:Reference number: Z22786

A:Accession: T44513

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-414 <CH1>

A:Cross-references: EMBL:AB025970; PIDN:BA85010.1

A:Experimental source: ATCC 14029

Query Match 100.0%; Score 35; DB 2; Length 414;

Best Local Similarity 100.0%; Pred. No. 22;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDFSMTL 6  
 DB 175 LDFSMTL 180

## RESULT 3

hypothetical protein XF1033 [imported] - Xylella fastidiosa (strain 9a5c)  
 C:Species: Xylella fastidiosa  
 C:Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 20-Aug-2000  
 C:Accession: D82732  
 R:Anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequences  
 Nature 406, 151-157, 2000  
 A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.  
 A:Reference number: A82515; MUID:20365717; PMID:10910347  
 A:Note: for a complete list of authors see reference number A59328 below  
 A:Accession: D82732  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-61 <SIM>  
 A:Cross-references: GB:AE003940; GB:AE003849; NID:g9105966; PIDN:AAF83843.1; GSPDB:GN001  
 A:Experimental source: strain 9a5c  
 R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A  
 Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carre, H  
 as-Neto, E.; Docena, C.; El-Dorri, H.; Facincan, A.P.; Ferreira, A.J.S.  
 submitted to GenBank, June 2000  
 A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franco, S.C.; Franco, M.C.; Frohm  
 J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laig  
 chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.E.; Marino, C.L.; Marques, M.V.; Martins, H  
 A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.  
 , F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A  
 Rodrigues, V.; Rosa, A.J.; de M. de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak  
 M.; Tsunako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z  
 A:Reference number: A59328  
 A:Contents: annotation  
 C:Genetics:  
 A:Gene: XF1033

Query Match 94.3%; Score 33; DB 2; Length 61;  
 Best Local Similarity 83.3%; Pred. No. 6.8;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDFSMTL 6  
 DB 2 MDFSMTL 7

## RESULT 4

probable pathogenicity island protein sscB [imported] - Salmonella enterica subsp. enter  
 C:Species: Salmonella enterica subsp. enterica serovar Typh  
 A:Note: this species has also been called Salmonella typhi  
 C:Date: 09-Nov-2001 #sequence\_revision 09-Nov-2001 #text\_change 09-Nov-2001  
 C:Accession: A10698  
 R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,  
 th, T.; Conerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,  
 , S.; Moule, S.; O'Garra, P.  
 Nature 413, 848-852, 2001  
 A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;  
 A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov  
 A:Reference number: AB0502; PMID:11677608  
 A:Accession: A10698  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-144 <PAR>  
 A:Cross-references: GB:AL513382; PIDN:CAD01962.1; PID:g16502804; GSPDB:GN00176  
 C:Genetics:  
 A:Gene: sscB

Query Match 94.3%; Score 33; DB 2; Length 144;  
 Best Local Similarity 83.3%; Pred. No. 17;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDFSMTL 6  
 DB 45 LDFSMTL 50

## RESULT 5

hypothetical protein jhp0093 - Helicobacter pylori (strain J99)  
 C:Species: Helicobacter pylori  
 A:Variety: strain J99  
 C:Date: 12-Feb-1999 #sequence\_revision 12-Feb-1999 #text\_change 08-Oct-1999  
 C:Accession: D11975  
 R:Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Dolg, P.C.; Smith, D.  
 , Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F  
 Nature 397, 176-180, 1999  
 A:Title: Genomic sequence comparison of two unrelated isolates of the human gastric p  
 A:Reference number: A71800; MUID:99120557; PMID:9923682  
 A:Accession: D11975  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-253 <ARN>  
 A:Cross-references: GB:AE001448; GB:AE001439; NID:g4154594; PIDN:AAD05674.1; PID:g415  
 A:Experimental source: strain J99  
 C:Genetics:  
 A:Gene: jhp0093

Query Match 94.3%; Score 33; DB 2; Length 253;  
 Best Local Similarity 83.3%; Pred. No. 32;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDFSMTL 6  
 DB 149 LDFSMTL 154

## RESULT 6

hypothetical protein HP0101 - Helicobacter pylori (strain 26695)  
 C:Species: Helicobacter pylori  
 C:Date: 09-Aug-1997 #sequence\_revision 09-Aug-1997 #text\_change 08-Oct-1999  
 C:Accession: E64532  
 R:Romb, J.F.; White, O.; Kierlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R  
 Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalaf, H.G.; Glodek, A.; McKe  
 son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watney,  
 Nature 388, 539-547, 1997  
 A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser,  
 A:Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.  
 A:Reference number: A64520; MUID:97394467; PMID:9252185  
 A:Accession: E64532  
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-253 <TON>  
 A:Cross-references: GB:AE000532; GB:AE000511; NID:g2313184; PIDN:AAD07180.1; PID:g231  
 C:Genetics:  
 A:Start codon: TTG

Query Match 94.3%; Score 33; DB 2; Length 253;  
 Best Local Similarity 83.3%; Pred. No. 32;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDFSMTL 6  
 DB 149 LDFSMTL 154

## RESULT 7

conserved hypothetical integral membrane protein NMA1694 [imported] - Neisseria menin  
 C:Species: Neisseria meningitidis  
 C:Date: 05-May-2000 #sequence\_revision 05-May-2000 #text\_change 02-Feb-2001  
 C:Accession: A81865  
 R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Mo

Holroyd, S.; Uggels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream, Nature 404, 502-506, 2000  
 A:Title: Complete DNA sequence of a serogroup A strain of *Neisseria meningitidis* 22491.  
 A:Reference number: AB1775; MUID:20222556; PMID:10761919  
 A:Accession: AB1865  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-518 <PAR>  
 A:Cross-references: GB:AL162756; GB:AL157959; NID:97380091; PIDN:CA84922.1; PID:9738033  
 A:Experimental source: serogroup A, strain 22491  
 C:Genetics:  
 A:Gene: NMA1694

Query Match 94.3%; Score 33; DB 2; Length 518;  
 Best Local Similarity 83.3%; Pred. No. 70;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDFSMTL 6  
 Db 1 MDFSMTL 6

## RESULT 8

conserved hypothetical protein NMB1485 [imported] - *Neisseria meningitidis* (strain MC58  
 C:Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 19-Jan-2001  
 C:Species: *Neisseria meningitidis*  
 C:Accession: C81077  
 R:Retellin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.  
 Hickey, E.K.; Hart, D.H.; Salberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;  
 ri, H.; Qin, H.; Vanthaeven, J.; Gill, J.; Scarlato, V.; Maignan, V.; Pizze, M.  
 Science 287, 1809-1815, 2000  
 A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve  
 A:Title: Complete genome sequence of *Neisseria meningitidis* serogroup B strain MC58.  
 A:Reference number: AB1000; MUID:20175755; PMID:10710307  
 A:Accession: C81077  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-518 <TEXT>  
 A:Cross-references: GB:AE002498; GB:AE002098; NID:97226724; PIDN:AMF41841.1; PID:9722672  
 A:Experimental source: serogroup B, strain MC58  
 C:Genetics:  
 A:Gene: NMB1485

Query Match 94.3%; Score 33; DB 2; Length 518;  
 Best Local Similarity 83.3%; Pred. No. 70;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDFSMTL 6  
 Db 1 MDFSMTL 6

## RESULT 9

NIP80 protein - yeast (*Saccharomyces cerevisiae*)  
 N:Alternate names: protein P2279; protein YPL174C  
 C:Species: *Saccharomyces cerevisiae*  
 C:Date: 10-Dec-1994 #sequence\_revision 31-May-1996 #text\_change 05-Dec-1997  
 A:Accession: S65186; S34343  
 R:Benes, V.; Rechmann, S.; Neutlich, U.; Voss, H.; Ansgorge, W.  
 Submitted to the Protein Sequence Database, May 1996  
 A:Reference number: S65183  
 A:Accession: S65186  
 A:Molecule type: DNA  
 A:Residues: 1-868 <BEN>  
 A:Cross-references: EMBL:Z73530; NID:91370366; PID:e246907; PID:91370367; MIPS:YPL174C  
 A:Experimental source: strain S288C (AB972)  
 R:Schlenstedt, G.; Silver, P.A.  
 Submitted to the EMBL Data Library, May 1993  
 A:Reference number: S34342  
 A:Accession: S34343  
 A:Molecule type: DNA

A:Residues: 169-429, 'V', 431-868 <SCH>  
 A:Cross-references: EMBL:X72227  
 C:Genetics:  
 A:Gene: SGD:NIP100; NIP80  
 A:Cross-references: MIPS:YPL174C; SGD:S0006095  
 A:Map position: 16L  
 C:Keywords: transmembrane protein  
 F:574-590/Domain: transmembrane #status: predicted <TM>

Query Match 94.3%; Score 33; DB 2; Length 868;  
 Best Local Similarity 83.3%; Pred. No. 12e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDFSMTL 6  
 Db 782 LDFSMTL 787

## RESULT 10

hypothetical protein F37D6.1 - *Caenorhabditis elegans*  
 C:Species: *Caenorhabditis elegans*  
 C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
 C:Accession: T21915  
 R:McMurray, A.  
 Submitted to the EMBL Data Library, June 1996  
 A:Reference number: Z19487  
 A:Accession: T21915  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-1214 <MTL>  
 A:Cross-references: EMBL:Z75540; PIDN:CAA9847.1; GSPDB:GN00019; CESP:F37D6.1  
 A:Experimental source: clone F37D6  
 C:Genetics:  
 A:Gene: CESP:F37D6.1  
 A:Map position: 1  
 A:Introns: 43/71; 59/3; 103/3; 149/2; 230/3; 278/3; 313/1; 439/2; 489/3; 571/1; 625/2;

Query Match 94.3%; Score 33; DB 2; Length 1214;  
 Best Local Similarity 83.3%; Pred. No. 1.8e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDFSMTL 6  
 Db 772 LDFSMTL 777

## RESULT 11

hypothetical protein AF1703 - *Archaeoglobus fulgidus*  
 C:Species: *Archaeoglobus fulgidus*  
 C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 21-Jul-2000  
 C:Accession: F69462  
 R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dod  
 .; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E  
 Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.  
 Nature 390, 364-370, 1997  
 A:Authors: Overbeek, T.; Cotton, M.D.; Spriggs, T.; Artach, P.; Kaine, B.P.; Sykes,  
 Smith, H.O.; Woese, C.R.; Venturi, J.C.  
 A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing arch  
 A:Reference number: A69450; MUID:98049343; PMID:9389475  
 A:Accession: F69462  
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-208 <RLF>  
 A:Cross-references: GB:AE000986; GB:AE000782; NID:92689309; PIDN:AB89558.1; PID:9264  
 C:Superfamily: Methanobacterium thermocautotrophicum conserved hypothetical protein MT

Query Match 91.4%; Score 32; DB 1; Length 208;  
 Best Local Similarity 83.3%; Pred. No. 41;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDFSMTL 6

DB 155 LDFAWL 160

## RESULT 12

T04971

hypothetical protein T16L1.30 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C&gt;Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 04-Mar-2000

C:Accession: T04971

A:Bevan, M.; Obermaier, B.; Deutschenhaur, S.; Piravandi, E.; Hohetsel, J.; Mewes, H.W.; submitted to the Protein Sequence Database, November 1998

A:Reference number: 215393

A:Accession: T04971

A:Molecule type: DNA

A:Residues: 1-371 &lt;BEV&gt;

A:Cross-references: EMBL:AL031394

A:Experimental source: cultivar Columbia; BAC clone T16L1

C:Genetics:

A:Map position: 4

A:introns: 69/1; 83/3; 123/3; 176/2; 201/2; 224/3; 275/3; 312/1; 333/1

A:Note: T16L1.30

C:Superfamily: Arabidopsis thaliana hypothetical protein T16L1.30

Query Match 91.4%; Score 32; DB 2; Length 371;  
Best Local Similarity 83.3%; Pred. No. 77;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDFSWL 6  
DB 325 LDFAWL 330

## RESULT 13

F83328

probable sodium/alanine symporter PA2533 [imported] - Pseudomonas aeruginosa (strain PAO)

C:Species: Pseudomonas aeruginosa

C&gt;Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 31-Dec-2000

C:Accession: F83328

R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Br

adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lartig, K.; Lam,

; Lory, S.; Olson, M.V.

A:Reference number: 959-964, 2000

A:Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic patho

A:Accession: F83328

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-449 &lt;STO&gt;

A:Cross-references: GB:AE004681; GB:AE004091; NID:99948587; PIDN:AA05921.1; GSPDB:GN001

A:Experimental source: strain PAO1

C:Genetics:

A:Gene: PA2533

C:Superfamily: sodium-dependent D-alanine/glycine transport protein

Query Match 91.4%; Score 32; DB 2; Length 449;  
Best Local Similarity 83.3%; Pred. No. 94;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDFSWL 6  
DB 407 LDFAWL 412

## RESULT 14

E95850

probable amino acid carrier protein [imported] - Sinorhizobium meliloti (strain 1021) me

C:Species: Sinorhizobium meliloti

C&gt;Date: 24-Aug-2001 #sequence\_revision 24-Aug-2001 #text\_change 30-Sep-2001

C:Accession: E95850

R:Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernan

Proc. Natl. Acad. Sci. U.S.A. 98: 9889-9894, 2001

A:Title: The complete sequence of the 1,683-kb psymb megaplasmid from the N2-fixing endo

A:Reference number: A95842; MUID:21396508; PMID:11481431

A:Accession: E95850

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-467 &lt;KUR&gt;

A:Cross-references: GB:AL591985; PIDN:CAC48469.1; PID:915139941; GSPDB:GN00167

A:Experimental source: strain 1021, megaplasmid psymb

R:Gallbert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubl

pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.

L.; Hyman, R.W.; Jones, T.

Science 293, 668-672, 2001

A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelau

heault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh,

A:Title: The composite genome of the legume symbiont Sinorhizobium meliloti.

A:Reference number: A96039; MUID:21368234; PMID:11474104

A:Contents: annotation

C:Genetics:

A:Gene: SMD20069

A:Genome: plasmid

C:Superfamily: sodium-dependent D-alanine/glycine transport protein

Query Match 91.4%; Score 32; DB 2; Length 467;  
Best Local Similarity 83.3%; Pred. No. 98;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDFSWL 6  
DB 407 LDFAWL 412

## RESULT 15

G95953

probable membrane-anchored protein [imported] - Sinorhizobium meliloti (strain 1021)

C:Species: Sinorhizobium meliloti

C&gt;Date: 24-Aug-2001 #sequence\_revision 24-Aug-2001 #text\_change 30-Sep-2001

C:Accession: G95953

R:Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Her

proc. Natl. Acad. Sci. U.S.A. 98: 9889-9894, 2001

A:Title: The complete sequence of the 1,683-kb psymb megaplasmid from the N2-fixing e

A:Reference number: A95842; MUID:21396508; PMID:11481431

A:Accession: G95953

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-450 &lt;KUR&gt;

A:Cross-references: GB:AL591985; PIDN:CAC49295.1; PID:915140781; GSPDB:GN00167

A:Experimental source: strain 1021, megaplasmid psymb

R:Gallbert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubl

pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.

L.; Hyman, R.W.; Jones, T.

Science 293, 668-672, 2001

A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelau

heault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh,

A:Title: The composite genome of the legume symbiont Sinorhizobium meliloti.

A:Reference number: A96039; MUID:21368234; PMID:11474104

A:Contents: annotation

C:Genetics:

A:Gene: exp1; SMD21319

A:Genome: plasmid

Query Match 91.4%; Score 32; DB 2; Length 490;  
Best Local Similarity 83.3%; Pred. No. 1e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDFSWL 6  
DB 466 VDFSWL 471

Search completed: May 30, 2003, 14:52:53

Job time : 7.5921 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 30, 2003, 14:41:40 ; Search time 3.11842 Seconds  
(without alignments)  
79.803 Million cell updates/sec

Title: US-09-643-260-11  
Perfect score: 35  
Sequence: 1 LDFSML 6

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues  
Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 08  
Maximum Match 1008  
Listing first 45 summaries

Database : SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	35	100.0	313	1	IRF1_CHICK
2	33	94.3	868	1	N180_YEAST
3	31	88.6	121	1	YGBA_YEAST
4	31	88.6	224	1	PDXH_MYCTU
5	31	88.6	229	1	BCL2_BOVIN
6	31	88.6	236	1	BCL2_CRILLO
7	31	88.6	236	1	BCL2_MOUSE
8	31	88.6	236	1	BCL2_RAT
9	31	88.6	239	1	BCL2_HUMAN
10	31	88.6	444	1	GLGA_DEIRA
11	31	88.6	495	1	SYC_AQUAE
12	31	88.6	612	1	YNB8_YEAST
13	31	88.6	612	1	YNB8_YEAST
14	31	88.6	678	1	VID3_AGRHR
15	31	88.6	1343	1	VGR2_RAT
16	30	85.7	438	1	ELBL_ADECT
17	30	85.7	745	1	IKRA_HUMAN
18	30	85.7	745	1	IKRA_MOUSE
19	30	85.7	756	1	IKRB_HUMAN
20	30	85.7	757	1	IKRB_MOUSE
21	30	85.7	757	1	IKRB_RAT
22	29	82.9	926	1	MAV3_SCHCO
23	29	82.9	233	1	BCL2_CHICK
24	29	82.9	304	1	YGT8_PSEAE
25	29	82.9	308	1	CITR_BACSO
26	29	82.9	328	1	YCDB_ECOLI
27	29	82.9	362	1	SIAG_HUMAN
28	29	82.9	401	1	HIS2_STNY3
29	29	82.9	404	1	ADMR_HUMAN
30	29	82.9	477	1	GLGA_ECOLI
31	29	82.9	477	1	GLGA_SALTY
32	29	82.9	477	1	GLGA_SALTY
33	29	82.9	494	1	DPOK_HUMAN

34	29	82.9	506	1	TDT_CHICK	P36195 gallus gall
35	29	82.9	518	1	TDT_MONDO	O02789 monodelphis
36	29	82.9	522	1	CPFA_RAT	P51669 rattus norv
37	29	82.9	529	1	TIMK_ECOLI	P08957 escherichia
38	29	82.9	529	1	TIMK_ECOLI	P07989 salmonella
39	29	82.9	529	1	TIMK_ECOLI	P40813 salmonella
40	29	82.9	530	1	TDM_MOUSE	P09838 mus musculu
41	29	82.9	561	1	Y423_MYCPN	P47662 mycoplasma
42	29	82.9	561	1	Y423_MYCPN	P75174 mycoplasma
43	29	82.9	630	1	Y242_MYCPN	P47484 mycoplasma
44	29	82.9	719	1	IF39_TOBAC	P56821 nicotiana t
45	29	82.9	3093	1	POL6_BSTVI	O65730 b genome po

## ALIGNMENTS

RESULT 1  
ID IRF1\_CHICK STANDARD; PRT; 313 AA.

AC 090876;  
DT 01-NOV-1997--(Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DE 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Interferon regulatory factor 1 (IRF-1).  
GN IRF1.  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
OC Gallus.  
OX NCBI\_TaxID=9031;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=95241453; PubMed=7536924;

RA Jungfirth C., Rebert M., Ozato K., Degen H.J., Schultz U.,  
RA David I.B.,  
RT Chicken Interferon consensus sequence-binding protein (ICSBP) and  
RT Interferon regulatory factor (IRF) 1 genes reveal evolutionary  
RT conservation in the IRF gene family."

RL Proc. Natl. Acad. Sci. U.S.A. 92:3105-3109(1995).  
--1- FUNCTION: SPECIFICALLY BINDS TO THE UPSTREAM REGULATORY REGION OF  
TYPE I IFN AND IFN-INDUCIBLE MHC CLASS I GENES (THE INTERFERON  
CONSSENSUS SEQUENCE (ICS)) AND ACTIVATES THOSE GENES (BY  
SIMILARITY).

--1- SUBCELLULAR LOCATION: Nuclear.  
--1- SIMILARITY: BELONGS TO THE IRF FAMILY.  
--1- SIMILARITY: BELONGS TO THE IRF FAMILY.

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DR EMBL: L39766; AAA62160.1; --  
DR HSSP: P15314; 11F1.  
DR InterPro: IPR001346; IRF.  
DR Pfam: PF00605; IRF.1.  
DR PRINTS: PR00267; INTERFERON.  
DR PRODOM: PD002355; IRF.1.  
DR SMART: SM00348; IRF.1.  
DR PROSITE: PS00601; IRF.1.  
DR Transcription regulation; DNA-binding; Activator; Nuclear protein.  
FT DNA BIND 7 109 TRYPDOPHAN PENTAD REPEAT.  
SQ SEQUENCE 313 AA; 36009 MW; 0895FA3736FA7463 CRC64;

Query Match 100.0%; Score 35; DB 1; Length 313;  
Best Local Similarity 100.0%; Pred. No. 8.9;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDFSML 6  
||||||

DB 295 LDFSWL 300

RESULT 2  
 NI80\_YEAST STANDARD; PRT; 868 AA.

AC P33420; 008917; 28. Created)  
 DT 01-FEB-1994 (Rel. 35, Last sequence update)  
 DT 01-NOV-1997 (Rel. 41, Last annotation update)  
 DE NIP80 protein (NIP100 protein).  
 GN NIP80 OR NIP100 OR YPL174C.  
 OS Saccharomyces cerevisiae (Baker's yeast).  
 CC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 CC Saccharomycetales; Saccharomycetaceae; Saccharomyces.  
 NCBI\_TaxID=4932;  
 [1]  
 RP SEQUENCE FROM N.A.  
 RA Schlenstedt G., Silver P.A.;  
 RL Submitted (May-1993) to the EMBL/GenBank/DBJ databases.  
 [2]  
 RP REVISIONS.  
 RA Silver P.A.;  
 RL Submitted (Apr-1997) to the EMBL/GenBank/DBJ databases.  
 [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=5288c / AB972;  
 RX MEDLINE=9731371; PubMed=9169875;  
 RA Bussey H., Storms R.K., Ahmed A., Albermann K., Allen E., Ansoorge W.,  
 RA Aranjio R., Aparicio A., Bartrell B.G., Badcock K., Benes V.,  
 RA Borstein D., Bowman S., Bruckner M., Carpenter J., Cherry J.M.,  
 RA Chung E., Churcher C.M., Coster F., Davis K., Davis R.W.,  
 RA Dierich F.S., Dells H., Dipalo T., Dubois E., Duesterhoeft A.,  
 RA Duncan M., Floeth M., Forlin N., Friesen J.D., Fritz C., Goffeau A.,  
 RA Hall J., Hebling U., Heumann K., Hilbert H., Hillier L.,  
 RA Hunick-Smith S., Hyman R., Johnston M., Kaiman S., Kiehn K.,  
 RA Komp C., Kurd O., Lashkari D., Lew H., Lin A., Lin D., Louis E.J.,  
 RA Marathe R., Messenguy F., Mewes H.-W., Mitterpat S., Moestl D.,  
 RA Mueller-Auer S., Namath A., Nentwich U., Oetner P., Pearson D.,  
 RA Peter F.X., Pohl T.M., Purnelle D., Schaefer M., Scharle W.,  
 RA Scherens B., Schramm S., Schroeder M., Sidcu A.M., Tetteil H.,  
 RA Urestrazu L.A., Ushinsky S., Vierendeels F., Visiers S., Voss H.,  
 RA Walsh S.V., Wambutt R., Wang Y., Wedder E., Wedler H., Winnett E.,  
 RA Zhong M.W., Zolner A., Vo D.H., Hanl J.;  
 RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome XVI.";  
 RL Nature 387:103-105(1997).  
 CC -1 SIMILARITY: CONTAINS 1 CAP-GLY DOMAIN.

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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

EMBL: X72227; CA51030.1; -  
 EMBL: Z73530; CA97881.1; -  
 DR PIR: S34343; S34343.  
 DR SGD: S0006095; NIP100.  
 DR InterPro: IPR000938; CAP-GLY.  
 DR Pfam: PF01302; CAP-GLY\_1.  
 DR PROSITE: PS00845; CAP-GLY\_1.  
 DR PROSITE: PS50245; CAP-GLY\_2; 1.  
 KW Cytoskeleton; Coiled coil.  
 FT DOMAIN 34 84 CAP-GLY.  
 FT DOMAIN 101 175 COILED COIL (POTENTIAL).  
 FT DOMAIN 207 375 COILED COIL (POTENTIAL).  
 FT DOMAIN 645 776 COILED COIL (POTENTIAL).  
 SO SEQUENCE 868 AA; 100289 MW; A72EA9E938845081 CRC64;

Query Match 94.3%; Score 33; DB 1; Length 868;  
 Best Local Similarity 83.3%; Pred. No. 62;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDFSWL 6  
 :|||||  
 Db 782 LDFSWL 787

RESULT 3  
 YGPD\_YEAST STANDARD; PRT; 121 AA.

AC P53186;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DE Hypothetical 13.6 kDa protein in MIG1-AGA2 intergenic region.  
 GN YG1034C.  
 OS Saccharomyces cerevisiae (Baker's yeast).  
 CC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 CC Saccharomycetales; Saccharomycetaceae; Saccharomyces.  
 NCBI\_TaxID=4932;  
 [1]  
 RP SEQUENCE FROM N.A.  
 RA Hebling U., Hofmann B., Dells H.;  
 RL Submitted (May-1996) to the EMBL/GenBank/DBJ databases.  
 [2]  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

EMBL: Z72556; CA96735.1; -  
 DR SGD: S0003002; YG1034C.  
 KW Hypothetical protein; ATP-binding.  
 FT NP\_BIND 77 84  
 SO SEQUENCE 121 AA; 13573 MW; 88D46FF50B6700F CRC64;

QY 1 LDFSWL 6  
 :|||||  
 Db 40 LDFSWL 45

Query Match 88.6%; Score 31; DB 1; Length 121;  
 Best Local Similarity 83.3%; Pred. No. 20;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RESULT 4  
 PDHX\_MYCTU STANDARD; PRT; 224 AA.

AC 006207;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DE 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Pyridoxamine 5'-phosphate oxidase (EC 1.4.3.5) (PMP/PMP oxidase)  
 DE (PMPox).  
 GN PDHX OR RV2607 OR MT2682 OR MYCTY1A10.26C.  
 OS Mycobacterium tuberculosis.  
 CC Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;  
 CC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.  
 NCBI\_TaxID=1773;  
 [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=H37RV;  
 RX MEDLINE=98295987; PubMed=9634230;  
 RA Cole S.T., Brosch R., Parkhill J., Garner T., Churcher C., Harris D.,  
 RA Gordon S.V., Eigmeier K., Gas S., Barry C.E. III, Tekala F.,  
 RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,  
 RA Davies R., Devlin K., Fellwell T., Gentles S., Hamlin N., Holroyd S.,  
 RA Hornsby T., Jagers K., Krogh A., McLean J., Moule S., Murphy L.,  
 RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,  
 Rutter S., Seeger K., Skelton S., Squares S., Squares R.,

RA Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;  
 RT "Deciphering the biology of Mycobacterium tuberculosis from the  
 RT complete genome sequence."  
 RL Nature 393:537-544(1998).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-CDG 1551 / Oshkosh;  
 RA Flatschmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,  
 RA Peterson J., DeBoy R., Dodson R., Gwin M.L., Haft D., Hickey E.,  
 RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,  
 RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,  
 RA Bishai W.;  
 RT Whole genome comparison of Mycobacterium tuberculosis clinical and  
 RT laboratory strains."  
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.  
 CC -1 FUNCTION: OXIDIZE PNP AND PNP INTO PYRIDOXAL 5'-PHOSPHATE (PLP)  
 CC (BY SIMILARITY).  
 CC -1 CATALYTIC ACTIVITY: Pyridoxamine 5'-phosphate + H(2)O + O(2) =  
 CC Pyridoxal 5'-phosphate + NH(3) + H(2)O(2).  
 CC -1 COFACTOR: FMN (BY SIMILARITY).  
 CC -1 PATHWAY: De novo synthesis of pyridoxine (vitamin B6) and  
 CC pyridoxal phosphate.  
 CC -1 SIMILARITY: BELONGS TO THE PYRIDOXAMINE 5'-PHOSPHATE OXIDASE  
 CC FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL: 295387; CAB08613.1; -  
 DR EMBL: AEO07101; AAK46998.1; -  
 DR HSSP: P28225; LDNL.  
 DR TIGR: MT2682; -  
 DR Tuberculist: RV2607; -  
 DR InterPro: IPR000659; Pyridox\_oxidase.  
 DR Pfam: PF01243; Pyridox\_oxidase; 1.  
 DR PRODOM: PD006312; Pyridox\_oxidase; 1.  
 DR TIGRFAMs: TIGR00558; pdxH; 1.  
 DR PROSITE: PS01064; PYRIDOX\_OXIDASE; 1.  
 DR Pyridoxine biosynthesis; Oxidoreductase; Flavoprotein; FMN;  
 DR Complete proteome.  
 KW SEQUENCE 224 AA; 25186 MW; 66ABCD0AAACE90DC1 CRC64;  
 SQ

Query Match 88.6%; Score 31; DB 1; Length 224;  
 Best Local Similarity 83.3%; Pred. No. 37;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDFSWL 6  
 11111  
 Db 32 LDFDML 37

RESULT 5  
 BCL2\_BOVIN STANDARD; PRT; 229 AA.  
 AC 002718;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Apoptosis regulator Bcl-2.  
 GN BCL2.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_Taxid=9913;  
 RP [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-Holstein; TISSUE-thymus;

RA Reyes R.A., Cockerell G.L.;  
 RT "Bovine leukemia virus associated-leukemogenesis is correlated  
 RT with suppression of programmed cell death and increased expression  
 RT of Bcl-2".  
 RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.  
 CC -1 FUNCTION: Suppresses apoptosis in a variety of cell systems  
 CC including factor-dependent lymphohematopoietic and neural cells.  
 CC Regulates cell death by controlling the mitochondrial membrane  
 CC permeability. Appears to function in a feedback loop system with  
 CC caspases. Inhibits caspase activity either by preventing the  
 CC release of cytochrome c from the mitochondria and/or by binding to  
 CC the apoptosis-activating factor (Apaf-1) (By similarity).  
 CC -1 SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK and  
 CC Bcl-x(L). Heterodimerization with BAX requires intact BH1 and BH2  
 CC domains, and is necessary for anti-apoptotic activity (By  
 CC similarity). Also interacts with Apaf-1 and RAf-1 (By similarity).  
 CC -1 SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular  
 CC membrane of the nuclear envelope and the endoplasmic reticulum (By  
 CC similarity).  
 CC -1 DOMAIN: The BH4 domain is required for anti-apoptotic activity and  
 CC for interaction with RAf-1 (By similarity).  
 CC -1 PTM: Phosphorylation/dephosphorylation on Ser-70 regulates Bcl2  
 CC anti-apoptotic activity. Growth factor-stimulated phosphorylation  
 CC on Ser-70 by PKC is required for the cell cycle (By similarity). In  
 CC occurs during the G2/M phase of the cell cycle (By similarity). In  
 CC the absence of growth factors, Bcl2 appears to be phosphorylated  
 CC by other protein kinases such as ERKs and stress-activated  
 CC kinases. Dephosphorylated by protein phosphatase 2A (PP2A) (By  
 CC similarity).  
 CC -1 PTM: Proteolytically cleaved by caspases during apoptosis. The  
 CC cleaved protein, lacking the BH4 domain, has pro-apoptotic  
 CC activity, causes the release of cytochrome c into the cytosol  
 CC promoting further caspase activity (By similarity).  
 CC -1 SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.  
 CC -1 SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.  
 CC -1 SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 3 (BH3) DOMAIN.  
 CC -1 SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 4 (BH4) DOMAIN.  
 CC -1 SIMILARITY: BELONGS TO THE BCL-2 FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL: U92434; AAB53319.1; -  
 DR HSSP: Q07817; IMAZ.  
 DR InterPro: IPR002475; BCL2\_family.  
 DR InterPro: IPR000712; BCL2\_BH.  
 DR InterPro: IPR003093; BCL2\_BH4.  
 DR InterPro: IPR004725; BCL2\_reg.  
 DR Pfam: PF00452; Bcl-2; 1.  
 DR Pfam: PF02180; BH4; 1.  
 DR SMART: SM00337; BCL; 1.  
 DR SMART: SM00265; BH4; 1.  
 DR TIGRFAMs: TIGR00865; bcl-2; 1.  
 DR PROSITE: PS50062; BCL2\_FAMILY; 1.  
 DR PROSITE: PS01080; BH1; 1.  
 DR PROSITE: PS01258; BH2; 1.  
 DR PROSITE: PS01259; BH3; 1.  
 DR PROSITE: PS01260; BH4\_1; 1.  
 DR PROSITE: PS50063; BH4\_2; 1.  
 KW Apoptosis; Transmembrane; Mitochondrion; Phosphorylation.  
 FT DOMAIN 10..30 BH4.  
 FT DOMAIN 64..68 POLY-PRO.  
 FT DOMAIN 69..72 POLY-ALA.  
 FT DOMAIN 83..97 BH3.  
 FT DOMAIN 126..145 BH1.  
 FT DOMAIN 177..192 BH2.  
 FT TRANSMEM 202..223 POTENTIAL.  
 FT SITE 34..35 CLEAVAGE (BY CASPASES) (BY SIMILARITY).  
 FT SITE

FT MOD\_RES 63 63 PHOSPHORYLATION (BY PKC) (BY SIMILARITY).  
 SQ SEQUENCE 229 AA; 25099 MW; ADDDDMF98FFFLID CRC64;  
 Query Match 88.6%; Score 31; DB 1; Length 229;  
 Best Local Similarity 100.0%; Pred. No. 38;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 DFWL 6  
 DB 201 DFWL 205  
 RESULT 6  
 BCL2\_CR10  
 ID BCL2\_CR10 STANDARD; PRT; 236 AA.  
 AC Q9JTV8;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Apoptosis regulator Bcl-2.  
 GN BCL2.  
 OS Cricetus longicaudatus (Long-tailed hamster) (Chinese hamster).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;  
 OC Cricetus;  
 OC NCBI\_Taxid=10030;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-Ovary;  
 RX MEDLINE=20431763; PubMed=10973819;  
 RA Tomicic M.T., Christmann M., Kaina B.;  
 RT "Cloning and functional analysis of cDNA encoding the hamster Bcl-2 protein".  
 RL Blochem. Biophys. Res. Commun. 275:899-903(2000).  
 RN [2]  
 RP SEQUENCE FROM N.A., AND CLEAVAGE BY CASPASES.  
 RX MEDLINE=21092839; PubMed=11181062;  
 RA Tomicic M.T., Kaina B.;  
 RT "Hamster Bcl-2 protein is cleaved in vitro and in cells by caspase-9 and caspase-3".  
 RL Blochem. Biophys. Res. Commun. 281:404-408(2001).  
 CC -1 FUNCTION: Suppresses apoptosis in a variety of cell systems including factor-dependent lymphohematopoietic and neural cells. Regulates cell death by controlling the mitochondrial membrane permeability. Appears to function in a feedback loop system with caspases. Inhibits caspase activity either by preventing the release of cytochrome c from the mitochondria and/or by binding to the apoptosis-activating factor (APAF-1) (By similarity).  
 CC -1 SUBUNIT: Forms homodimers, and heterodimers with BAX, BAK, and BH2 domains, and is necessary for anti-apoptotic activity (By similarity).  
 CC -1 SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular membrane of the nuclear envelope and the endoplasmic reticulum.  
 CC -1 DOMAIN: The BH4 domain is required for anti-apoptotic activity and for interaction with RAF-1 (By similarity).  
 CC -1 PTM: Phosphorylation/dephosphorylation on Ser-70 regulates Bcl2 anti-apoptotic activity. Growth factor-stimulated phosphorylation on Ser-70 by PKC is required for the anti-apoptotic activity and occurs during the G2/M phase of the cell cycle (By similarity). In the absence of growth factors, Bcl2 appears to be phosphorylated by other protein kinases such as ERKs and stress-activated kinases (By similarity). Dephosphorylated by protein phosphatase 2A (PP2A) (By similarity).  
 CC -1 PTM: Proteolytically cleaved by caspases during apoptosis. The cleaved protein, lacking the BH4 domain, has pro-apoptotic activity, causes the release of cytochrome c into the cytosol promoting further caspase activity.  
 CC -1 SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.  
 CC -1 SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.  
 CC -1 SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 3 (BH3) DOMAIN.  
 CC -1 SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 4 (BH4) DOMAIN.  
 CC -1 SIMILARITY: BELONGS TO THE BCL-2 FAMILY.

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 CC -----  
 DR EMBL: AJ271720; CAB92245.1; -  
 DR HSP: 007817; 1MA2.  
 DR InterPro: IPR002475; BCL2\_family.  
 DR InterPro: IPR000712; Bcl2\_BH.  
 DR InterPro: IPR003093; Bcl2\_BH4.  
 DR InterPro: IPR004725; Bcl2\_reg.  
 DR Pfam: PF00452; Bcl-2; 1.  
 DR Pfam: PF02180; BH4; 1.  
 DR SMART: SM00337; BCL; 1.  
 DR SMART: SM0265; BH4; 1.  
 DR TIGR: TIGR00865; bcl-2; 1.  
 DR PROSITE: PS50062; BCL2\_FAMILY; 1.  
 DR PROSITE: PS01080; BH1; 1.  
 DR PROSITE: PS01258; BH2; 1.  
 DR PROSITE: PS01259; BH3; 1.  
 DR PROSITE: PS01260; BH4; 1.  
 DR PROSITE: PS50063; BH4\_2; 1.  
 KW Apoptosis; Transmembrane; Mitochondrion; Phosphorylation.  
 FT DOMAIN 10 30 BH4.  
 FT DOMAIN 90 104 BH3.  
 FT DOMAIN 133 152 BH1.  
 FT DOMAIN 184 199 BH2.  
 FT TRANSMEM 209 230 POTENTIAL.  
 FT SITE 64 65 CLEAVAGE (BY CASPASE-3 AND CASPASE-9).  
 FT MOD\_RES 70 70 PHOSPHORYLATION (BY PKC) (BY SIMILARITY).  
 SQ SEQUENCE 236 AA; 26491 MW; BECADFLEF337228 CRC64;  
 Query Match 88.6%; Score 31; DB 1; Length 236;  
 Best Local Similarity 100.0%; Pred. No. 39;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 DFWL 6  
 DB 208 DFWL 212  
 RESULT 7  
 BCL2\_MOUSE  
 ID BCL2\_MOUSE STANDARD; PRT; 236 AA.  
 AC P10417; P10418;  
 DT 01-MAR-1989 (Rel. 10, Created)  
 DT 01-APR-1993 (Rel. 25, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Apoptosis regulator Bcl-2.  
 GN BCL2 OR BCL-2.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 OC NCBI\_Taxid=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).  
 RC STRAIN-BALB/c; TISSUE-Liver;  
 RX MEDLINE=87187643; PubMed=3032455;  
 RA Negishi M., Sillini E., Kozak C., Tsujimoto Y., Croce C.M.;  
 RT "Molecular analysis of mbcl-2: structure and expression of the murine gene homologous to the human gene involved in follicular lymphoma".  
 RL Cell 49:455-463(1987).  
 RN [2]  
 RP REVISIONS TO 221-222.  
 RX MEDLINE=92375724; PubMed=1508712;  
 RA Eguichi Y., Ewert D.L., Tsujimoto Y.;  
 RT "Isolation and characterization of the chicken bcl-2 gene: expression in a variety of tissues including lymphoid and neuronal organs in adult and embryo.";

RL Nucleic Acids Res. 20:4187-4192(1992).

RN [3] PHOSPHORYLATION BY PKC, AND MUTAGENESIS OF SERINE RESIDUES.

RP MEDLINE-97277291; PubMed-9115213.

RX Ito T., Deng X., Carr B., May W.S. Jr.:

RA "Bcl-2 phosphorylation required for anti-apoptosis function."

RT J. Biol. Chem. 272:11671-11673(1997).

RL [4] DEPHOSPHORYLATION BY PP2A.

RP MEDLINE-99069407; PubMed-9852076;

RX Deng X., Ito T., Carr B., Mumby M., May W.S. Jr.:

RA "Reversible phosphorylation of Bcl2 following interleukin 3 or

RT bryostatin 1 is mediated by direct interaction with protein

RT phosphatase 2A".

RL J. Biol. Chem. 273:34157-34163(1998).

CC -1- FUNCTION: Suppresses apoptosis in a variety of cell systems

CC including factor-dependent lymphohematopoietic and neural cells.

CC Regulates cell death by controlling the mitochondrial membrane

CC permeability. Appears to function in a feedback loop system with

CC caspases. Inhibits caspase activity either by preventing the

CC release of cytochrome c from the mitochondria and/or by binding to

CC the apoptosis-activating factor (APAF-1).

CC -1- SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK and

CC Bcl-x(L). Heterodimerization with BAX requires intact BH1 and BH2

CC domains, and is necessary for anti-apoptotic activity (By

CC similarity). Also interacts with APAF-1 and Raf-1.

CC -1- SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular

CC membrane of the nuclear envelope and the endoplasmic reticulum.

CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; alpha (shown here) and beta;

CC are produced by alternative splicing.

CC -1- TISSUE SPECIFICITY: Expressed in a variety of tissues.

CC -1- DOMAIN: The BH4 domain is required for anti-apoptotic activity and

CC for interaction with Raf-1.

CC -1- PTM: Phosphorylation/dephosphorylation on Ser-70 regulates Bcl2

CC anti-apoptotic activity. Growth factor-stimulated phosphorylation

CC on Ser-70 by PKC is required for the anti-apoptosis activity and

CC occurs during the G2/M phase of the cell cycle. In the absence of

CC growth factors, Bcl2 appears to be phosphorylated by other protein

CC kinases such as ERKs and stress-activated kinases.

CC Dephosphorylated by protein phosphatase 2A (PP2A).

CC -1- PTM: Proteolytically cleaved by caspases during apoptosis. The

CC cleaved protein, lacking the BH4 domain, has pro-apoptotic

CC activity, causes the release of cytochrome c into the cytosol

CC promoting further caspase activity.

CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.

CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.

CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 3 (BH3) DOMAIN.

CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 4 (BH4) DOMAIN.

CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.

CC -----

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CC -----

DR EMBL: L31532; AAA37282.1; -

DR EMBL: M15506; AAA37282.1; JOINED.

DR EMBL: M15506; AAA37281.1; -

DR PIR: A25960; TVMSA1.

DR PIR: B25960; TVMSB1.

DR PIR: E37332; E37332.

DR HSSP: Q07817; IMAZ.

DR MGD: MGI:88138; Bcl2.

DR InterPro: IPR002475; BCL2\_family.

DR InterPro: IPR000712; Bcl2\_BH.

DR InterPro: IPR003093; Bcl2\_BH4.

DR InterPro: IPR004725; Bcl2\_reg.

DR Pfam: PF00452; Bcl-2; 1.

DR Pfam: PF02180; BH4; 1.

DR SMART: SM00337; BCL\_1.

DR SMART: SM00265; BH4; 1.

DR TIGRfam: TIGR00865; bcl-2; 1.

DR PROSITE: PSS0062; BCL2\_FAMILY; 1.

DR PROSITE: PS01080; BH1; 1.

DR PROSITE: PS01258; BH2; 1.

DR PROSITE: PS01259; BH3; 1.

DR PROSITE: PS01260; BH4\_1; 1.

DR PROSITE: PS01260; BH4\_2; 1.

DR Apoptosis; Alternative splicing; Transmembrane; Mitochondrion;

KW Phosphorylation.

FT DOMAIN 10 30 BH4.

FT DOMAIN 90 104 BH3.

FT DOMAIN 133 152 BH1.

FT DOMAIN 184 199 BH2.

FT TRANSMEM 209 230 POTENTIAL.

FT SITE 34 35 CLEAVAGE (BY CASPASES) (BY SIMILARITY).

FT MOD\_RES 70 70 PHOSPHORYLATION (BY PKC).

FT VARSPIC 193 236 DAVEILGPRPRLEFDEISLSTLSTLALVGACTIGAVL

FT SEQUENCE 236 AA; 26425 MW; AA85EFB0766BE0A CRC64;

FT GHR -> VGACTIVE (IN ISOFORM BETA).

QY 2 DFSML 6 88.6%; Score 31; DB 1; Length 236;

Db 208 DFSML 212 Best Local Similarity 100.0%; Pred. No. 39;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 8

BCL2\_RAT STANDARD; PRT; 236 AA.

AC P49950; Q62837; Q64032;

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Apoptosis regulator Bcl-2.

GN BCL2 OR BCL-2.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Rattus.

OX NCBI\_TaxID=10116;

RN [1] SEQUENCE FROM N.A.

RP TISSUE-Brain;

RC MEDLINE-94193015; PubMed-8144041;

RA Sato T., Irie S., Krajewski S., Reed J.C.;

RT Cloning and sequencing of a cDNA encoding the rat Bcl-2 protein.;

RL Gene 140:291-292(1994).

RN [2] SEQUENCE FROM N.A.

RP STRAIN-Sprague-Dawley; TISSUE-Ovary;

RC MEDLINE-95129487; PubMed-7828536;

RA Tilly J.U., Tilly K.I., Kenton M.L., Johnson A.L.;

RT "Expression of members of the bcl-2 gene family in the immature rat

RT ovary: equine chorionic gonadotropin-mediated inhibition of granulosa

RT cell apoptosis is associated with decreased bax and constitutive

RT bcl-2 and bcl-xlong messenger ribonucleic acid levels.";

RL Endocrinology 136:232-241(1995).

RN [3] SEQUENCE OF 19-172 FROM N.A.

RP MEDLINE-95059917; PubMed-7969891;

RA Castrén E., Ohga Y., Berezaghi M.P., Tzimagiorgis G., Thoenen H.,

RA Lindholm D.;

RT "bcl-2 messenger RNA is localized in neurons of the developing and

RT adult rat brain.";

RL Neuroscience 61:165-177(1994).

CC -1- FUNCTION: Suppresses apoptosis in a variety of cell systems

CC including factor-dependent lymphohematopoietic and neural cells.

CC Regulates cell death by controlling the mitochondrial membrane

CC permeability. Appears to function in a feedback loop system with

CC caspases. Inhibits caspase activity either by preventing the

CC release of cytochrome c from the mitochondria and/or by binding to  
 CC the apoptosis-activating factor (APAF-1).  
 CC -1- SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK and  
 CC Bcl-x(l). Heterodimerization with BAX requires intact BH1 and BH2  
 CC domains, and is necessary for anti-apoptotic activity (By  
 CC similarity). Also interacts with APAF-1 and RAf-1 (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular  
 CC membrane of the nuclear envelope and the endoplasmic reticulum.  
 CC -1- TISSUE SPECIFICITY: Expressed in a variety of tissues, with  
 CC highest levels in reproductive tissues. In the adult brain,  
 CC expression is localized in mitral cells of the olfactory bulb,  
 CC granule and pyramidal neurons of hippocampus, pontine nuclei,  
 CC cerebellar granule neurons, and in ependymal cells. In prenatal  
 CC brain, expression is higher and localized in the neuroepithelium  
 CC and in the cortical plate.  
 CC -1- DOMAIN: The BH4 domain is required for anti-apoptotic activity and  
 CC for interaction with RAf-1 (By similarity).  
 CC -1- PTM: Phosphorylation/dephosphorylation on Ser-70 regulates Bcl2  
 CC anti-apoptotic activity. Growth factor-stimulated phosphorylation  
 CC on Ser-70 by PKC is required for the anti-apoptosis activity and  
 CC occurs during the G2/M phase of the cell cycle. In the absence of  
 CC growth factors, Bcl2 appears to be phosphorylated by other protein  
 CC kinases such as ERKs and stress-activated kinases.  
 CC -1- PTM: Phosphorylated by protein phosphatase 2A (PP2A) (By similarity).  
 CC -1- PTM: Proteolytically cleaved by caspases during apoptosis. The  
 CC cleaved protein, lacking the BH4 domain, has pro-apoptotic  
 CC activity, causes the release of cytochrome c into the cytosol  
 CC promoting further caspase activity (By similarity).  
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 3 (BH3) DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 4 (BH4) DOMAIN.  
 CC -1- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.  
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 CC -----  
 CC EMBL: L14680; AAA53662.1; -  
 CC EMBL: U34964; AA77687.1; -  
 CC HSSP: Q07817; IMAZ.  
 CC InterPro: IPR002475; BCL2\_family.  
 CC InterPro: IPR000712; Bcl2\_BH.  
 CC InterPro: IPR003093; Bcl2\_BH4.  
 CC InterPro: IPR004725; Bcl2\_Reg.  
 CC Pfam: PF00452; Bcl-2; 1.  
 CC Pfam: PF02180; BH4; 1.  
 CC SMART: SM00337; BCL; 1.  
 CC SMART: SM00265; BH4; 1.  
 CC TIGFAM: TIGR00865; bcl-2; 1.  
 CC PROSITE: PS00062; BCL2\_FAMILY; 1.  
 CC PROSITE: PS01080; BH1; 1.  
 CC PROSITE: PS01258; BH2; 1.  
 CC PROSITE: PS01259; BH3; 1.  
 CC PROSITE: PS01260; BH4; 1.  
 CC PROSITE: PS00063; BH4\_2; 1.  
 CC Apoptosis; Transmembrane; Mitochondrion; Phosphorylation.  
 CC DOMAIN 10 30 BH4.  
 CC DOMAIN 90 104 BH3.  
 CC DOMAIN 133 152 BH1.  
 CC DOMAIN 184 199 BH2.  
 CC TRANSMEM 209 230 POTENTIAL.  
 CC SITE 34 35 CLEAVAGE (BY CASPASES) (BY SIMILARITY).  
 CC MOD\_RES 70 70 PHOSPHORYLATION (BY PKC) (BY SIMILARITY).  
 CC CONFLICT 42 42 A -> R (IN REF. 2).  
 CC CONFLICT 157 157 E -> G (IN REF. 1).  
 CC CONFLICT 164 164 S -> Y (IN REF. 2).  
 CC CONFLICT 212 212 L -> Q (IN REF. 2).

SO SEQUENCE 236 AA; 26622 MW; E768CB9071A872A CRC64;  
 Query Match 88.6%; Score 31; DB 1; Length 236;  
 Best Local Similarity 100.0%; Pred. No. 39;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 DFSWL 6  
 DB 208 DFSWL 212  
 RESULT 9  
 BCL2\_HUMAN STANDARD; PRT; 239 AA.  
 ID BCL2\_HUMAN  
 AC P10415; P10416; Q16197; Q13842;  
 DT 01-MAR-1989 (Rel. 10, Created)  
 DT 01-APR-1993 (Rel. 25, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Apoptosis regulator Bcl-2.  
 GN BCL2.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORM ALPHA AND BETA).  
 RX MEDLINE=86259760; PubMed=3523487;  
 RA Tsujimoto Y., Croce C.M.;  
 RT "Analysis of the structure, transcripts, and protein products of  
 RT bcl-2, the gene involved in human follicular lymphoma.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 83:5214-5218(1986).  
 RN [2]  
 RP REVISIONS TO 96; 110 AND 237.  
 RX MEDLINE=92375724; PubMed=1508712;  
 RA Eguchi Y., Ewert D.L., Tsujimoto Y.;  
 RT "Isolation and characterization of the chicken bcl-2 gene: expression  
 RT in a variety of tissues including lymphoid and neuronal organs in  
 RT adult and embryo.";  
 RL Nucleic Acids Res. 20:4187-4192(1992).  
 RN [3]  
 RP SEQUENCE FROM N.A. (ISOFORM ALPHA).  
 RX MEDLINE=87002488; PubMed=2875799;  
 RA Cleary M.L., Smith S.D., Sklar J.;  
 RT "Cloning and structural analysis of cDNAs for bcl-2 and a hybrid bcl-  
 RT 2/immunoglobulin transcript resulting from the t(14;18)  
 RT translocation.";  
 RL Cell 47:19-28(1986).  
 RN [4]  
 RP SEQUENCE FROM N.A. (ISOFORM ALPHA).  
 RX MEDLINE=86196071; PubMed=2834197;  
 RA Seto M., Jaeger U., Hockett R.D., Granger W., Bennett S.,  
 RA Goldman P., Korsmeyer S.J.;  
 RT "Alternative promoters and exons, somatic mutation and deregulation  
 RT of the Bcl-2-Ig fusion gene in lymphoma.";  
 RL EMBO J. 7:123-131(1988).  
 RN [5]  
 RP SEQUENCE OF 1-131 FROM N.A. (ISOFORM ALPHA), AND VARIANTS NHL.  
 RX MEDLINE=92096610; PubMed=139299;  
 RA Tanaka S., Louie D.C., Kant J.A., Reed J.C.;  
 RT "Frequent incidence of somatic mutations in translocated BCL2  
 RT oncogenes of non-Hodgkin's lymphomas.";  
 RL Blood 79:229-237(1992).  
 RN [6]  
 RP SUBCELLULAR LOCATION.  
 RX MEDLINE=91066924; PubMed=2250705;  
 RA Hockenbery D., Nunez G., Millman C., Schreiber R.D., Korsmeyer S.J.;  
 RT "Bcl-2 is an inner mitochondrial membrane protein that blocks  
 RT programmed cell death.";  
 RL Nature 348:334-336(1990).  
 RN [7]  
 RP MUTAGENESIS.  
 RX MEDLINE=94239528; PubMed=8183370;  
 RA Yin X.-M., Olvera Z.N., Korsmeyer S.J.;

RT BH1 and BH2 domains of Bcl-2 are required for inhibition of  
RT apoptosis and heterodimerization with Bax.";  
RT Nature 369:321-323(1994).  
RN [8]  
RP CLEAVAGE BY CASPASES, AND MUTAGENESIS.  
RX MEDLINE-98057466; PubMed-9395403;  
RA Cheng E.H.-Y., Kirsch D.G., Clem R.J., Ravi R., Kastan M.B., Bedi A.,  
RA Dueno K., Hardwick J.M.;  
RT "Conversion of Bcl-2 to a Bax-like death effector by caspases.";  
RL Science 278:1966-1968(1997).  
RN [9]  
RP REVIEW ON PHOSPHORYLATION.  
RX MEDLINE-21260650; PubMed-11368354;  
RA Ruvoilo P.P., Deng X., May W.S.;  
RT "Phosphorylation of Bcl2 and regulation of apoptosis.";  
RL Leukemia 15:515-522(2001).  
RN [10]  
RP PHOSPHORYLATION BY ASK1/JNK1.  
RX MEDLINE-20036804; PubMed-10567572;  
RA Yamamoto K., Ichijo H., Korsmeyer S.J.;  
RT "BCL-2 is phosphorylated and inactivated by an ASK1/Jun N-terminal  
RT protein kinase pathway normally activated at G(2)/M.";  
RL Mol. Cell. Biol. 19:8469-8478(1999).  
RN [11]  
RP FUNCTION: Suppresses apoptosis in a variety of cell systems  
CC including factor-dependent lymphohematopoietic and neural cells.  
CC Regulates cell death by controlling the mitochondrial membrane  
CC permeability. Appears to function in a feedback loop system with  
CC caspases. Inhibits caspase activity either by preventing the  
CC release of cytochrome c from the mitochondria and/or by binding to  
CC the apoptosis-activating factor (APAF-1).  
CC [12]  
CC SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK and  
CC Bcl-x(L). Heterodimerization with BAX requires intact BH1 and BH2  
CC domains, and is necessary for anti-apoptotic activity (By  
CC similarity). Also interacts with APAF-1 and RAIF-1.  
CC [13]  
CC SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular  
CC membrane of the nuclear envelope and the endoplasmic reticulum.  
CC [14]  
CC ALTERNATIVE PRODUCTS: 2 isoforms, alpha (shown here) and beta;  
CC are produced by alternative splicing.  
CC [15]  
CC TISSUE SPECIFICITY: Expressed in a variety of tissues.  
CC [16]  
CC DOMAIN: The BH4 domain is required for anti-apoptotic activity and  
CC for interaction with RAIF-1.  
CC [17]  
CC PTM: Phosphorylation/dephosphorylation on Ser-70 regulates Bcl2  
CC anti-apoptotic activity. Growth factor-stimulated phosphorylation  
CC on Ser-70 by PKC is required for the anti-apoptosis activity and  
CC occurs during the G2/M phase of the cell cycle. In the absence of  
CC growth factors, Bcl2 appears to be phosphorylated by other protein  
CC kinases such as ERKs and stress-activated kinases.  
CC [18]  
CC DEPHOSPHORYLATED BY PROTEIN PHOSPHATASE 2A (PP2A) (By similarity).  
CC [19]  
CC PTM: Proteolytically cleaved by caspases during apoptosis. The  
CC cleaved protein, lacking the BH4 domain, has pro-apoptotic  
CC activity, causes the release of cytochrome c into the cytosol  
CC promoting further caspase activity.  
CC [20]  
CC DISEASE: Involved in follicular lymphoma (FL) (also known as type  
CC II chronic lymphatic leukemia) by a chromosomal translocation  
CC t(14;18)(q32;q21) which involves Bcl2 and Immunoglobulin gene  
CC regions.  
CC [21]  
CC SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 1 (BH1) DOMAIN.  
CC [22]  
CC SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 2 (BH2) DOMAIN.  
CC [23]  
CC SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 3 (BH3) DOMAIN.  
CC [24]  
CC SIMILARITY: CONTAINS 1 BCL-2 HOMOLOG 4 (BH4) DOMAIN.  
CC [25]  
CC SIMILARITY: BELONGS TO THE BCL-2 FAMILY.  
CC [26]  
CC DATABASE: NAME=Atlas Genet. Cytogenet. Oncol. Haematol.;  
CC WWW="http://www.infobiogen.fr/services/chronocancer/Genes/BCL2ID49.html".  
CC [27]  
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CC [28]  
CC EMBL: M13994; AAA51813.1; ALT\_SEQ.

DR EMBL: M13995; AAA51814.1; ALT\_SEQ.  
DR EMBL: M14745; AAA35591.1; -  
DR EMBL: X06487; CAA29778.1; -  
DR EMBL: S72602; AAD14111.1; ALT\_SEQ.  
DR PIR: A29409; TVH0BL.  
DR PIR: B29409; TVH0BL.  
DR PIR: A24428; TVH0BC.  
DR PIR: C37332; C37332.  
DR PIR: D37332; D37332.  
DR HSP: Q07817; 1MAZ.  
DR Genew: HGNC:990; BCL2.  
DR MIM: 151430; -  
DR InterPro: IPR002475; BCL2\_family.  
DR InterPro: IPR000712; Bcl2\_BH.  
DR InterPro: IPR003093; Bcl2\_BH4.  
DR InterPro: IPR004725; Bcl2\_reg.  
DR Pfam: PF00452; BCL-2; 1.  
DR Pfam: PF02180; BH4; 1.  
DR SMART: SM00337; BCL; 1.  
DR SMART: SM00265; BH4; 1.  
DR TIGRFAMs: TIGR00865; bcl-2; 1.  
DR PROSITE: PS50062; BCL2\_FAMILY; 1.  
DR PROSITE: PS01080; BH1; 1.  
DR PROSITE: PS01258; BH2; 1.  
DR PROSITE: PS01259; BH3; 1.  
DR PROSITE: PS01260; BH4; 1.  
DR PROSITE: PS50063; BH4-2; 1.  
KW Proto-oncogene: Apoptosis; Alternative splicing; Transmembrane;  
KW Mitochondrion; Phosphorylation; Chromosomal translocation;  
KW Polymorphism; Disease mutation.  
KW DOMAIN 10  
FT DOMAIN 93 107  
FT BH3 107  
FT BH1 107  
FT BH2 107  
FT TRANSMEM 212 233  
FT SITE 34 35  
FT MOD\_RES 70 70  
FT VARSPPLIC 196 239  
FT  
FT VARIANT 7 7  
FT  
FT VARIANT 59 59  
FT  
FT VARIANT 93 93  
FT  
FT MUTAGEN 34 34  
FT MUTAGEN 64 64  
FT MUTAGEN 145 145  
FT  
FT MUTAGEN 188 188  
FT  
FT CONFLICT 48 48  
FT CONFLICT 59 59  
FT CONFLICT 117 117  
FT CONFLICT 129 129  
SO SEQUENCE 239 AA; 26266 MW; 3C49P2B714DC9CB CRC64;  
Query Match 88.6%; Score 31; DB 1; Length 239;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
RESULT 10  
ID GIGA\_DEIRA STANDARD; PRT; 444 AA.  
AC G9RWS1;  
DT 15-JUN-2002 (Rel. 41, Created)

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DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE Glycogen synthase (EC 2.4.1.21) [Starch [bacterial glycogen]
DE synthase].
GN G1GA OR DR0594.
OS Deinococcus radiodurans.
OC Bacteria; Thermus/Deinococcus group; Deinococci; Deinococcales;
OC Deinococcaceae; Deinococcus.
ON NCBI_TaxID=1299;
RX STRAIN=RI.
RP SEQUENCE FROM N.A.
RC MEDLINE=20036896; PubMed=10567266;
RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
RA Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
RA Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
RA Makarova K.S., Aravind L., Lam P., McDonald L., Utterback T., Zaleski C.,
RA Kechum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
RA Fraser C.M.;
RT "Genome sequence of the radioresistant bacterium Deinococcus
RT radiodurans R1."
RL Science 286:1571-1577(1999).
CC -1- FUNCTION: Synthesizes alpha-1,4-glucan chains using ADP-glucose.
CC -1- CATALYTIC ACTIVITY: ADP-glucose + [(1,4)-alpha-D-glucosyl](N) =
CC ADP + [(1,4)-alpha-D-glucosyl](N+1).
CC -1- PATHWAY: Glycogen biosynthesis; second step.
CC -1- SIMILARITY: BELONGS TO THE BACTERIAL/PLANT GLYCOGEN SYNTHASE
CC FAMILY.
CC -----
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CC -----
DR EMBL; AE001917; AAF10170.1; ALT_INIT.
DR TIGR; DR0594; -.
DR InterPro; IPR001296; Glycos_transf_1.
DR Pfam; PF00534; Glycos_transf_1; 2.
DR Glycogen biosynthesis; Transferrase; Glycosyltransferase;
DR Complete proteome.
FT BINDING 15 ADP-GLUCOSE (BY SIMILARITY).
FT SEQUENCE 444 AA; 48457 MW; 767605781A915302 CRC64;
SQ
Query Match 88.6%; Score 31; DB 1; Length 444;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LDFSW 5
DB 426 LDFSW 430

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RX MEDLINE=98196666; PubMed=9537320;
RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
RA Graham D.E., Overbeek R., Sneed M.A., Keller M., Anjay M., Huber R.,
RA Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
RT "The complete genome of the hyperthermophilic bacterium Aquifex
RT aeolicus."
RL Nature 392:353-358(1998).
CC -1- CATALYTIC ACTIVITY: ATP + L-cysteine + tRNA(Cys) = AMP +
CC diphosphate + L-cysteinyl-tRNA(Cys).
CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
CC STRONG, TO METHIONYL-TRNA SYNTHETASE.
CC -----
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CC -----
DR EMBL; AE000721; AAC07125.1; -.
DR InterPro; IPR002308; Cys_tRNA-synt_1a.
DR InterPro; IPR001412; tRNA-synt_1.
DR Pfam; PF01406; tRNA-synt_1e; 1.
DR PRINTS; PR00983; TRNASYNTHCS.
DR TIGRfam; TIGR0435; CYS3.1.
DR PROSITE; PS00178; AA_TRNA_LIGASE_1; FALSE_NEG.
DR Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
DR Complete proteome.
FT SITE 31 "HIGH" REGION.
FT SITE 266 "KMSKS" REGION.
FT BINDING 269 ATP (BY SIMILARITY).
FT SEQUENCE 495 AA; 57135 MW; A454658B2BBAE8M4 CRC64;
SQ
Query Match 88.6%; Score 31; DB 1; Length 495;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LDFSW 5
DB 302 LDFSW 306

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RESULT 11
SYN_AQUAE STANDARD; PRT; 495 AA.
ID AC 067163;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Cysteine-tRNA synthetase (EC 6.1.1.16) (Cysteine--tRNA ligase)
DE (CYSTRS).
GN CYSS OR AO1068.
OS Aquifex aeolicus.
OC Bacteria; Aquificae; Aquificae (class); Aquificales; Aquificaceae;
OC Aquifex.
OX NCBI_TaxID=63363;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VF5;

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RESULT 12
SYN8_YEAST STANDARD; PRT; 612 AA.
ID AC P53876;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Hypothetical 69.6 kDa protein in HDAL-PUB1 intergenic region.
GN YN1018C OR N2831.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RA Andre B., Iragui Houssein I., Urtizazu L.A., Vissers S.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
DE -1- SIMILARITY: TO YEAST YN1034W.
CC -----
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CC -----
DR EMBL; Z71294; CAA95880.1; -.

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DR SGD; S0004963; YNL018C.  
 KW Hypothetical protein.  
 SQ SEQUENCE 612 AA; 69551 MW; E655B2D96317FC62 CRC64;

Query Match  
 Best Local Similarity 88.6%; Score 31; DB 1; Length 612;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 LDFSWL 6  
 DB 17 LDFOWL 22

RESULT 13  
 YND4\_YEAST STANDARD; PRT; 612 AA.  
 AC P53963;  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE Hypothetical 69.4 kDa protein in NCE3-HHT2 intergenic region.  
 GN YNL034W OR N2740.  
 OS Saccharomyces cerevisiae (Baker's Yeast).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.  
 OX NCBI\_TaxID=4932;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Duesterhoeft A., Floeth M., Fritz C., Heuss-Neitzel D.,  
 RA Hilbert H., Moestl D.;  
 RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: TO YEAST YNL018C.  
 CC -----  
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 CC -----  
 CC EMBL; Z71310; CAA95897.1; -  
 DR SGD; S0004979; YNL034W.  
 KW Hypothetical protein.  
 SQ SEQUENCE 612 AA; 69373 MW; E39B7080BDE0285 CRC64;

Query Match  
 Best Local Similarity 88.6%; Score 31; DB 1; Length 612;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 LDFSWL 6  
 DB 17 LDFOWL 22

RESULT 14  
 YND3\_AGRH STANDARD; PRT; 678 AA.  
 ID YND3\_AGRH  
 AC P13463;  
 DT 01-JAN-1990 (Rel. 13, Created)  
 DT 01-JAN-1990 (Rel. 13, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Protein YND3.  
 GN Agrobacterium rhizogenes.  
 OS Agrobacterium rhizogenes.  
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;  
 OC Rhizobiaceae; Rhizobium.  
 OX NCBI\_TaxID=359;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-A4;  
 RX MEDLINE=89039712; PubMed=3185501;

RA Hirayama T., Muranaka T., Ohkawa H., Oka A.;  
 RT "Organization and characterization of the vircD genes from  
 RT Agrobacterium rhizogenes."  
 RL Mol. Gen. Genet. 213:229-237(1988).  
 CC -----  
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 CC -----  
 CC EMBL; X12867; CAA31352.1; -  
 DR PIR; S12456; S12456.  
 KW Crown gall tumor; Plasmid.  
 SQ SEQUENCE 678 AA; 72777 MW; A5BCEBA58AC26532 CRC64;

Query Match  
 Best Local Similarity 100.0%; Score 31; DB 1; Length 678;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 DFWL 6  
 DB 418 DFWL 422

RESULT 15  
 VGR2\_RAT STANDARD; PRT; 1343 AA.  
 ID VGR2\_RAT  
 AC O08775;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Vascular endothelial growth factor receptor 2 precursor (EC 2.7.1.112)  
 DE (VGR2-2) (protein-tyrosine kinase receptor flk-1) (Fetal liver kinase  
 DE 1).  
 GN KDR OR FLK1.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Retina;  
 RA Wen Y., Edelman J.L., De Vries G.W., Sachs G.;  
 RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: RECEPTOR FOR VEGF OR VEGF-C. HAS A TYROSINE-PROTEIN  
 CC KINASE ACTIVITY. THE VEGF-KINASE LIGAND/RECEPTOR SIGNALING SYSTEM  
 CC PLAYS A KEY ROLE IN VASCULAR DEVELOPMENT AND REGULATION OF  
 CC VASCULAR PERMEABILITY (BY SIMILARITY).  
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein  
 CC tyrosine phosphate.  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- SIMILARITY: BELONGS TO THE CSF-1/PDGF RECEPTOR FAMILY OF TYROSINE-  
 CC PROTEIN KINASES.  
 CC -----  
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 CC -----  
 CC EMBL; U93306; AAB97508.1; -  
 DR EMBL; U93307; AAB97509.1; -  
 DR HSSP; P11362; IFGK.  
 DR InterPro; IPR000719; Euk\_Pkinase.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003598; Ig\_C2.  
 DR InterPro; IPR003600; Ig\_Like.  
 DR InterPro; IPR001824; RTKinaseITL.

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DR InterPro: IPR001245; Tyr_kinase.
DR Pfam: PF00047; 1g; 6.
DR Pfam: PF00069; pkinase; 1.
DR ProDom: PD000001; Euk_pkinase; 2.
DR SMART: SM00410; IG-like; 4.
DR SMART: SM00408; IGC2; 1.
DR SMART: SM00219; Tyrc; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE: PS00240; RECEPTOR_TYR_KIN_ITI; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
KW Signal: Transferase; Tyrosine-protein kinase; Receptor; Transmembrane;
KW Glycoprotein; Phosphorylation; ATP-binding; Immunoglobulin domain;
KW Repeat.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 1343 VASCULAR ENDOTHELIAL GROWTH FACTOR
FT TRANSMEM 761 760 RECEPTOR 2.
FT DOMAIN 783 1343 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 46 109 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 141 207 IG-LIKE C2-TYPE DOMAIN 1.
FT DOMAIN 239 304 IG-LIKE C2-TYPE DOMAIN 2.
FT DOMAIN 345 400 IG-LIKE C2-TYPE DOMAIN 3.
FT DOMAIN 438 533 IG-LIKE C2-TYPE DOMAIN 4.
FT DOMAIN 560 645 IG-LIKE C2-TYPE DOMAIN 5.
FT DOMAIN 677 740 IG-LIKE C2-TYPE DOMAIN 6.
FT DOMAIN 830 1158 IG-LIKE C2-TYPE DOMAIN 7.
FT NP_BIND 836 844 PROTEIN KINASE.
FT BINDING 864 864 ATP (BY SIMILARITY).
FT ACT_SITE 1024 1024 ATP (BY SIMILARITY).
FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 96 96 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 143 143 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 158 158 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 245 245 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 318 318 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 374 374 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 395 395 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 507 507 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 576 576 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 609 609 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 615 615 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 627 627 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 671 671 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 700 700 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 717 717 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT MOD_RES 1055 1055 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
SQ SEQUENCE 1343 AA; 150393 MW; AD7E509EB62D3FF4 CRC64;

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Query Match 88.6%; Score 31; DB 1; Length 1343;  
Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDFSW 5  
|||||  
DB 256 LDFSW 260

Search completed: May 30, 2003, 15:48:56  
Job time : 4.11842 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 30, 2003, 14:32:11 ; Search time 14.7632 Seconds

(without alignments)  
83.741 Million cell updates/sec

Title: US-09-643-260-11

Perfect score: 35

Sequence: 1 LDFSWL 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: SP:archaea:\*  
2: SP:bacteria:\*  
3: SP:fungi:\*  
4: SP:human:\*  
5: SP:invertebrate:\*  
6: SP:mammal:\*  
7: SP:mhc:\*  
8: SP:organelle:\*  
9: SP-phage:\*  
10: SP-plant:\*  
11: SP-rodent:\*  
12: SP-virus:\*  
13: SP-vertebrate:\*  
14: SP-unclassified:\*  
15: SP-ivirius:\*  
16: SP:bacteriaph:\*  
17: SP-archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	35	100.0	315	13	091838
2	35	100.0	391	16	P95247
3	35	100.0	407	2	055047
4	35	100.0	414	2	09f738
5	35	100.0	414	2	0950Y1
6	35	100.0	415	16	08VJK7
7	35	100.0	1115	10	0942A0
8	33	94.3	61	16	09PEJ5
9	33	94.3	144	16	082619
10	33	94.3	144	16	084950
11	33	94.3	253	16	024927
12	33	94.3	258	16	092MX2
13	33	94.3	513	16	09JYP7
14	33	94.3	518	16	09JTN7
15	33	94.3	1214	5	020129
16	32	91.4	208	17	028570

17	32	91.4	355	10	08RWE1	08rwe1 arabidopsis
18	32	91.4	371	10	081871	081871 arabidopsis
19	32	91.4	449	16	0910V1	0910V1 pseudomonas
20	32	91.4	467	16	092X93	092X93 rhizobium m
21	32	91.4	490	16	P66442	P66442 rhizobium m
22	31	88.6	44	4	096PA0	096PA0 homo sapien
23	31	88.6	56	8	0952P8	0952P8 diadema ant
24	31	88.6	56	8	0952P5	0952P5 diadema ant
25	31	88.6	56	8	0952P4	0952P4 diadema ant
26	31	88.6	56	8	0952N9	0952N9 diadema ant
27	31	88.6	56	8	0952N5	0952N5 diadema ant
28	31	88.6	56	8	0952M6	0952M6 diadema ant
29	31	88.6	56	8	0952M4	0952M4 diadema ant
30	31	88.6	56	8	0952M3	0952M3 diadema ant
31	31	88.6	56	8	0952K9	0952K9 diadema ant
32	31	88.6	56	8	0952J4	0952J4 diadema ant
33	31	88.6	56	8	0952I2	0952I2 diadema ant
34	31	88.6	56	8	0952H7	0952H7 diadema ant
35	31	88.6	56	8	094EP3	094EP3 diadema ant
36	31	88.6	56	8	094EP5	094EP5 diadema ant
37	31	88.6	56	8	0952N2	0952N2 diadema ant
38	31	88.6	56	8	094N67	094N67 diadema ant
39	31	88.6	56	8	0952P6	0952P6 diadema ant
40	31	88.6	56	8	094M49	094M49 diadema ant
41	31	88.6	56	8	08WEP4	08WEP4 diadema ant
42	31	88.6	56	8	08WEP9	08WEP9 diadema ant
43	31	88.6	56	8	08WEP3	08WEP3 diadema ant
44	31	88.6	56	8	08WEP1	08WEP1 diadema set
45	31	88.6	56	8	08WEP5	08WEP5 diadema mex

#### ALIGNMENTS

RESULT 1

091838 PRELIMINARY; PRT; 315 AA.

ID 091838;  
AC 01-OCT-2000 (TREMBLrel. 15, Created)  
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE Interferon regulatory factor 1 (Interferon regulatory factor-1).  
GN IRF-1.  
OS Coturnix coturnix (common quail), and  
OS Coturnix coturnix japonica (Japanese quail).  
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
OC Coturnix.  
OX NCBI\_TaxID=9091, 93934;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC SPECIES=C.coturnix;  
RA Zoeller B., Mueller I., Nanda I., Guttenbach M., Dosch E., Schmid M.,  
RA Jungwirth C.;  
RT "Sequence analysis of avian interferon regulatory factors (IRF)  
RT reveals close relation of the chicken and quail interferon induced  
RT transcriptional apparatus. Cytogenetic studies and sequence comparison  
RT of the avian IRF-1, ICSP and a MHC class II gene reveals that the  
RT avian cell line C-32 is derived from quail.";  
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC SPECIES=C.coturnix japonica; STRAIN=BREED:FRANZOESISCHE MASTWACHTEL;  
RA Zoeller B., Ingold R.M., Nanda I., Guttenbach M.;  
RT "Sequence comparison of avian interferon regulatory factors and  
RT identification of the avian CEC-32 cell as a quail cell line.";  
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AJ271052; CAC01088.1; -;  
DR HSSP; P15314; IIF1.  
DR InterPro; IPR001346; IRF.  
DR Pfam; PF00605; IRF.1  
DR PRINTS; PR00267; INTERFERGFC.

DR PRODM: PD002355; IRF: 1.  
 DR SMART: SM00348; IRF: 1.  
 DR PROSITE: PS00601; IRF: 1.  
 SQ SEQUENCE 315 AA; 36257 MW; 7E32521A2D2D62D0 CRC64;

Query Match 100.0%; Score 35; DB 13; Length 315;  
 Best Local Similarity 100.0%; Pred. No. 47;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDFSML 6  
 DB 297 LDFSML 302

## RESULT 2

P95247 PRELIMINARY; PRT; 391 AA.  
 ID P95247  
 AC P95247  
 DT 01-MAY-1997 (TRENBLREL. 03, Created)  
 DT 01-MAY-1997 (TRENBLREL. 03, Last sequence update)  
 DT 01-JUN-2002 (TRENBLREL. 21, Last annotation update)  
 DE Hypothetical 37.4 kDa protein (PPE family protein).  
 GN RV3352C OR MTCY98.21C OR MT2419.  
 OS Mycobacterium tuberculosis.  
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;  
 OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.  
 OX NCBI\_TaxID=1773;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=H37RV;  
 RX MEDLINE=98295987; PubMed=9634230;  
 RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,  
 RA Gordon S.V., Eigmeier K., Gas S., Barry C.E. III, Tekala F.,  
 RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,  
 RA Davies R., Devlin K., Fellwell T., Gentles S., Hamlin N., Holroyd S.,  
 RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,  
 RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,  
 RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,  
 RA Sultson J.E., Taylor K., Whitehead S., Barrell B.G.;  
 RT "Deciphering the biology of Mycobacterium tuberculosis from the  
 RT complete genome sequence."  
 RL Nature 393:537-544(1998).

RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CDC 1551 / OSHKOSH;  
 RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,  
 RA Peterson J., Deboy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,  
 RA Kolony J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,  
 RA Delcher A., Utterback T., Feldman J., Kouri H., Gill J., Mikula A.,  
 RA Bishal W.;  
 RT "Whole genome comparison of Mycobacterium tuberculosis clinical and  
 RT laboratory strains."  
 RL Submitted (APR-2001) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: Z83860; CAB06149.1; -  
 DR EMBL: AE007082; AAK46712.1; -  
 DR TIGR: MT2419; -  
 DR TubercuList; RV3352c; -  
 DR InterPro; IPR000030; Microbac\_PPE.  
 DR Pfam; PF00823; PPE; 1.  
 KW Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 391 AA; 37355 MW; 360B67EEF6CE46A CRC64;

Query Match 100.0%; Score 35; DB 16; Length 391;  
 Best Local Similarity 100.0%; Pred. No. 59;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDFSML 6  
 DB 3 LDFSML 8

## RESULT 3

O55047

ID O55047 PRELIMINARY; PRT; 407 AA.  
 AC O55047;  
 DT 01-NOV-1996 (TRENBLREL. 01, Created)  
 DT 01-NOV-1996 (TRENBLREL. 01, Last sequence update)  
 DT 01-DEC-2001 (TRENBLREL. 19, Last annotation update)  
 DE Form I operon ORF protein genes, insertion sequence IS630  
 DE protein.  
 OS Shigella sonnei.  
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
 OC Shigella.  
 OX NCBI\_TaxID=624;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=536;  
 RA Houny H-S.;  
 RT "Genetic analysis and identification of an IS630 element in the form I  
 RT operon of Shigella sonnei 536."  
 RL Submitted (AUG-1995) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: U34305; AAA84874.1; -  
 SQ SEQUENCE 407 AA; 47980 MW; 23BFAF09EBD55D7 CRC64;

Query Match 100.0%; Score 35; DB 2; Length 407;  
 Best Local Similarity 100.0%; Pred. No. 61;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDFSML 6  
 DB 175 LDFSML 180

## RESULT 4

O9F738 PRELIMINARY; PRT; 414 AA.  
 ID O9F738  
 AC O9F738;  
 DT 01-MAR-2001 (TRENBLREL. 16, Created)  
 DT 01-MAR-2001 (TRENBLREL. 16, Last sequence update)  
 DT 01-DEC-2001 (TRENBLREL. 19, Last annotation update)  
 DE Wbgy.  
 GN Wbgy.  
 OS Shigella sonnei.  
 OC Plasmid plny.  
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
 OC Shigella.  
 OX NCBI\_TaxID=624;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=5361;  
 RX MEDLINE=20448976; PubMed=10992522;  
 RA Shepherd J., Wang L., Reeves P.R.;  
 RT "Comparison of the O antigen gene clusters of Escherichia coli  
 RT (Shigella) Sonnei and Plesiomonas shigelloides O17: Sonnei gained its  
 RT current plasmid borne O antigen genes from Plesiomonas shigelloides in  
 RT a recent event."  
 RL Infect. Immun. 68:6056-6061(2000).  
 DR EMBL: AF285971; AAG17422.1; -  
 KW Plasmid.  
 SQ SEQUENCE 414 AA; 49034 MW; EA6CA44A19ACD8CD CRC64;

Query Match 100.0%; Score 35; DB 2; Length 414;  
 Best Local Similarity 100.0%; Pred. No. 62;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDFSML 6  
 DB 175 LDFSML 180

## RESULT 5

O9S0Y1 PRELIMINARY; PRT; 414 AA.  
 ID O9S0Y1  
 AC O9S0Y1;  
 DT 01-MAY-2000 (TRENBLREL. 13, Created)  
 DT 01-MAY-2000 (TRENBLREL. 13, Last sequence update)

DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)  
 DE ORF5 (ORF5) (ORF5G).  
 GN MBGV OR ORF5G.  
 OS Plesiomonas shigelloides (Aeromonas shigelloides), and  
 OS Shigella sonnei.  
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
 OC Plesiomonas.  
 NCBI\_TaxID=703, 624;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES-P.shigelloides; STRAIN-SEROTYPE O17;  
 RA Child T., Okamura N., Yoshida Y., Ohtani K., Arakawa E., Watanabe H.,  
 RT "Complete DNA sequence of the O-antigen (rfb) gene cluster in  
 RT Plesiomonas shigelloides serotype O17 having the same O-antigen as  
 RT Shigella sonnei: comparison with that of S. sonnei."  
 RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES-P.shigelloides; STRAIN-SEROTYPE O17;  
 RA MEDLINE=99036814; PubMed=9817819;  
 RA Hwang H.H., Venkatesan M.M.;  
 RT "Genetic analysis of Shigella sonnei form I antigen: identification of  
 RT novel IS630 as an essential element for the form I expression."  
 RL Microb. Pathog. 25:165-173(1998).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES-P.shigelloides; STRAIN-C27;  
 RX PubMed=10992522;  
 RA Shepherd J., Wang L., Reeves P.R.;  
 RT "Comparison of the O antigen gene clusters of Escherichia coli  
 RT (Shigella) Sonnei and Plesiomonas shigelloides O17: Sonnei gained its  
 RT current plasmid borne O antigen genes from Plesiomonas shigelloides in  
 RT a recent event."  
 RL Infect. Immun. 68:6056-6061(2000).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES-S.sonnei;  
 RA Xu D.O., Cisar J.O., Ambulos N. Jr., Burr D., Kopecko D.J.;  
 RT "Molecular cloning and characterization of the O-antigen gene cluster  
 RT of Shigella sonnei: genetic stability, proposed biosynthetic pathway  
 RT and essential genes for expression of form I O polysaccharide in  
 RT Salmonella vaccine vector strain."  
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AB025970; BAA85010.1;  
 DR EMBL: AF285970; AA017412.1;  
 DR EMBL: AF294823; AAK85169.1;  
 SQ SEQUENCE 414 AA; 49038 MW; E92985FE7F19D953 CRC64;  
 QY 1 LDFSWM 6  
 DB 175 LDFSWM 180  
 Query Match 100.0%; Score 35; DB 2; Length 414;  
 Best Local Similarity 100.0%; Pred. No. 62;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 6  
 08VUK7 PRELIMINARY; PRT; 415 AA.  
 AC 08VUK7;  
 DT 01-MAR-2002 (TREMBLrel. 20, Created)  
 DT 01-MAR-2002 (TREMBLrel. 20, last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, last annotation update)  
 DE PPE family protein.  
 GN MT2422.  
 OS Mycobacterium tuberculosis.  
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;  
 OC Actinomycetales; Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.  
 NCBI\_TaxID=1773;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-CDC 1551 / OSHKOSH;

RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,  
 RA Peterson J., DeBoy R., Dodson R., Gwin M.L., Haft D., Hickey E.,  
 RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,  
 RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,  
 RA Bhalal W.;  
 RT "Whole genome comparison of Mycobacterium tuberculosis clinical and  
 RT laboratory strains."  
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AE007082; AAK46715.1;  
 DR TIGR: MT2422;  
 DR InterPro: IPR000030; Microbac\_PPE.  
 DR Pfam: PF00823; PPE; 1.  
 SQ SEQUENCE 415 AA; 40093 MW; 8B4BC671EBF4521 CRC64;  
 QY 1 LDFSWM 6  
 DB 34 LDFSWM 39  
 Query Match 100.0%; Score 35; DB 16; Length 415;  
 Best Local Similarity 100.0%; Pred. No. 63;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 7  
 0942A0 PRELIMINARY; PRT; 1115 AA.  
 AC 0942A0;  
 DT 01-DEC-2001 (TREMBLrel. 19, Created)  
 DT 01-DEC-2001 (TREMBLrel. 19, last sequence update)  
 DT 01-MAR-2002 (TREMBLrel. 20, last annotation update)  
 DE Beta galactosidase-like protein.  
 GN P0431606.9.  
 OS Oryza sativa (Rice).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC Ehrhartoideae; Oryzaceae; Oryza.  
 NCBI\_TaxID=4530;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-CV. NIPPONBARE;  
 RA Sasaki T., Matsumoto T., Yamamoto K.;  
 RT "Oryza sativa nippobare(GA3) genomic DNA, chromosome 1, PAC  
 RT clone:P0431606."  
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AP003683; BAB64698.1;  
 DR InterPro: IPR004200; Bgal\_small\_C.  
 DR InterPro: IPR004199; Bgal\_small\_N.  
 DR InterPro: IPR001649; GH\_2.  
 DR Pfam: PF02930; Bgal\_small\_C; 1.  
 DR Pfam: PF02929; Bgal\_small\_N; 1.  
 DR Pfam: PF00703; Glyco\_hydro\_2; 1.  
 DR Pfam: PF02836; Glyco\_hydro\_2; 1.  
 DR Pfam: PF02837; Glyco\_hydro\_2; 1.  
 DR PROSITE: PS00719; GLYCOSYL\_HYDROL\_F2\_1; UNKNOWN\_1.  
 DR PROSITE: PS00608; GLYCOSYL\_HYDROL\_F2\_2; UNKNOWN\_1.  
 SQ SEQUENCE 1115 AA; 126078 MW; 1AABFAA305CA8C5 CRC64;  
 QY 1 LDFSWM 6  
 DB 697 LDFSWM 702  
 Query Match 100.0%; Score 35; DB 10; Length 1115;  
 Best Local Similarity 100.0%; Pred. No. 1,7e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 8  
 09PEJ5 PRELIMINARY; PRT; 61 AA.  
 AC 09PEJ5;  
 DT 01-OCT-2000 (TREMBLrel. 15, Created)  
 DT 01-OCT-2000 (TREMBLrel. 15, last sequence update)  
 DT 01-MAR-2002 (TREMBLrel. 20, last annotation update)

DE Hypothetical protein Xf1033.  
 GN Xf1033.  
 OS Xylella fastidiosa.  
 OC Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;  
 OC Xylella.  
 OX NCBI\_TaxID=2371;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=9A5C;  
 RC MEDLINE=20365717; PubMed=10910347;  
 RA Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M.,  
 RA Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,  
 RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Brites M.R.S.,  
 RA Bueno M.R.F., Camargo A.A., Camargo L.E.A., Carraro D.M., Carter H.,  
 RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,  
 RA Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorri H.,  
 RA Facchini A.P., Ferreira A.J.S., Ferreira V.C., Ferro J.A.,  
 RA Fraga J.S., Frances S.C., Franco M.C., Frohne M., Furlan L.R.,  
 RA Garner M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,  
 RA Ho P.L., Hohnsbeil J.D., Junqueira M.L., Kemper E.L., Kltajima J.P.,  
 RA Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,  
 RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,  
 RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,  
 RA Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,  
 RA Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,  
 RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,  
 RA Nhami A.J., Nobrega F.G., Nunes L.R., Oliveira M.A.,  
 RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,  
 RA Peixoto B.R., Pereira G.A.G., Pereira H.A.Jr., Pesquero J.B.,  
 RA Queiroz R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,  
 RA de Rosa V.E.Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,  
 RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A.Jr.,  
 RA da Silva J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,  
 RA de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsubako M.H.,  
 RA Vallada H., Van Sluys M.A., Verjovsky-Almeida S., Vettore A.L.,  
 RA Zago M.A., Zatz M., Melandis J., Setubal J.C.;  
 RT "The genome sequence of the plant pathogen Xylella fastidiosa.";  
 RT Nature 406:151-159(2000).  
 DR EMBL, AE003940; AAF83843.1;  
 KW Hypothetical protein; Complete proteome.  
 SO SEQUENCE 61 AA; 6849 MW; 6CD0800BD7BAE107 CRC64;

Query Match 94.3%; Score 33; DB 16; Length 61;  
 Best Local Similarity 83.3%; Pred. No. 22;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 IDFSWL 6  
 :|||||  
 DB 2 MDESWL 7

RESULT 9  
 O826L9 PRELIMINARY; PRT; 144 AA.  
 ID O826L9;  
 AC O826L9;  
 DT 01-MAR-2002 (TREMBLrel. 20, Created)  
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE Putative pathogenicity island protein.  
 GN SCSB OR STY11717.  
 OS Salmonella typhi.  
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
 OC Salmonella.  
 OX NCBI\_TaxID=601;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CT18;  
 RC MEDLINE=21534947; PubMed=11677608;  
 RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,  
 RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahia M.,  
 RA Baker S., Basham D., Brooks K., Chillingworth T., Connerton P.,  
 RA Cronin A., Davies P., Davies R.M., Dowd L., White N., Farrar J.,  
 RA Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagsels K.,

RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,  
 RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,  
 RA Whitehead S., Barrall B.G.;  
 RT "Complete genome sequence of a multiple drug resistant Salmonella  
 RT enterica serovar Typhi CT18.";  
 RL Nature 413:848-852(2001).  
 DR EMBL, AL627271; CAD01962.1;  
 DR InterPro; IPR001440; TPR.  
 DR Pfam; PF00515; TPR; 2.  
 DR PRINTS; PR01595; SYCDHAPRONE.  
 KW Hypothetical protein; Complete proteome.  
 SO SEQUENCE 144 AA; 16390 MW; EC0EDA7F0E325E08 CRC64;

Query Match 94.3%; Score 33; DB 16; Length 144;  
 Best Local Similarity 83.3%; Pred. No. 52;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 IDFSWL 6  
 :|||||  
 DB 45 IDFSWL 50

RESULT 10  
 O84950 PRELIMINARY; PRT; 144 AA.  
 ID O84950;  
 AC O84950;  
 DT 01-NOV-1998 (TREMBLrel. 08, Created)  
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE SCSB (Secretion system chaparrone).  
 GN SCSB OR STM1403.  
 OS Salmonella typhimurium.  
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
 OC Salmonella.  
 OX NCBI\_TaxID=602;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=SL1344;  
 RA Cirillo D.M., Valdivia R.H., Monack D., Falkow S.;  
 RT "Macrophage-dependent induction of the Salmonella pathogenicity island  
 RT 2 type III secretion system and its role in intracellular survival.";  
 RL Mol. Microbiol. 0:0-0(1998).  
 [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=LT2;  
 RC MEDLINE=9900132; PubMed=9786193;  
 RA Hensel M., Shea J.E., Waterman R., Mundy R., Nikolaus T., Banks G.,  
 RA Vazquez-Torres A., Gleason C., Fang F.C., Holden D.W.;  
 RT "Genes encoding putative effector proteins of the type III secretion  
 RT system of Salmonella pathogenicity island 2 are required for bacterial  
 RT virulence and proliferation in macrophages.";  
 RL Mol. Microbiol. 30:163-174(1998).  
 [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=LT2 / SGSC1412 / ATCC 700720;  
 RC MEDLINE=21534948; PubMed=11677609;  
 RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,  
 RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,  
 RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,  
 RA Ryan E., Sun H., Florea L., Miller W., Stoenack T., Nhan M.,  
 RA Waterston R., Wilson R.K.;  
 RT "Complete genome sequence of Salmonella enterica serovar Typhimurium  
 RT LT2.";  
 RL Nature 413:852-856(2001).  
 DR EMBL, AF020808; AAC28884.1;  
 DR EMBL, AJ224892; CAAL2190.1;  
 DR EMBL, AE008761; AAL20327.1;  
 DR InterPro; IPR001440; TPR.  
 DR Pfam; PF00515; TPR; 2.  
 DR PRINTS; PR01595; SYCDHAPRONE.  
 KW Complete proteome.  
 SO SEQUENCE 144 AA; 16375 MW; B60EDA7F0E325B08 CRC64;

Query Match 94.3%; Score 33; DB 16; Length 144;  
 Best Local Similarity 83.3%; Pred. No. 52;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDFSML 6  
 DB 45 LDFSML 50

## RESULT 11

O24927 PRELIMINARY; PRT; 253 AA.  
 AC 024927;  
 DT 01-JAN-1998 (TREMBlrel. 05, Created)  
 DT 01-JAN-1998 (TREMBlrel. 05, last sequence update)  
 DT 01-MAR-2002 (TREMBlrel. 20, last annotation update)  
 DE Hypothetical protein HP0101.  
 GN HP0101.  
 OS Helicobacter pylori (Campylobacter pylori).  
 OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;  
 OC Helicobacter.  
 OX NCBI\_TaxID=210;

SEQUENCE FROM N.A.  
 RC STRAIN=26655 / ATCC 700392;  
 RX MEDLINE=97394467; PubMed=9252185;  
 RA Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,  
 RA Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A.,  
 RA Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S.,  
 RA Loftus B., Richardson D., Dodson R., Khakhria H.G., Glodek A.,  
 RA McKenney K., Fitzgerald L.M., Lee N., Adams M.D., Hickey E.K.,  
 RA Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M.,  
 RA Cotton M.D., Weidman J.M., Fujii C., Bowman C., Wathey L., Wallin E.,  
 RA Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,  
 RA Venter J.C.;  
 RT "The complete genome sequence of the gastric pathogen Helicobacter  
 pylori." Nature 388:539-547(1997).  
 RL Nature 388:539-547(1997).  
 DR EMBL: AE00532; M07180.1;  
 DR TIGR: HP0101;  
 DR InterPro: IPR002718; HP\_OMP.  
 DR Pfam: PF01856; HP\_OMP; 1.  
 KW Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 253 AA; 29463 MW; C9A6BBE2C5A90003 CRC64;

Query Match 94.3%; Score 33; DB 16; Length 253;  
 Best Local Similarity 83.3%; Pred. No. 93;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDFSML 6  
 DB 149 LDFSML 154

## RESULT 12

O92MX2 PRELIMINARY; PRT; 253 AA.  
 AC 092MX2;  
 DT 01-MAY-1999 (TREMBlrel. 10, Created)  
 DT 01-MAY-1999 (TREMBlrel. 10, last sequence update)  
 DT 01-MAY-2000 (TREMBlrel. 13, last annotation update)  
 DE PUTATIVE.  
 GN JHP0093.  
 OS Helicobacter pylori J99 (Campylobacter pylori J99).  
 OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;  
 OC Helicobacter.  
 OX NCBI\_TaxID=85963;

SEQUENCE FROM N.A.  
 RP MEDLINE=99120557; PubMed=9923682;  
 RA Alm R.A., Ling L.-S.L., Mait D.T., King B.L., Brown E.D., Dolg P.C.,  
 RA Smith D.R., Noonan B., Guild B.C., deJonge B.L., Camel G.,  
 RA Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,

RA Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,  
 RA Trust T.J.;  
 RT "Genomic sequence comparison of two unrelated isolates of the human  
 RT gastric pathogen Helicobacter pylori." Nature 397:176-180(1999).  
 RL Nature 397:176-180(1999).  
 DR EMBL: AE001448; M05674.1;  
 KW Complete proteome.  
 SQ SEQUENCE 253 AA; 29526 MW; 5C5F5239737E90AE CRC64;

Query Match 94.3%; Score 33; DB 16; Length 253;  
 Best Local Similarity 83.3%; Pred. No. 93;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDFSML 6  
 DB 149 LDFSML 154

## RESULT 13

O9JYP7 PRELIMINARY; PRT; 518 AA.  
 AC 09JYP7;  
 DT 01-OCT-2000 (TREMBlrel. 15, Created)  
 DT 01-OCT-2000 (TREMBlrel. 15, last sequence update)  
 DT 01-JUN-2002 (TREMBlrel. 21, last annotation update)  
 DE Hypothetical protein NMB1485.  
 GN NMB1485.  
 OS Neisseria meningitidis (serogroup B).  
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
 OX NCBI\_TaxID=491;

SEQUENCE FROM N.A.  
 RC STRAIN=MC58 / SEROGROUP B;  
 RX MEDLINE=20175755; PubMed=10710307;  
 RA Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,  
 RA Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,  
 RA Nelson W.C., Gwinn M.L., Deboy R., Peterson J.D., Hickey E.K.,  
 RA Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,  
 RA Mason T., Clecko A., Parksey D.S., Blair E., Cifton H., Clark E.B.,  
 RA Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J.,  
 RA Gill J., Scarlato V., Maignani V., Pizsa M., Grandi G., Sun L.,  
 RA Smith H.O., Fraser C.M., Moxon E.R., Kappuli R., Venter J.C.;  
 RT "Complete genome sequence of Neisseria meningitidis serogroup B strain  
 MC58." Science 287:1809-1815(2000).  
 RL Science 287:1809-1815(2000).  
 DR EMBL: AE002498; MAF41841.1;  
 DR TIGR: NMB1485;  
 DR InterPro: IPR000644; CBS\_domain.  
 DR InterPro: IPR005170; CorC\_HLYC.  
 DR Pfam: PF00571; CBS; 2.  
 DR Pfam: PF03471; CorC\_HLYC; 1.  
 DR SMART: SM00116; CBS; 2.  
 KW Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 518 AA; 57342 MW; C9D9324DA672DC96 CRC64;

Query Match 94.3%; Score 33; DB 16; Length 518;  
 Best Local Similarity 83.3%; Pred. No. 1,9e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDFSML 6  
 DB 1 MDFSML 6

## RESULT 14

O9JTN9 PRELIMINARY; PRT; 518 AA.  
 AC 09JTN9;  
 DT 01-OCT-2000 (TREMBlrel. 15, Created)  
 DT 01-OCT-2000 (TREMBlrel. 15, last sequence update)  
 DT 01-JUN-2002 (TREMBlrel. 21, last annotation update)  
 DE Conserved hypothetical integral membrane protein.  
 GN NMA1694.

OS Neisseria meningitidis (serogroup A).  
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
 OX NCBI\_TaxID=65699;

Search completed: May 30, 2003, 14:38:59  
 Job time : 16.7632 secs

RP SEQUENCE FROM N.A.

RC STRAIN-22491 / SEROGROUP A / SEROTYPE 4A.  
 RX MEDLINE=20222556; PubMed-10761919;

RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.,

RA Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,

RA Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S.,

RA Jagels K., Leather S., Moule S., Mungall K., Quail M.A.,

RA Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,

RA Whitehead S., Spratt B.G., Barrall B.G.;  
 "Complete DNA sequence of a serogroup A strain of Neisseria

RT meningitidis 22491."

RL Nature 404:502-506(2000).

DR EMBL: AL162756: CAB84922.1; "

DR InterPro: IPR000644; CBS\_domain.

DR InterPro: IPR005170; CorC\_HlyC.

DR Pfam: PF00571; CBS; 2.

DR Pfam: PF03471; CorC\_HlyC; 1.

DR SMART: SM00116; CBS; 2.

DR SMART: SM00116; CBS; 2.

DR SMART: SM00116; CBS; 2.

DR SMART: SM00116; CBS; 2.

DR SMART: SM00116; CBS; 2.

DR SMART: SM00116; CBS; 2.

DR SMART: SM00116; CBS; 2.

DR SMART: SM00116; CBS; 2.

DR SMART: SM00116; CBS; 2.

DR SMART: SM00116; CBS; 2.

DR SMART: SM00116; CBS; 2.

DR SMART: SM00116; CBS; 2.

DR SMART: SM00116; CBS; 2.

DR SMART: SM00116; CBS; 2.

DR SMART: SM00116; CBS; 2.

DR SMART: SM00116; CBS; 2.

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DR SMART: SM00116; CBS; 2.

DR SMART: SM00116; CBS; 2.

DR SMART: SM00116; CBS; 2.

DR SMART: SM00116; CBS; 2.

DR SMART: SM00116; CBS; 2.

DR SMART: SM00116; CBS; 2.

DR SMART: SM00116; CBS; 2.

DR SMART: SM00116; CBS; 2.

DR SMART: SM00116; CBS; 2.

DR SMART: SM00116; CBS; 2.

DR SMART: SM00116; CBS; 2.

DR SMART: SM00116; CBS; 2.

DR SMART: SM00116; CBS; 2.

DR SMART: SM00116; CBS; 2.

DR SMART: SM00116; CBS; 2.

DR SMART: SM00116; CBS; 2.

OY 1 LDFSWL 6  
 Db 1 LDFSWL 6

RESULT 15

ID Q20129 PRELIMINARY; PRT: 1214 AA.

AC Q20129; 01-NOV-1996 (TRENBLREL. 01, Created)

DT 01-NOV-1996 (TRENBLREL. 01, Last sequence update)

DT 01-DEC-2001 (TRENBLREL. 19, Last annotation update)

DE F37D6.1 protein.

GN F37D6.1.

OS Caenorhabditis elegans.

OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;

OC Rhabditidae; Peloderinae; Caenorhabditis.

OX NCBI\_TaxID=6239;

RP SEQUENCE FROM N.A.

RA McMurray A.A.;

RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.

RP SEQUENCE FROM N.A.

RX MEDLINE=99069613; PubMed-9851916;

RA none;

RT "Genome sequence of the nematode C.elegans: A platform for

RT investigating biology."

RL Science 282:2012-2018(1998).

DR EMBL: 275540; CA99847.1; "

DR InterPro: IPR001357; BRCT.

DR Pfam: PF00533; BRCT; 6.

DR SMART: SM00282; BRCT; 6.

DR PROSITE: PS50172; BRCT; 4.

SO SEQUENCE 1214 AA; 138080 MW; FDCDEA1300CEFA4E CRC64;

Query Match 94.3%; Score 33; DB 5; Length 1214;

Best Local Similarity 83.3%; Pred. NO. 4.6e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDFSWL 6  
 Db 772 LDFSWI 777

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 30, 2003, 14:32:12 ; Search time 6.5921 Seconds  
(without alignments)  
87.500 Million cell updates/sec

Title: US-09-643-260-13

Perfect score: 33

Sequence: 1 LDMSAL 6

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

1: PIR\_73:\*\*\*  
2: PIR\_1:\*\*\*  
3: PIR\_3:\*\*\*  
4: PIR\_4:\*\*\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	33	100.0	330	2	B69416
2	31	93.9	192	2	F82645
3	31	93.9	333	2	S75980
4	31	93.9	984	2	S67527
5	31	93.9	1394	2	S66876
6	31	93.9	2297	2	T34918
7	30	90.9	163	2	D84320
8	30	90.9	208	2	D75556
9	30	90.9	261	2	A69807
10	30	90.9	280	2	D87195
11	30	90.9	365	2	F82398
12	30	90.9	380	2	D82088
13	30	90.9	384	2	AG0149
14	30	90.9	401	2	D83618
15	30	90.9	442	2	T20638
16	30	90.9	476	2	E82758
17	30	90.9	572	2	T37128
18	30	90.9	638	2	F75547
19	30	90.9	1026	2	T39612
20	30	90.9	1293	2	T30871
21	30	90.9	1471	2	F86218
22	30	90.9	1616	2	T00713
23	29	87.9	32	2	A24047
24	29	87.9	94	2	S77047
25	29	87.9	119	2	S74925
26	29	87.9	119	2	S75488
27	29	87.9	119	2	S74836
28	29	87.9	119	2	S75590
29	29	87.9	150	2	A83754

30	29	87.9	171	2	S75475	transposase slr152
31	29	87.9	177	2	AG2498	hypothetical prote
32	29	87.9	211	2	A44177	female protein - g
33	29	87.9	214	2	G83488	probable permease
34	29	87.9	215	2	H82830	conserved hypothet
35	29	87.9	223	1	YLHUP	serum amyloid P-co
36	29	87.9	232	2	F82729	conserved hypothet
37	29	87.9	242	2	A48593	serum amyloid P-co
38	29	87.9	242	2	G87696	hypothetical prote
39	29	87.9	279	2	F70612	hypothetical prote
40	29	87.9	282	2	S76906	transposase slr1043
41	29	87.9	282	2	S76382	transposase slr023
42	29	87.9	282	2	S76312	transposase slr035
43	29	87.9	282	2	S77237	transposase slr135
44	29	87.9	282	2	S75484	transposase slr199
45	29	87.9	286	1	C42053	gap junction prote

#### ALIGNMENTS

RESULT 1  
B69416  
hypothetical protein AF1331 - Archaeoglobus fulgidus  
C:Species: Archaeoglobus fulgidus  
C>Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 22-Oct-1999  
C/Accession: B69416  
R:Kien, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dod  
.. Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kitzness, E  
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.  
Mature\_390\_364-370\_1997  
A:Authors: Uffereback, T.; Cotton, M.D.; Spriggs, T.; Artlich, P.; Kaine, B.P.; Sykes,  
Smith, H.O.; Woese, C.R.; Venter, J.C.  
A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing arch  
A:Reference number: A69250, MIMD:98049343, PMID:9389475  
A:Accession: B69416  
A>Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-330 <KIE>  
A/Cross-references: GB:AE001012; GB:AE000782; MIMD:92689335; PIMD:AA89926.1; PIMD:9264

Query Match 100.0%; Score 33; DB 2; Length 330;  
Best Local Similarity 100.0%; Pred. No. 63;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
DB 177 LDMSAL 182

RESULT 2  
F82645  
tryptophan repressor binding protein XF1733 [imported] - Xylella fastidiosa (strain 9  
C:Species: Xylella fastidiosa  
C>Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 20-Aug-2000  
R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Seq  
Nature 406, 151-157, 2000  
A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.  
A:Reference number: A82515; MIMD:20365717; PMID:10910347  
A>Note: for a complete list of authors see reference number A59328 below  
A/Accession: F82645  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-192 <SIM>  
A/Cross-references: GB:AE003996; GB:AE003849; MIMD:99106790; PIMD:AA84542.1; GSPDB:GN  
A:Experimental source: strain 9a5c  
R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvares, R.  
Birones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer  
as-Neto, E.; Docena, C.; El-Dorri, H.; Facinani, A.P.; Ferreira, A.J.S.  
submitted to Genbank, June 2000  
A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Fr  
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; La

chado, M.A.; Madela, A.M.B.N.; Madela, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E.  
 A.Autors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;  
 F.O.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmeri, D.A.  
 Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawaak  
 M.; Tsunako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z  
 A:Reference number: A59328  
 A:Contents: annotation  
 C:Genetics:  
 A:Gene: XF1733

Query Match 93.9%; Score 31; DB 2; Length 192;  
 Best Local Similarity 83.3%; Pred. No. 93;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDMSAL 6  
 :|||||  
 DB 43 MDMSAL 48

RESULT 3  
 S75980  
 hypothetical protein slr0537 - *Synechocystis* sp. (strain PCC 6803)  
 C:Species: *Synechocystis* sp.  
 A:Variety: PCC 6803  
 C:Date: 25-Apr-1997 #sequence\_revision 25-Apr-1997 #text\_change 20-Jun-2000  
 C:Accession: S75980  
 R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;  
 O. K.; Okumura, S.; Shimo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda  
 DNA Res. 3, 109-136, 1996  
 A:Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis*  
 5.

A:Reference number: S74322; MUID:97061201; PMID:8905231  
 A:Accession: S75980  
 A:Status: nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1333 <KAN>  
 A:Cross-references: EMBL:D64006; GB:AB001339; NID:g1001291; PIDN:BA10827.1; PID:g100134  
 A:Note: The nucleotide sequence was submitted to the EMBL Data Library, June 1996  
 C:Superfamily: probable ribokinase

Query Match 93.9%; Score 31; DB 2; Length 333;  
 Best Local Similarity 83.3%; Pred. No. 16e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDMSAL 6  
 :|||||  
 DB 146 MDMSAL 151

RESULT 4  
 S67527  
 protein kinase (EC 2.7.1.-) PRK2 - human  
 C:Species: *Homo sapiens* (man)  
 C:Date: 29-Jan-1998 #sequence\_revision 06-Feb-1998 #text\_change 21-Jul-2000  
 C:Accession: S67527; I67464  
 R:Palmer, R.H.; Ridden, J.; Parker, P.J.  
 Eur. J. Biochem. 227, 344-351, 1995  
 A:Title: Cloning and expression patterns of two members of a novel protein-kinase-C-rela  
 A:Reference number: I53327; MUID:95154310; PMID:7851406  
 A:Accession: S67527

A:Molecule type: mRNA  
 A:Residues: 1-984 <PAL>  
 A:Cross-references: EMBL:S75548; NID:g914099; PIDN:AAB3346.1; PID:g914100  
 A:Experimental source: fetal brain  
 A:Accession: I67464  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-984 <RES>  
 A:Cross-references: GB:S75548; NID:g914099; PIDN:AAB3346.1; PID:g914100  
 C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolo  
 C:Keywords: ATP; phosphotransferase  
 F:655-916/Domain: protein kinase homology <KIN>

F:663-671/Region: protein kinase ATP-binding motif  
 F:686/Active site: Lys #status predicted

Query Match 93.9%; Score 31; DB 2; Length 984;  
 Best Local Similarity 83.3%; Pred. No. 5e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDMSAL 6  
 :|||||  
 DB 919 IDMSAL 924

RESULT 5  
 S66876  
 ATP-dependent transport protein homolog YOR011w - yeast (*Saccharomyces cerevisiae*)  
 N:Alternate names: ATP-dependent permease homolog; protein O2601; protein UNA841  
 C:Species: *Saccharomyces cerevisiae*  
 C:Date: 12-Jul-1996 #sequence\_revision 12-Jul-1996 #text\_change 19-Apr-2002  
 C:Accession: S66876; S66877; S54617; S61995; S72144  
 R:Pettersson, B.; Sterky, F.; Uhlen, M.  
 submitted to the Protein Sequence Database, July 1996  
 A:Reference number: S66882  
 A:Accession: S66876

A:Molecule type: DNA  
 A:Residues: 1-841 <PE>  
 A:Cross-references: EMBL:Z74919; MIPS:YOR011w  
 A:Experimental source: strain S288C  
 Ride Haan, M.; Maarse, A.C.; Grievell, L.A.; Maarse, A.C.  
 submitted to the Protein Sequence Database, July 1996  
 A:Reference number: S66877  
 A:Accession: S66877

A:Molecule type: DNA  
 A:Residues: 355-1394 <DEH>  
 A:Cross-references: EMBL:Z74919; MIPS:YOR011w  
 A:Experimental source: strain S288C  
 Ride Haan, M.; Maarse, A.C.; Grievell, L.A.  
 submitted to the EMBL Data Library, May 1995  
 A:Reference number: S54617  
 A:Accession: S54617

A:Molecule type: DNA  
 A:Residues: 355-1394 <DEM>  
 A:Cross-references: EMBL:X87331  
 R:Stierky, F.; Uhlen, M.  
 submitted to the EMBL Data Library, December 1995  
 A:Reference number: S61981  
 A:Accession: S61995

A:Molecule type: DNA  
 A:Residues: 389-841 <STE>  
 A:Cross-references: EMBL:U43491; NID:g1150992; PIDN:AAC49491.1; PID:g1151007  
 R:Stierky, F.; Holmberg, A.; Pettersson, B.; Uhlen, M.  
 Yeast 12, 1091-1095, 1996  
 A:Title: The sequence of a 30 kb fragment on the left arm of chromosome XV from *Sacch*  
 A:Reference number: S72130; MUID:97051599; PMID:8896276  
 A:Accession: S72144

A:Status: nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 389-841 <ST2>  
 A:Cross-references: EMBL:U43491; NID:g1150992; PIDN:AAC49491.1; PID:g1151007  
 A:Note: The nucleotide sequence was submitted to the EMBL Data Library, December 1995  
 C:Genetics:  
 A:Gene: SGD:AUS1  
 A:Cross-references: SGD:S0005537  
 A:Map position: 15R  
 A:Note: YOR011w

C:Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homolog  
 C:Keywords: ATP; nucleotide binding; P-loop; transmembrane protein  
 F:49-249/Domain: ATP-binding cassette homology <ABC1>  
 F:391-407/Domain: transmembrane #status predicted <TM1>  
 F:421-437/Domain: transmembrane #status predicted <TM2>  
 F:476-493/Domain: transmembrane #status predicted <TM3>  
 F:501-517/Domain: transmembrane #status predicted <TM4>  
 F:527-543/Domain: transmembrane #status predicted <TM5>  
 F:640-656/Domain: transmembrane #status predicted <TM6>

F:766-954/Domain: ATP-binding cassette homology <ABC2>  
 F:782-789/Region: nucleotide-binding motif A (P-loop)  
 F:1107-1123/Domain: transmembrane #status predicted <TM7>  
 F:1166-1182/Domain: transmembrane #status predicted <TM8>  
 F:1226-1242/Domain: transmembrane #status predicted <TM9>

Query Match 93.9%; Score 31; DB 2; Length 1394;  
 Best Local Similarity 83.3%; Pred. No. 7.2e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LDMSAL 6  
 Db 1017 LDMSAL 1022

RESULT 6  
 T34918  
 polyketide synthase - streptomyces coelicolor

C:Species: Streptomyces coelicolor  
 C>Date: 05-Nov-1999 #sequence\_revision 05-Nov-1999 #text\_change 17-Nov-2000

C:Accession: T34918  
 R:Oliver, K.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.  
 submitted to the EMBL data library, January 1998

A:Reference number: Z21558  
 A:Accession: T34918  
 A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA  
 A:Residues: 1-2297 <OLI>  
 A:Cross-references: EMBL:AL021409; PIDN:CAAL16183.1; GSPDB:GN00070; SCOEDB:SC3F7.12

A:Experimental source: strain A3(2)  
 C:Genetics:  
 A:Gene: SCOEDB:SC3F7.12  
 C:Superfamily: 3-oxoacyl-[acyl-carrier-protein] synthase I homology; acetate-CoA ligase

C:Keywords: carrier protein  
 F:80-583/Domain: acetate-CoA ligase homology <ACLI>  
 F:701-771/Domain: acyl carrier protein homology <ACP>

F:818-1205/Domain: 3-oxoacyl-[acyl-carrier-protein] synthase I homology <OAS>  
 F:1315-1600/Domain: [acyl-carrier-protein] S-malonyltransferase homology <AMT>

Query Match 93.9%; Score 31; DB 2; Length 2297;  
 Best Local Similarity 83.3%; Pred. No. 1.2e+03;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LDMSAL 6  
 Db 1641 LDMSAL 1646

RESULT 7  
 DB4320  
 hypothetical protein Vng1679h [imported] - Halobacterium sp. NRC-1

C:Species: Halobacterium sp. NRC-1  
 C>Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 02-Feb-2001

C:Accession: DB4320  
 R:Ng, W.V.; Kennedy, S.P.; Mahlitz, G.G.; Bergquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.; Lethausen, B.; Keller, K.; Cruz, R.; Danson, M.D.; Hough, D.W.; Maddocks, D.G.; Jablo

Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000  
 A:Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ehardt, H.; Lowe, T.M.; Li

A:Title: Genome sequence of Halobacterium species NRC-1.  
 A:Reference number: A84160; MUID:20504483; PMID:11016950

A:Accession: DB4320  
 A:Status: preliminary  
 A:Molecule type: DNA

A:Residues: 1-163 <STO>  
 A:Cross-references: GB:AE004437; NID:g10581148; PIDN:AA919928.1; GSPDB:GN00138

C:Genetics:  
 A:Gene: VNC1679H  
 Query Match 90.9%; Score 30; DB 2; Length 163;  
 Best Local Similarity 83.3%; Pred. No. 1.2e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LDMSAL 6  
 Db 142 LDMSAL 147

RESULT 8  
 D75556  
 phosphoribosylanthranilate isomerase - Deinococcus radiodurans (strain R1)

C:Species: Deinococcus radiodurans  
 C>Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 17-Mar-2000

C:Accession: D75556  
 R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.  
 M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.;  
 S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.  
 Science 286, 1571-1577, 1999

A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.  
 A:Reference number: A75250; MUID:20036896; PMID:10567266

A:Accession: D75556  
 A:Status: preliminary

A:Molecule type: DNA  
 A:Residues: 1-208 <WHI>  
 A:Cross-references: GB:AE001875; GB:AE000513; NID:g6457790; PIDN:AA09715.1; PID:g645

A:Experimental source: strain R1  
 C:Genetics:  
 A:Gene: DR0123  
 A:Map position: 1  
 C:Superfamily: phosphoribosylanthranilate isomerase; trpE homology

Query Match 90.9%; Score 30; DB 2; Length 208;  
 Best Local Similarity 83.3%; Pred. No. 1.6e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LDMSAL 6  
 Db 144 LDMSAL 149

RESULT 9  
 A69807

3-hydroxyisobutyrate dehydrogenase homolog yfjR - Bacillus subtilis

C:Species: Bacillus subtilis  
 C>Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 18-Aug-2000

C:Accession: A69807  
 R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Ber  
 C.; Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.;  
 A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari,  
 Nature 390, 249-256, 1997

A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fuma, S.; Galizzi, A.; Gal  
 lech, J.; Harwood, C.R.; Hentzel, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M  
 koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardino  
 A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mau  
 y, M.; Ogawa, K.; Ogilwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portete  
 Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadleir, Y.; Sato, T.; Scanl  
 A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Se  
 akuchil, M.; Tamakoshi, A.; Tanaka, T.; Terpilata, P.; Tognoni, A.; Tosato, V.; Uchida  
 T.; Winters, P.; Wipac, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida  
 A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis

A:Reference number: A69580; MUID:98044033; PMID:9386377  
 A:Accession: A69807

A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA

A:Residues: 1-261 <KUN>  
 A:Cross-references: GB:Z99108; GB:AL009126; NID:g2633055; PIDN:CAB12628.1; PID:g26331

A:Experimental source: strain 168  
 C:Genetics:  
 A:Gene: yfjR

C:Superfamily: 3-hydroxyisobutyrate dehydrogenase; 3-hydroxyisobutyrate dehydrogenase  
 F:2-240/Domain: 3-hydroxyisobutyrate dehydrogenase homology #status atypical <HIR>

Query Match 90.9%; Score 30; DB 2; Length 261;  
 Best Local Similarity 83.3%; Pred. No. 2e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDMSAL 6  
 DB 251 LDMSAL 256

## RESULT 10

D87195  
 Probable xylanase/chitin deacetylase [Imported] - Clostridium acetobutylicum  
 C:Species: Clostridium acetobutylicum  
 C:Date: 14-Sep-2001 #sequence\_revision 14-Sep-2001 #text\_change 14-Sep-2001  
 C:Accession: D87195  
 R:Rolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.  
 J. Bacteriol. 183, 4823-4838, 2001  
 A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cld  
 A:Reference number: A96900; MUID:21359325; PMID:21359325  
 A:Accession: D87195  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-280 <RUR>  
 A:Cross-References: GB:AE001437; PIDN:AAK80351.1; PID:g15025409; GSPDB:GN00168  
 A:Experimental source: Clostridium acetobutylicum ATCC824  
 C:Genetics:  
 A:Gene: CAC2396

Query Match 90.9%; Score 30; DB 2; Length 280;  
 Best Local Similarity 83.3%; Pred. No. 2.1e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDMSAL 6  
 DB 212 LDMSAL 217

## RESULT 11

F82398  
 Transcription regulator Arac/XylS family VCA0926 [Imported] - Vibrio cholerae (strain NI  
 C:Species: Vibrio cholerae  
 C:Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 02-Feb-2001  
 C:Accession: F82398  
 R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwin, M.L.; Dodson, R.J.;  
 Chardon, D.; Ermolaeva, M.D.; Vamathevan, J.; Baas, S.; Qin, H.; Dragol, I.; Sellers, R.  
 L. R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.  
 Nature 406, 477-483, 2000  
 A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.  
 A:Reference number: A82035; MUID:20406833; PMID:10952301  
 A:Accession: F82398  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-365 <HEI>  
 A:Cross-References: GB:AE004420; GB:AE003853; NID:g9658361; PIDN:AAF96823.1; GSPDB:GN001  
 A:Experimental source: serogroup O1, strain NI6961; biotype El Tor  
 C:Genetics:  
 A:Gene: VCA0926  
 A:Map position: 2

Query Match 90.9%; Score 30; DB 2; Length 365;  
 Best Local Similarity 83.3%; Pred. No. 2.8e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDMSAL 6  
 DB 70 VDMASL 75

## RESULT 12

D82088  
 Chromate resistance protein-related protein VC2339 [Imported] - Vibrio cholerae (strain  
 C:Species: Vibrio cholerae  
 C:Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 02-Feb-2001  
 C:Accession: D82088  
 R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwin, M.L.; Dodson, R.J.;

Chardon, D.; Ermolaeva, M.D.; Vamathevan, J.; Baas, S.; Qin, H.; Dragol, I.; Sellers  
 L. R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.  
 Nature 406, 477-483, 2000  
 A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.  
 A:Reference number: A82035; MUID:20406833; PMID:10952301  
 A:Accession: D82088  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-380 <HEI>  
 A:Cross-References: GB:AE004304; GB:AE003853; NID:g9656905; PIDN:AAF95482.1; GSPDB:GN  
 C:Experimental source: serogroup O1, strain NI6961; biotype El Tor  
 C:Genetics:  
 A:Gene: VC2339  
 A:Map position: 1  
 C:Superfamily: Chromate resistance protein A

Query Match 90.9%; Score 30; DB 2; Length 380;

Best Local Similarity 83.3%; Pred. No. 2.9e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDMSAL 6  
 DB 344 LDMSAL 349

## RESULT 13

AG0149  
 Probable membrane protein YPO1221 [Imported] - Yersinia pestis (strain CO92)  
 C:Species: Yersinia pestis  
 C:Date: 02-Nov-2001 #sequence\_revision 02-Nov-2001 #text\_change 02-Nov-2001  
 C:Accession: AG0149  
 R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.  
 deno-Farraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.  
 H.; M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barril  
 Nature 413, 523-527, 2001  
 A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.  
 A:Reference number: AB0001; MUID:21470413; PMID:11586360  
 A:Accession: AG0149  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-384 <RUR>  
 A:Cross-References: GB:AL590842; PIDN:CAC90058.1; PID:g15979278; GSPDB:GN00175  
 C:Genetics:  
 A:Gene: YPO1221

Query Match 90.9%; Score 30; DB 2; Length 384;  
 Best Local Similarity 83.3%; Pred. No. 2.9e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDMSAL 6  
 DB 228 LDMSAL 233

## RESULT 14

D83618  
 beta-Ketoadipyl CoA thiolase Pcar PA0228 [Imported] - Pseudomonas aeruginosa (strain  
 C:Species: Pseudomonas aeruginosa  
 C:Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 31-Dec-2000  
 C:Accession: D83618  
 R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.;  
 Adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.R.; Folger, K.R.; Kas, A.; Lapid, K.; L.  
 Lory, S.; Olson, M.V.  
 Nature 406, 959-964, 2000  
 A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa  
 A:Reference number: A82950; MUID:20437337; PMID:10984043  
 A:Accession: D83618  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-401 <STO>  
 A:Cross-References: GB:AE004460; GB:AE004091; NID:g9946055; PIDN:AA03617.1; GSPDB:GN  
 A:Experimental source: strain PA01  
 C:Genetics:

A:Gene: pcaf; PA0228  
C:Superfamily: acetyl-CoA acetyltransferase

Query Match 90.9%; Score 30; DB 2; Length 401;  
Best Local Similarity 83.3%; Pred. No. 3.1e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0;

OY 1 LDMSAL 6  
:|||||  
Db 45 VDMSAL 50

## RESULT 15

T20638  
hypothetical protein T06H11.4 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 18-Feb-2000

C:Accession: T20638; T24630

R:Kershaw, J.

submitted to the EMBL Data Library, June 1995

A:Reference number: Z19303

A:Accession: T20638

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-442 <NTL>

A:Cross-references: EMBL:Z49887; PIDN:CAA90060.1; GSPDB:GN00028; CESP:T06H11.4

A:Experimental source: clone F09B9

R:Kershaw, J.

submitted to the EMBL Data Library, June 1995

A:Reference number: Z19914

A:Accession: T24630

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-442 <NT2>

A:Cross-references: EMBL:Z49889; PIDN:CAA90069.1; GSPDB:GN00028; CESP:T06H11.4

A:Experimental source: clone T06H11

C:Genetics:

A:Gene: CESP:T06H11.4

A:Map position: X

A:Intons: 45/1; 95/2; 150/2; 208/3; 250/2; 292/3

C:Superfamily: molybdenum cofactor biosynthesis protein moca-2

## Query Match

90.9%; Score 30; DB 2; Length 442;  
Best Local Similarity 83.3%; Pred. No. 3.4e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDMSAL 6  
:|||||  
Db 39 VDMSAL 44

Search completed: May 30, 2003, 14:52:56  
Job time : 8.5921 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 30, 2003, 14:32:11 ; Search time 14.7632 Seconds  
(without alignments)  
83.741 Million cell updates/sec

Title: US-09-643-260-13  
Perfect score: 33  
Sequence: 1 IDWSAL 6

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues  
Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

SPREMBL.21: \*  
1: sp\_archaea: \*  
2: sp\_bacteria: \*  
3: sp\_fungi: \*  
4: sp\_human: \*  
5: sp\_invertebrate: \*  
6: sp\_mammal: \*  
7: sp\_mhc: \*  
8: sp\_organelle: \*  
9: sp\_phase: \*  
10: sp\_plant: \*  
11: sp\_rodent: \*  
12: sp\_virus: \*  
13: sp\_vertebrate: \*  
14: sp\_unclassified: \*  
15: sp\_virus: \*  
16: sp\_bacteriap: \*  
17: sp\_archaeap: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	33	100.0	295	16	09RL11	09rl11 streptomyc
2	33	100.0	330	17	028938	028938 archaeoglob
3	31	93.9	192	16	09PCP5	09pcp5 xyliella fas
4	31	93.9	266	2	09E085	09e085 corynebacte
5	31	93.9	345	5	09VXR2	09vxx2 drosophila
6	31	93.9	399	5	09NE98	09nev8 leishmania
7	31	93.9	652	5	09V553	09v553 drosophila
8	31	93.9	666	5	08SX14	08sx14 drosophila
9	31	93.9	1006	3	007324	007324 saccharomyc
10	31	93.9	1040	3	094147	094147 saccharomyc
11	31	93.9	1394	3	008409	008409 saccharomyc
12	31	93.9	2297	16	054155	054155 streptomyc
13	31	93.9	10917	2	093NM6	093nm6 streptomyc
14	30	90.9	90	2	050164	050164 mycobacteri
15	30	90.9	124	5	09VP65	09vp65 drosophila
16	30	90.9	154	5	09NSH2	09nsh2 caenorhabdi

17	30	90.9	163	17	09HPE2	09hpe2 halobacteri
18	30	90.9	208	16	09RY28	09ry28 deinococcus
19	30	90.9	231	2	09RHB7	09rnb7 bradyrhizob
20	30	90.9	256	11	09CXU7	09cxu7 mus musculu
21	30	90.9	280	16	097GH1	097gh1 clostridium
22	30	90.9	360	5	016933	016933 ancylostoma
23	30	90.9	365	16	09RL23	09rl23 vibrio chol
24	30	90.9	380	16	09KPM8	09kpm8 yersinia pe
25	30	90.9	384	16	08ZGR2	08zgr2 rhizobium l
26	30	90.9	391	16	098PD4	098pd4 pseudomonas
27	30	90.9	401	16	0916R0	0916r0 streptomyc
28	30	90.9	403	16	091L11	091l11 streptomyc
29	30	90.9	442	5	019242	019242 caenorhabdi
30	30	90.9	453	11	09CUA9	09cu9 mus musculu
31	30	90.9	476	16	09PP46	09pp46 xyliella fas
32	30	90.9	564	11	09CTV2	09ctv2 mus musculu
33	30	90.9	572	16	09S1S8	09s1s8 streptomyc
34	30	90.9	600	4	090FT3	090ft3 homo sapien
35	30	90.9	638	16	09RXV9	09rxv9 schistosach
36	30	90.9	1026	3	042948	042948 streptomyc
37	30	90.9	1293	2	005170	005178 streptomyc
38	30	90.9	1432	2	093NM8	093nm8 streptomyc
39	30	90.9	1471	10	09FRS5	09frs5 arabidopsis
40	30	90.9	4801	2	09AIT3	09ait3 xanthomonas
41	29	87.9	94	16	P74807	P74807 synchocyst
42	29	87.9	110	11	09CT20	09ct20 mus musculu
43	29	87.9	119	16	P72947	P72947 synchocyst
44	29	87.9	119	16	P73748	P73748 synchocyst
45	29	87.9	119	16	P73980	P73980 synchocyst

## ALIGNMENTS

## RESULT 1

09RL11 ID 09RL11 PRELIMINARY; PRT: 295 AA.  
AC 09RL11;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
DE Hypothetical protein SC00307.  
GN SC00307 OR SC569.16.  
OS Streptomyces coelicolor.  
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;  
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.  
OX NCBI\_TaxID=1902;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-A3(2);  
RA Seeger K.J., Harris D.;  
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN-A3(2);  
RA James K.D., Parkhill J., Barrell B.G., Razaandream M.A.;  
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN-A3(2);  
RA Redenbach M., Kleser H.M., Denapalte D., Eichner A., Cullum J.,  
RA Kinashil H., Hopwood D.A.;  
RT "A set of ordered cosmids and a detailed genetic and physical map for  
the 8 Mb streptomycetes coelicolor A3(2) chromosome.";  
RL Mol. Microbiol. 21:77-96(1996).  
RN [4]  
RP SEQUENCE FROM N.A.  
RC STRAIN-A3(2) / M145;  
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,  
RA Thompson N.R., James K.D., Harris D.E., Quail M.A., Kleser H.,  
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,  
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,

RA Huang C.-H., Kleser T., Jarke L., Murphy L., Oliver K., O'Neill S.,  
 RA Rabinowitsch E., Raedemacher M.A., Rutherford K., Rutter S.,  
 RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,  
 RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,  
 RA Hopwood D.A.;  
 RT "Complete genome sequence of the model actinomycete Streptomyces  
 RT coelicolor A3(2)";  
 RL Nature 417:141-147(2002).  
 DR EMBL: AL117385; CAB55664.1; -  
 DR InterPro: IPR002086; Aldehyde\_dehydr.  
 DR InterPro: IPR001387; HTH\_3.  
 DR Pfam: PF01381; HTH\_3; 1.  
 DR SMART: SM00530; HTH\_XRE; 1.  
 DR PROSITE: PS00687; ALDEHYDE\_DEHYDR\_GLU; UNKNOWN\_1.  
 DR Hypothetical protein.  
 KW SEQUENCE 295 AA; 32188 MW; 91AF744D77736075 CRC64;  
 Query Match 100.0%; Score 33; DB 16; Length 295;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDMSAL 6  
 DB 234 LDMSAL 239

RESULT 2  
 ID 028938 PRELIMINARY; PRT; 330 AA.  
 AC 028938;  
 DT 01-JAN-1998 (TREMBlrel. 05, Created)  
 DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)  
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)  
 DE Hypothetical protein AF1331.  
 GN AF1331.  
 OS Archaeoglobus fulgidus.  
 OC Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;  
 OC Archaeoglobaceae; Archaeoglobus.  
 OK NCBI\_TaxID=2234;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=VC-16 / DSM 4304 / ATCC 49558;  
 RC MEDLINE=98049343; PubMed=9389475;  
 RX Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,  
 RA Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,  
 RA Richardson D.L., Kierlavage A.R., Graham D.E., Kyrpides N.C.,  
 RA Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,  
 RA Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,  
 RA Peterson S., Reich C.I., McNeill L.K., Badger J.H., Glodek A., Zhou L.,  
 RA Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,  
 RA Cotton M.D., Spriggs T., Artlich P., Kaine B.P., Sykes S.M.,  
 RA Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,  
 RA Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,  
 RA Venter J.C.;  
 RT "The complete genome sequence of the hyperthermophilic, sulphate-  
 RT reducing archaeon Archaeoglobus fulgidus";  
 RL Nature 390:364-370(1997).  
 DR EMBL: AE001012; AAB89926.1; -  
 DR TIGR: AF131;  
 KW Hypothetical protein; Complete proteome.  
 SO SEQUENCE 330 AA; 38741 MW; 1B32F8BF5E9C7621 CRC64;

Query Match 100.0%; Score 33; DB 17; Length 330;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDMSAL 6  
 DB 177 LDMSAL 182

ID 09PCP5 PRELIMINARY; PRT; 192 AA.  
 AC 09PCP5;  
 DT 01-OCT-2000 (TREMBlrel. 15, Created)  
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)  
 DE Xylophagan repressor binding protein.  
 GN Xyl133.  
 OS Xylella fastidiosa.  
 OC Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;  
 OC Xylella.  
 OK NCBI\_TaxID=2371;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=9A5C;  
 RC MEDLINE=20365717; PubMed=10910347;  
 RX Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M.,  
 RA Alvimenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,  
 RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Bionnes M.R.S.,  
 RA Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carer H.,  
 RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,  
 RA Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorry H.,  
 RA Facincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,  
 RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furian L.R.,  
 RA Garner M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,  
 RA Ho P.L., Hohnsels J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,  
 RA Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,  
 RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,  
 RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,  
 RA Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,  
 RA Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,  
 RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,  
 RA Nham A.Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,  
 RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,  
 RA Peloto B.R., Pereira G.A.G., Pereira H.A.Jr., Pesquero J.B.,  
 RA Queiroz R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,  
 RA de Rosa V.E.Jr., de Sa R.G., Santelli R.V., Sawaaki H.E.,  
 RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A.Jr.,  
 RA da Silveira J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,  
 RA de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsubako M.H.,  
 RA Vallada H., Van Sluys M.A., Verjovsky-Almeida S., Vettore A.L.,  
 RA Zago M.A., Zatz M., Melandis J., Setubal J.C.;  
 RT "The genome sequence of the plant pathogen Xylella fastidiosa";  
 RL Nature 406:151-159(2000).  
 RT Nature 406:151-159(2000).  
 DR EMBL: AE003996; AAF84542.1; -  
 DR InterPro: IPR001226; Flavodoxin.  
 DR Pfam: PF00258; Flavodoxin; 1.  
 DR PROSITE: PS00201; FLAVODOXIN; UNKNOWN\_1.  
 KW Complete proteome.  
 SO SEQUENCE 192 AA; 20309 MW; 38474F2CAC40A7D4 CRC64;

Query Match 93.9%; Score 31; DB 16; Length 192;  
 Best Local Similarity 83.3%; Pred. No. 2.6e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDMSAL 6  
 DB 43 LDMSAL 48

RESULT 4  
 ID 09E085 PRELIMINARY; PRT; 266 AA.  
 AC 09E085;  
 DT 01-MAR-2001 (TREMBlrel. 16, Created)  
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)  
 DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)  
 DE Hypothetical 29.4 kDa protein.  
 GN OFE55.  
 OS Corynebacterium equi (Rhodococcus equi).  
 OG Plasmid pREAR701 (p33701), and plasmid virulence.  
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;  
 OC Actinomycetales; Corynebacteriaceae; Nocardiaceae; Rhodococcus.  
 OK NCBI\_TaxID=43767;

RN [1]  
 RC SEQUENCE FROM N.A.  
 RC STRAIN=ATCC33701; PLASMID=PREAT701 (P33701);  
 RA Takai S., Sekizaki T., Kakuda T., Nakamura M., Suzuki K., Ogino N.;  
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC33701, AND 103; PLASMID=PREAT701 (P33701), AND VIRULENCE;  
 RX PubMed-11083803;  
 RA Takai S., Hines S.A., Sekizaki T., Nicholson V.M., Alperin D.A.,  
 RA Oskai M., Takamatsu D., Nakamura M., Suzuki K., Ogino N., Kakuda T.,  
 RA Dan H., Prescott J.F.;  
 RT "DNA sequence and comparison of virulence plasmids from Rhodococcus  
 RT equi ATCC 33701 and 103";  
 RL Infect. Immun. 68:6840-6847(2000).  
 DR EMBL: AP001204; BAB16664.1; -;  
 DR EMBL: AF116907; BAG21758.1; -;  
 KW Hypothetical protein; Plasmid.  
 SQ SEQUENCE 266 AA; 29450 MW; 26B9B089717FFB6 CRC64;

Query Match 93.9%; Score 31; DB 2; Length 266;  
 Best Local Similarity 83.3%; Pred. NO. 3.5e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSAL 6  
 DB 30 LDMSAI 35

RESULT 5

Q9VXR2 PRELIMINARY; PRT; 345 AA.  
 AC Q9VXR2;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
 DE CG8191 protein (REL1665p).  
 GN CG8191.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachyera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 NC NCB1\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BERKELEY;  
 RX MEDLINE-20196006; PubMed-10731132;  
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
 RA Abiri J.F., Aghayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Bertman B.P., Bhandari D., Bolshakov S.,  
 RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotier P.,  
 RA Burks K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
 RA Foster C., Gabrielian A.E., Gary N.S., Gelbart W.M., Glasser K.,  
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Idegian C.,  
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Klumel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., Moherson D.,  
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,

RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Sytkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of Drosophila melanogaster";  
 RL Science 287:2185-2195(2000).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BERKELEY;  
 RA Stapleton M., Brokstein P., Hong L., Aghayani A., Carlson J.,  
 RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,  
 RA George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,  
 RA Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,  
 RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,  
 RA Celniker S.;  
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AE003500; AAF48496.1; -;  
 DR EMBL: AY071134; AAL48756.1; -;  
 DR Flybase; FBgn0030675; CG8191.  
 SQ SEQUENCE 345 AA; 39831 MW; 0613409F8F007B9C CRC64;

Query Match 93.9%; Score 31; DB 5; Length 345;  
 Best Local Similarity 83.3%; Pred. No. 4.6e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSAL 6  
 DB 136 LDMSAI 141

RESULT 6

Q9NE98 PRELIMINARY; PRT; 399 AA.  
 AC Q9NE98;  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
 DE Hypothetical 43.5 kDa protein.  
 GN I4803.06.  
 OS Leishmania major.  
 OC Eukaryota; Euzoenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.  
 NC NCB1\_TaxID=5664;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=FRIDLIN;  
 RA Masuy D., Purnelle B., Goffeau A., Ivens A.C., Quail M.,  
 RA Rasmundrem M.A., Bartell B.G.;  
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=FRIDLIN;  
 RX MEDLINE-98146435; PubMed-9477341;  
 RA Ivens A.C., Lewis S.M., Bagherzadeh A., Zhang L., Chan H.M.,  
 RA Smith D.F.;  
 RT "A physical map of the Leishmania major Friedlin genome.";  
 RL Genome Res. 8:135-145(1998).  
 DR EMBL: AL161416; CAB77684.1; -;  
 KW Hypothetical protein.  
 SQ SEQUENCE 399 AA; 43458 MW; BB86021C2BBB3E18 CRC64;

Query Match 93.9%; Score 31; DB 5; Length 399;  
 Best Local Similarity 83.3%; Pred. No. 5.3e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSAL 6  
 DB 388 LDMSAI 393

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RESULT 7
ID 09V553 PRELIMINARY; PRT; 652 AA.
AC 09V553:
DT 01-MAY-2000 (TEMBLrel. 13, Created)
DT 01-MAY-2000 (TEMBLrel. 13, Last sequence update)
DE 01-JUN-2001 (TEMBLrel. 17, Last annotation update)
DE CG8027 protein.
GN CG8027.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
RX MEDLINE-20196006; PubMed-10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champagne M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Milos G.L.G.,
RA Abtill J.F., Adhyani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Bens P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borovica D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
RA Burla K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Gary N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwan C.,
RA Jaitani M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Kethum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laeso P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mallet B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclob J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Rehner K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spler E., Spreading A.C., Stapleton M., Strong R., Sun E.,
RA Svrtkars R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weisslock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhan M., Zhan G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
DR EMBL; AE003834; AAF58967.1;
DR FlyBase; FBgn0033392; CG8027.
DR InterPro; IPR000800; Notch.
DR Pfam; PF00066; notch.1.
DR SMART; SM00004; NL; 1.
SQ SEQUENCE 652 AA; 75752 MW; 2728764810039458 CRC64;

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Query Match 93.9%; Score 31; DB 5; Length 652;
Best Local Similarity 83.3%; Pred. No. 8.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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OY 1 LDMSAL 6.
DB 447 LDMSAM 452

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RESULT 8
ID 08SX14 PRELIMINARY; PRT; 666 AA.
AC 08SX14:
DT 01-JUN-2002 (TEMBLrel. 21, Created)
DT 01-JUN-2002 (TEMBLrel. 21, Last sequence update)
DE 01-JUN-2002 (TEMBLrel. 21, Last annotation update)
DE RE35033p.
GN CG8027.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
RX MEDLINE-941169519; PubMed-7764548;
RA Lee Y.S., Shimizu J., Yoda K., Yamasaki M.,
RA "Molecular cloning of a gene, DHS1, which complements a drug-
RA hypersensitive mutation of the yeast Saccharomyces cerevisiae."
RA Biosci. Biotechnol. Biochem. 58:391-395(1994).
RL EMBL; X87331; CAA60760.1;
SQ SEQUENCE 666 AA; 77745 MW; F6FDB6D1C1C39248 CRC64;

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Query Match 93.9%; Score 31; DB 5; Length 666;
Best Local Similarity 83.3%; Pred. No. 8.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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OY 1 LDMSAL 6
DB 461 LDMSAM 466

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RESULT 9
ID 007324 PRELIMINARY; PRT; 1006 AA.
AC 007324:
DT 01-NOV-1996 (TEMBLrel. 01, Created)
DT 01-NOV-1996 (TEMBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TEMBLrel. 21, Last annotation update)
DE ATP dependent permease (Yeast homolog).
GN AUS1 AND YOR011W.
OS Saccharomyces cerevisiae (Baker's Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBI_TaxID=4932;
RX MEDLINE-94019318; PubMed-8413243;
RA Dumont M.E., Schlichter J.B., Cardillo T.S., Hayes M.K., Bethlendy G.,
RA Sherman F.;
RT "CYC2 encodes a factor involved in mitochondrial import of yeast
RT cytochrome c."
RL Mol. Cell. Biol. 13:6442-6451(1993).
SQ SEQUENCE FROM N.A.
RX STRAIN-FY1679;
RX MEDLINE-941169519; PubMed-7764548;
RA Lee Y.S., Shimizu J., Yoda K., Yamasaki M.,
RA "Molecular cloning of a gene, DHS1, which complements a drug-
RA hypersensitive mutation of the yeast Saccharomyces cerevisiae."
RL EMBL; X87331; CAA60760.1;

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DR SGD: S0005537; AUSL.
DR InterPro: IPR003593; AAA_ATPase.
DR InterPro: IPR003439; ABC_transportr.
DR InterPro: IPR001202; WW_Rsp5_WMP.
DR Pfam: PF00005; ABC_tran; 1.
DR ProDom: PD000006; ABC_transportr; 1.
DR SMART: SM00382; AAA; 1.
DR PROSITE: PS01159; WW_DOMAIN_1; UNKNOWN_1.
DR ATP-binding.
SQ SEQUENCE 1006 AA; 113961 MW; 0EA9408A1AD1CA7F CRC64;

Query Match          93.9%; Score 31; DB 3; Length 1006;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSAL 6
Db 629 IDMSAL 634

RESULT 10
094147 PRELIMINARY; PRT; 1040 AA.
ID 094147;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE ORF YOR011W (Fragment).
GN AUSL OR YOR011W.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RX NCBL_TaxID=4932;
RN RA PETERSSON B., STERKY F., UHLEN M.;
RP Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
RL [2]
RN RA De haan M., Grievell L.A., Maarse A.C.;
RP Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
RL [3]
RN RP SEQUENCE FROM N.A.
RA MIPS;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: Z74920; CAA99202.1; -.
DR SGD: S0005537; AUSL.
DR InterPro: IPR003593; AAA_ATPase.
DR InterPro: IPR003439; ABC_transportr.
DR InterPro: IPR001202; WW_Rsp5_WMP.
DR Pfam: PF00005; ABC_tran; 1.
DR ProDom: PD000006; ABC_transportr; 1.
DR SMART: SM00382; AAA; 1.
DR PROSITE: PS01159; WW_DOMAIN_1; UNKNOWN_1.
DR ATP-binding.
FT NON_TER 1
SQ SEQUENCE 1040 AA; 117840 MW; B32B0F1D33906B5C CRC64;

Query Match          93.9%; Score 31; DB 3; Length 1040;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSAL 6
Db 663 IDMSAL 668

RESULT 11
008409 PRELIMINARY; PRT; 1394 AA.
ID 008409;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)

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DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Chromosome XV reading frame ORF YOR011W.
GN AUSL OR YOR011W.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RX NCBL_TaxID=4932;
RN RA PETERSSON B., STERKY F., UHLEN M.;
RP Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
RL [2]
RN RA De haan M., Grievell L.A., Maarse A.C.;
RP Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
RL [3]
RN RP SEQUENCE FROM N.A.
RA MIPS;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: Z74919; CAA99199.1; -.
DR SGD: S0005537; AUSL.
DR InterPro: IPR003593; AAA_ATPase.
DR InterPro: IPR003439; ABC_transportr.
DR InterPro: IPR001202; WW_Rsp5_WMP.
DR Pfam: PF00005; ABC_tran; 2.
DR ProDom: PD000006; ABC_transportr; 2.
DR SMART: SM00382; AAA; 1.
DR PROSITE: PS00211; ABC_TRANSPORTER; UNKNOWN_1.
DR PROSITE: PS01159; WW_DOMAIN_1; UNKNOWN_1.
DR ATP-binding.
SQ SEQUENCE 1394 AA; 157749 MW; 357A35A0FCF0C93B CRC64;

Query Match          93.9%; Score 31; DB 3; Length 1394;
Best Local Similarity 83.3%; Pred. No. 1.8e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSAL 6
Db 1017 IDMSAL 1022

RESULT 12
054155 PRELIMINARY; PRT; 2297 AA.
ID 054155;
AC 054155;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Polyketide synthase.
GN SC05892 OR SC3F7.12.
OS Streptomyces coelicolor.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycinae; Streptomycetaceae; Streptomyces.
OX NCBL_TaxID=1902;
RX NCBL_TaxID=1902;
RN RA PETERSSON B., STERKY F., UHLEN M.;
RP Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
RL [2]
RN RA Oliver K., Harris D.;
RP Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
RL [3]
RN RP SEQUENCE FROM N.A.
RA STRAIN-A3(2);
RC STRAIN-A3(2);
RA Parkhill J., Barrrell B.G., Rastandream M.A.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RN RP SEQUENCE FROM N.A.
RC STRAIN-A3(2);
RC MEDLINE=97000351; PubMed=8843436;
RA Redendach M., Kleser H.M., Denapate D., Eichner A., Cullum J.,
RA Kinasht H., Hopwood D.A.;
RT "A set of ordered cosmids and a detailed genetic and physical map for
the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
RT Mol. Microbiol. 21:77-96(1996).

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RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN-A3(2) / M145;
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
RA Thomson S.R., James K.D., Harris D.E., Quail M.A., Kleeser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornaby T., Howarth S.,
RA Huang C.-H., Kleeser T., Laire L., Murphy L., Oliver K., O'Neil S.,
RA Rabinovitch E., Rajandream M.A., Rutherford K., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA Warren T., Wietzorrek A., Woodward J., Barrett B.G., Parkhill J.,
RA Hopwood D.A.;
RT *Complete genome sequence of the model actinomycete Streptomyces
RT coelicolor A3(2).;
RL Nature 417:141-147(2002).
DR EMBL; AL021409; CAA16183.1; -
DR HSSP; P25715; IMLA.
DR InterPro: IPR001227; Ac_transferase.
DR InterPro: IPR003408; Ala_synthase.
DR InterPro: IPR004839; AminoTransfer1/2.
DR InterPro: IPR000873; AMP-bind.
DR InterPro: IPR000794; ketoacyl-synt.
DR InterPro: IPR001917; NHTransf_2.
DR InterPro: IPR003880; Ppantne_attach.
DR Pfam; PF02498; Acyl_transf; 1.
DR Pfam; PF02498; Ala_synthase; 1.
DR Pfam; PF02498; aminotran_1_2; 1.
DR Pfam; PF00501; AMP-binding; 1.
DR Pfam; PF00501; ketoacyl-synt; 1.
DR Pfam; PF02801; ketoacyl-synt.C; 1.
DR Pfam; PF00550; pp-binding; 1.
DR PRINTS; PR00156; AMPBINDING.
DR PROSITE; PS00599; AA_TRANSF_CLASS_2; UNKNOWN_1.
DR PROSITE; PS00075; ACP_DOMAIN; 2.
DR PROSITE; PS00606; B_KETOACYL_SYNTHASE; 1.
DR Phosphopantetheine; Transferase.
KM SEQUENCE 2297 AA; 241989 MW; C67B58461535EE46 CRC64;

Query Match 93.9%; Score 31; DB 16; Length 2297;
Best Local Similarity 83.3%; Pred. No. 2.9e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSAL 6
DB 1641 IDMSAL 1646

RESULT 13
O93NM6 PRELIMINARY; PRT; 10917 AA.
ID O93NM6;
AC O93NM6;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE AmpHC.
GN AMPHC.
OS Streptomyces nodosus.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomyces; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=40318;
RN [1]
RP SEQUENCE FROM N.A.
RA Caffrey P., Lynch S.V., Flood E.M., Finnan S.M., O'Leary M.,
RT "The amphoterin biosynthetic gene cluster from Streptomyces
RT nodosus.";
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF357202; AAK73514.1; -
DR InterPro: IPR001227; Ac_transferase.
DR InterPro: IPR002328; ADH_zinc.
DR InterPro: IPR002085; Adh_zn_family.
DR InterPro: IPR004410; Fadd.
DR InterPro: IPR000794; Ketoacyl-synt.
DR InterPro: IPR003880; Ppantne_attach.

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DR Pfam; PF00698; Acyl_transf; 6.
DR Pfam; PF00107; adh_zinc; 1.
DR Pfam; PF00109; ketoacyl-synt; 6.
DR Pfam; PF02801; ketoacyl-synt.C; 6.
DR Pfam; PF00550; pp-binding; 6.
DR TIGRfams; TIGR0128; fadd; 6.
DR PROSITE; PS00075; ACP_DOMAIN; 6.
DR PROSITE; PS00059; ADH_ZINC; UNKNOWN_1.
DR PROSITE; PS00606; B_KETOACYL_SYNTHASE; UNKNOWN_6.
DR PROSITE; PS00012; PHOSPHOPANTHETHEINE; UNKNOWN_5.
KM Phosphopantetheine.
SO SEQUENCE 10917 AA; 1132905 MW; 15AC5956B5810A1 CRC64;

Query Match 93.9%; Score 31; DB 2; Length 10917;
Best Local Similarity 83.3%; Pred. No. 1.3e+04;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSAL 6
DB 8165 IDMSAL 8170

RESULT 14
O50164 PRELIMINARY; PRT; 90 AA.
ID O50164;
AC O50164;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-NOV-1996 (TREMBLrel. 01, Last annotation update)
DE U2965.
OS Mycobacterium leprae.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacteriaceae; Mycobacterium.
OX NCBI_TaxID=1769;
RN [1]
RP SEQUENCE FROM N.A.
RA Smith D.R.;
RL Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Robison K.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U15187; AAA63116.1; -
DR SEQUENCE 90 AA; 9642 MW; F0187130F441A846 CRC64;

Query Match 90.9%; Score 30; DB 2; Length 90;
Best Local Similarity 83.3%; Pred. No. 1.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSAL 6
DB 65 LDMSAL 70

RESULT 15
O9VP65 PRELIMINARY; PRT; 124 AA.
ID O9VP65;
AC O9VP65;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE CG12975 protein (RES7810p).
GN CG12975.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Ceiniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

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RA Amanatides P.C., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Mortan J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.-H.C., Blazef R.G., Champe M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
 RA Abri J.F., Agbayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,  
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,  
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
 RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Glodde A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Idegami C.,  
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,  
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spler E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissendach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of *Drosophila melanogaster*.";  
 RL Science 287:2185-2195(2000).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BERKELEY;  
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,  
 RA Champe M., Chavez C., Dorsett V., Drensek D., Farfan D., Frise E.,  
 RA George R., Gonzalez M., Guartin H., Krommiller B., Li P., Liao G.,  
 RA Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,  
 RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,  
 RA Celinker S.;  
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF003593; AAF51690.1; -;  
 DR EMBL; AY071539; AAL49161.1; -;  
 DR FlyBase; FBgn0037061; CG12975.  
 SQ SEQUENCE 124 AA: 13920 MW: 3C37D84DEAF8767F CRC64;

Query Match 90.9%; Score 30; DB 5; Length 124;  
 Best Local Similarity 83.3%; Pred. NO. 2.6e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSAL 6  
 Db 49 LDMSAV 54

Search completed: May 30, 2003, 14:39:02  
 Job time : 16.7632 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 30, 2003, 14:32:12 ; Search time 6.5921 Seconds

(without alignments)  
87.500 Million cell updates/sec

Title: US-09-643-260-14

Perfect score: 35

Sequence: 1 LDMSFL 6

Scoring table: BLOSUM62

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : PIR\_73:\*

1: p1r1:\*

2: p1r2:\*

3: p1r3:\*

4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	35	100.0	136	2 S74785	hypothetical prote
2	35	100.0	362	2 T32669	hypothetical prote
3	35	100.0	573	2 A61969	sulfate permease f
4	35	100.0	2658	2 A86216	protein T23618.2 f
5	33	94.3	962	2 T05845	hypothetical prote
6	32	91.4	176	2 T32618	hypothetical prote
7	32	91.4	203	2 B97600	hypothetical prote
8	32	91.4	203	2 AB2822	conserved hypotet
9	32	91.4	339	2 C86874	ABC transporter pe
10	32	91.4	377	2 T36246	probable glycolate
11	32	91.4	404	2 A64151	hypothetical prote
12	32	91.4	556	2 S76624	integral membrane
13	32	91.4	927	2 AG1739	transmembrane prot
14	32	91.4	927	2 AH1369	transmembrane prote
15	32	91.4	939	2 AE2275	hypothetical prote
16	32	91.4	1466	2 T39557	vacuolar protein s
17	31	88.6	21	2 A60420	lens intrinsic mem
18	31	88.6	135	2 S59886	C2 protein - toma
19	31	88.6	135	1 OOCVCA	hypothetical prote
20	31	88.6	135	2 S07593	hypothetical prote
21	31	88.6	204	2 AB0188	phosphoribosyl-ATP
22	31	88.6	225	2 T17795	hypothetical prote
23	31	88.6	242	2 B96571	hypothetical prote
24	31	88.6	264	2 S51829	alpha-amylase inh
25	31	88.6	266	2 B84848	hypothetical prote
26	31	88.6	350	2 G98302	thermophilic desul
27	31	88.6	350	2 AG2980	dibenzothienophene d
28	31	88.6	355	2 A12867	endo-1,4-beta-xyla
29	31	88.6	356	1 A42053	gap junction prote

30	31	88.6	357	2 A49024	connexin40 - dog
31	31	88.6	358	2 S23111	connexin 40 - mous
32	31	88.6	358	2 I38429	connexin40 - human
33	31	88.6	365	2 E97644	endo-1,4-beta-xyla
34	31	88.6	369	2 B37819	connexin-42 - chic
35	31	88.6	383	2 T38772	protein phosphatas
36	31	88.6	400	2 T11921	MDH2 dehydrogenas
37	31	88.6	400	2 I50219	connexin 45.6 - ch
38	31	88.6	402	2 I46053	connexin44 - bovin
39	31	88.6	416	2 S25764	connexin 46 - rat
40	31	88.6	440	2 I39176	intrinsic membrane
41	31	88.6	442	2 T49624	gap junction prote
42	31	88.6	510	2 A45338	connexin-56 - chic
43	31	88.6	569	2 T43531	probable potassium
44	31	88.6	570	2 H87368	copper-binding pro
45	31	88.6	575	2 D84668	hypothetical prote

## ALIGNMENTS

## RESULT 1

S74785 hypothetical protein slr1082 - Synechocystis sp. (strain PCC 6803)

C:Species: Synechocystis sp.

A:Variety: PCC 6803

C:Date: 25-Apr-1997 #sequence\_revision 25-Apr-1997 #text\_change 21-Jul-2000

C:Accession: S74785

R:Kaneko, T., Sato, S., Kotani, H., Tanaka, A., Asamizu, E., Nakamura, Y., Miyajima, O., K., Okumura, S., Shimpo, S., Takeuchi, C., Wada, T., Watanabe, A., Yamada, M., Yas

DNA Res. 3, 109-136, 1996

A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocys

S. A:Reference number: S74782; MUID:97061201; PMID:8905231

A:Accession: S74785

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-136 <KAN>

A:Cross-references: EMBL:D90901; GB:AB001339; NID:q1651897; PIDN:BA16936.1; PID:q165

C:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

C:Superfamily: Synechocystis hypothetical protein slr0489

Query Match

Best Local Similarity 100.0%; Score 35; DB 2; Length 136;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query 1 LDMSFL 6

Db 42 LDMSFL 47

RESULT 2

T32669 hypothetical protein F16B4.2 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 29-Oct-1999

R:Davidson, S.; Wohldmann, P.; Bauer, C.; O'Neal, D.

submitted to the EMBL Data Library/ December 1997

A:Description: The sequence of C. elegans cosmid F16B4.

A:Reference number: Z21208

A:Accession: T32669

A:Molecule type: DNA

A:Residues: 1-362 <DAV>

A:Cross-references: EMBL:AF039048; PIDN:AB94233.1; GSPDB:GN00023; CESP:F16B4.2

C:Experimental source: strain Bristol N2; clone F16B4

A:Gene: CESP:F16B4.2

A:Map position: 5

A:Introns: 48/2; 112/2; 160/3; 255/3; 291/2; 333/3

Query Match

Best Local Similarity 100.0%; Score 35; DB 2; Length 362;

Best Local Similarity 100.0%; Pred. No. 47;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDMSFL 6  
|||||  
DB 26 LDMSFL 31

## RESULT 3

AE1969 sulfate permease family protein [imported] - Nostoc sp. (strain PCC 7120)

C:Species: Nostoc sp.  
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120  
C>Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 30-Jun-2002  
C:Accession: AE1969  
R:Kaneko, T.; Nakamura, Y.; Molk, C.P.; Kunitz, T.; Sasamoto, S.; Watanabe, A.; Iriyuch  
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S  
DNA Res. 8, 205-213, 2001  
A:Title: Complete genomic sequence of the filamentous nitrogen-fixing Cyanobacterium Ana  
A:Reference number: AB1807; MUID:21595285; PMID:11759840  
A:Accession: AE1969  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-573 <KUR>  
A:Cross-references: GB:BA000019; PIDN:BA073261.1; PID:g17130651; GSPDB:GN00179  
A:Experimental source: strain PCC 7120  
C:Genetics:  
A:Gene: all1304  
C:Superfamily: Integral membrane protein HP0228

Query Match 100.0%; Score 35; DB 2; Length 573;  
Best Local Similarity 100.0%; Pred. No. 74;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDMSFL 6  
|||||  
DB 357 LDMSFL 362

## RESULT 4

AB6216 protein T23G18.2 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)  
C>Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 31-Mar-2001  
C:Accession: AB6216  
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,  
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;  
ansen, N.F.; Hughes, B.; Hultzer, L.  
Nature 408, 816-820, 2000  
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.  
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maitl, R.; Marziani,  
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,  
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
A:Reference number: AB6141; MUID:21016719; PMID:11130712  
A:Accession: AB6216  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-2658 <STO>  
A:Cross-references: GB:AE005172; NID:g6579214; PIDN:AA18257.1; GSPDB:GN00141  
C:Genetics:  
A:Gene: T23G18.2  
A:Map position: 1

Query Match 100.0%; Score 35; DB 2; Length 2658;  
Best Local Similarity 100.0%; Pred. No. 3,66+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDMSFL 6  
|||||  
DB 2221 LDMSFL 2226

RESULT 5  
T05845 hypothetical protein F17L22.160 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)  
C>Date: 09-Apr-1999 #sequence\_revision 09-Apr-1999 #text\_change 24-Nov-1999  
C:Accession: T05845  
R:Bevan, M.; Van Der Schueren, J.; Chuang, Y.J.; Voel, M.; Robben, J.; Volckaert, G.;  
submitted to the Protein Sequence Database, February 1999  
A:Reference number: Z15454  
A:Accession: T05845  
A:Molecule type: DNA  
A:Residues: 1-962 <BEV>  
A:Cross-references: EMBL:AL035527  
A:Experimental source: cultivar Columbia; BAC clone F17L22  
C:Genetics:  
A:Map position: 4  
A:Note: F17L22.160  
C:Superfamily: Arabidopsis thaliana hypothetical protein F17L22.160

Query Match 94.3%; Score 33; DB 2; Length 962;  
Best Local Similarity 83.3%; Pred. No. 2,9e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDMSFL 6  
|||||  
DB 889 LDMSFL 894

## RESULT 6

T32618 hypothetical protein F42A6.5 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans  
C>Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 29-Oct-1999  
C:Accession: T32618  
R:Du, Z.; Scheet, P.; Andrews, S.  
submitted to the EMBL Data Library, December 1997  
A:Description: The sequence of C. elegans cosmid F42A6.  
A:Reference number: Z21201  
A:Accession: T32618  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-176 <DUZ>  
A:Cross-references: EMBL:AF038613; PIDN:AB92050.1; GSPDB:GN00022; CESP:F42A6.5  
A:Experimental source: strain Bristol N2; clone F42A6  
C:Genetics:  
A:Gene: CESP:F42A6.5  
A:Map position: 4  
A:introns: 51/3; 109/3

Query Match 91.4%; Score 32; DB 2; Length 176;  
Best Local Similarity 83.3%; Pred. No. 77;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDMSFL 6  
|||||  
DB 37 LDMSFL 42

## RESULT 7

B97600 hypothetical protein AGR\_C-3633 [imported] - Agrobacterium tumefaciens (strain C58, C

C:Species: Agrobacterium tumefaciens  
C>Date: 30-Sep-2001 #sequence\_revision 30-Sep-2001 #text\_change 11-Jan-2002  
C:Accession: B97600  
R:Goodner, B.; Hinkle, G.; Gattling, S.; Miller, N.; Blanchard, M.; Quirolo, B.; Goldm  
Science 294, 2323-2328, 2001  
A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium  
A:Reference number: A97359; PMID:11743194  
A:Accession: B97600  
A:Status: preliminary  
A:Molecule type: DNA

A:Residues: 1-203 <KUR>  
 A:Cross-references: GB:AE007869; PIDN:AAK87755.1; PID:915157123; GSPDB:GN00169  
 C:Genetics:  
 A:Gene: AGR\_C\_3633  
 A:Map position: circular chromosome

Query Match 91.4%; Score 32; DB 2; Length 203;  
 Best Local Similarity 83.3%; Pred. No. 89;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDMSFL 6  
 |||:|  
 Db 140 LDMSFL 145

RESULT 8  
 conserved hypothetical protein Atul999 [Imported] - Agrobacterium tumefaciens (strain C5  
 C:Species: Agrobacterium tumefaciens  
 C:Date: 11-Jan-2002 #sequence\_revision 11-Jan-2002 #text\_change 11-Jan-2002  
 C:Accession: AB2822  
 R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Moo, I.  
 ; Karp, P.; Romero, P.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClell  
 Science 294, 2317-2323, 2001  
 A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,  
 ster, E.W.  
 A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.  
 A:Reference number: AB2577; PMID:11743193  
 A:Accession: AB2822  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-203 <KUR>  
 A:Cross-references: GB:AE008688; PIDN:AAL42992.1; PID:917740453; GSPDB:GN00186  
 C:Genetics:  
 A:Gene: Atul999  
 A:Map position: circular chromosome

Query Match 91.4%; Score 32; DB 2; Length 203;  
 Best Local Similarity 83.3%; Pred. No. 89;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDMSFL 6  
 |||:|  
 Db 140 LDMSFL 145

RESULT 9  
 C86874  
 ABC transporter permease protein ecsb [Imported] - Lactococcus lactis subsp. lactis (str  
 C:Species: Lactococcus lactis subsp. lactis  
 C:Date: 23-Mar-2001 #sequence\_revision 23-Mar-2001 #text\_change 03-Aug-2001  
 C:Accession: C86874  
 R:Boletín, A.; Wincker, P.; Mauger, S.; Jallón, O.; Malarme, K.; Weissenbach, J.; Ehrli  
 Genome Res. 11, 731-753, 2001  
 A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis s  
 A:Reference number: A86625; MUID:21235186; PMID:11337471  
 A:Accession: C86874  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-339 <STO>  
 A:Cross-references: GB:AE005176; PID:912725040; PIDN:AAK06093.1; GSPDB:GN00146  
 A:Experimental source: strain IL1403  
 C:Genetics:  
 A:Gene: ecsb

Query Match 91.4%; Score 32; DB 2; Length 339;  
 Best Local Similarity 83.3%; Pred. No. 1.5e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDMSFL 6  
 |||:|

Db 158 LDMAFL 163

RESULT 10  
 T36246  
 Probable glycolate oxidase - Streptomyces coelicolor  
 C:Species: Streptomyces coelicolor  
 C:Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 28-Jul-2000  
 C:Accession: T36246  
 R:Saunders, D.C.; Harris, D.; Bentley, S.D.; Partridge, J.; Barrell, B.G.; Rajandream,  
 submitted to the EMBL Data Library, March 1999  
 A:Reference number: Z21602  
 A:Accession: T36246  
 A:Molecule type: DNA  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Residues: 1-377 <SAU>  
 A:Cross-references: EMBL:AL035640; PIDN:CAB38520.1; GSPDB:GN00070; SCOEDB:SC63.05  
 A:Experimental source: strain A3(2)  
 C:Genetics:  
 A:Gene: SCOEDB:SC63.05  
 A:Superfamily: (S)-2-hydroxy-acid oxidase (S)-2-hydroxy-acid oxidase homology  
 F:2-296/Domain: (S)-2-hydroxy-acid oxidase homology <2HX>

Query Match 91.4%; Score 32; DB 2; Length 377;  
 Best Local Similarity 83.3%; Pred. No. 1.7e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDMSFL 6  
 |||:|  
 Db 207 LDMSFL 212

RESULT 11  
 A64151  
 hypothetical protein HI0396 - Haemophilus influenzae (strain Rd KW20)  
 C:Species: Haemophilus influenzae  
 C:Date: 18-Aug-1995 #sequence\_revision 18-Aug-1995 #text\_change 08-Oct-1999  
 C:Accession: A64151  
 R:Feilschmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Keriavag  
 ; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodet, A.; Kelley, J.M.; Weidman  
 ; D.M.; Brandon, R.C.; Pine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.  
 Science 269, 496-512, 1995  
 A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Vente  
 A:Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.  
 A:Reference number: A64000; MUID:95350630; PMID:7542800  
 A:Accession: A64151  
 A:Status: nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-404 <TIGR>  
 A:Cross-references: GB:U32723; GB:L42023; MID:91573363; PIDN:AAK22055.1; PID:91573367  
 A:Note: best homolog was a hypothetical protein from Escherichia coli

Query Match 91.4%; Score 32; DB 2; Length 404;  
 Best Local Similarity 83.3%; Pred. No. 1.8e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDMSFL 6  
 |||:|  
 Db 366 LDMAFL 371

RESULT 12  
 S76624  
 Integral membrane protein HP0228 homolog 2 - Synecchocystis sp. (strain PCC 6803)  
 N:Alternate names: low affinity sulfate transporter; protein slr096  
 C:Species: Synecchocystis sp.  
 A:Valley: PCC 6803  
 C:Date: 25-Apr-1997 #sequence\_revision 25-Apr-1997 #text\_change 20-Jun-2000  
 C:Accession: S76624  
 R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima,  
 O. K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yas  
 DNA Res. 3, 109-136, 1996  
 A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synecchocys

S:  
 A:Reference number: S74322; MWID:97061201; PMID:8905231  
 A:Accession: S76624  
 A:Status: nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-556 <RAN>  
 A:Cross-references: EMBL:DB4004; GB:AB001339; NID:g1001701; PIDN:BA10568.1; PID:g100173  
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996  
 C:Superfamily: Integral membrane protein HP0228

Query Match 91.4%; Score 32; DB 2; Length 556;  
 Best Local Similarity 83.3%; Pred. No. 2.5e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDMSFL 6  
 DB 364 VDMNFL 369

## RESULT 13

transmembrane protein [imported] - *Listeria innocua* (strain C1p11262)  
 C:Species: *Listeria innocua*  
 C:Date: 27-Nov-2001 #sequence\_revision 27-Nov-2001 #text\_change 27-Nov-2001

R:Glaser, P.; Frangoul, L.; Buchleser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker, D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entlian, K.D.; Fshl, H.; Jones, L.M.; Karst, U.  
 Science 294, 849-852, 2001

A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkut, G.; Madueno, E.; Maltournam, A.; Maok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlend, A.; Title: Comparative genomics of *Listeria* species  
 A:Reference number: AB1077; MWID:21537279; PMID:11679669  
 A:Accession: AG1739  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-927 <GLA>

A:Cross-references: GB:AL592022; PIDN:CAC97687.1; PID:g16441982; GSPDB:GN00178  
 A:Experimental source: strain C1p11262  
 C:Genetics:  
 A:Gene: lln2460

Query Match 91.4%; Score 32; DB 2; Length 927;  
 Best Local Similarity 83.3%; Pred. No. 4.2e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDMSFL 6  
 DB 83 LDMNFL 88

## RESULT 14

transmembrane protein [imported] - *Listeria monocytogenes* (strain EGD-e)  
 C:Species: *Listeria monocytogenes*  
 C:Date: 27-Nov-2001 #sequence\_revision 27-Nov-2001 #text\_change 27-Nov-2001

R:Glaser, P.; Frangoul, L.; Buchleser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker, D.; Jones, L.M.; Karst, U.  
 Science 294, 849-852, 2001  
 A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkut, G.; Madueno, E.; Maltournam, A.; Maok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlend, A.; Title: Comparative genomics of *Listeria* species  
 A:Reference number: AB1077; MWID:21537279; PMID:11679669

A:Accession: AG1739  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-927 <GLA>

A:Cross-references: GB:NC\_003210; PIDN:CAD00438.1; PID:g16411848; GSPDB:GN00177  
 A:Experimental source: strain EGD-e  
 C:Genetics:  
 A:Gene: lmo2360

Query Match 91.4%; Score 32; DB 2; Length 927;  
 Best Local Similarity 83.3%; Pred. No. 4.2e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDMSFL 6  
 DB 83 LDMNFL 88

## RESULT 15

hypothetical protein alr3756 [imported] - *Nostoc* sp. (strain PCC 7120)  
 AE2275

C:Species: *Nostoc* sp.  
 A:Note: *Nostoc* sp. strain PCC 7120 is a synonym of *Anabaena* sp. strain PCC 7120  
 C:Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 30-Jun-2002

R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Irigu Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata DNA Res. 8, 205-213, 2001

A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium  
 A:Reference number: AB1807; MWID:21595285; PMID:11759840  
 A:Accession: AE2275  
 A:Status: preliminary  
 A:Molecule type: DNA

A:Residues: 1-939 <KUR>  
 A:Cross-references: GB:BA000019; PIDN:BAW75455.1; PID:g17132890; GSPDB:GN00179  
 A:Experimental source: strain PCC 7120  
 C:Genetics:  
 A:Gene: alr3756

Query Match 91.4%; Score 32; DB 2; Length 939;  
 Best Local Similarity 83.3%; Pred. No. 4.3e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDMSFL 6  
 DB 648 LDMSTL 653

Search completed: May 30, 2003, 14:52:57  
 Job time : 7.5921 secs

Good

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 30, 2003, 14:32:11 ; Search time 14.7632 Seconds  
(Without alignments)  
83.741 Million cell updates/sec

Title: US-09-643-260-14  
Perfect score: 35  
Sequence: 1 LDMSFL 6

Scoring table: BLOSUM62  
Gap 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues  
Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

SPRMBL\_21: \*  
1: sp\_archaea: \*  
2: sp\_bacteria: \*  
3: sp\_fungi: \*  
4: sp\_human: \*  
5: sp\_invertebrate: \*  
6: sp\_mammal: \*  
7: sp\_mhc: \*  
8: sp\_organelle: \*  
9: sp\_phage: \*  
10: sp\_plant: \*  
11: sp\_rodent: \*  
12: sp\_virus: \*  
13: sp\_vertebrate: \*  
14: sp\_unclassified: \*  
15: sp\_virus: \*  
16: sp\_bacteriap: \*  
17: sp\_archaeap: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	35	100.0	136	P72919	P72919 synchocyst
2	35	100.0	362	5	044634
3	35	100.0	573	16	08YXB1
4	35	100.0	2621	10	09LMZ3
5	35	100.0	2658	10	09SGE4
6	33	94.3	732	5	061565
7	33	94.3	788	5	09VXS9
8	33	94.3	962	10	09SVS7
9	32	91.4	176	5	044486
10	32	91.4	203	16	098GA7
11	32	91.4	203	16	08BDW9
12	32	91.4	284	16	086850
13	32	91.4	284	16	09RKS7
14	32	91.4	339	16	09CE52
15	32	91.4	377	16	09Z4X8
16	32	91.4	556	16	055814

17	32	91.4	927	16	0928S2	0928S2 listeria in
18	32	91.4	927	16	08YAS2	08YAS2 listeria mo
19	32	91.4	939	16	08YOR3	08YOR3 anabaena sp
20	32	91.4	1466	3	042930	042930 schizosacch
21	31	88.6	124	11	09D247	09D247 mus musculu
22	31	88.6	131	12	09QEP1	09QEP1 tomato leaf
23	31	88.6	134	12	072708	072708 cotton leaf
24	31	88.6	134	12	072711	072711 cotton leaf
25	31	88.6	134	12	056991	056991 papaya leaf
26	31	88.6	134	12	09ODE5	09ODE5 papaya leaf
27	31	88.6	134	12	09ICX4	09ICX4 tobacco gem
28	31	88.6	134	12	09IF69	09IF69 tomato leaf
29	31	88.6	134	12	0993Y9	0993Y9 tomato leaf
30	31	88.6	134	12	099DR2	099DR2 chili leaf
31	31	88.6	134	12	09IME1	09IME1 pepper leaf
32	31	88.6	134	12	091BQ2	091BQ2 ageratum ye
33	31	88.6	134	12	091M49	091M49 cotton leaf
34	31	88.6	134	12	088558	088558 tomato leaf
35	31	88.6	134	12	098742	098742 tomato leaf
36	31	88.6	134	12	08VO19	08VO19 cotton leaf
37	31	88.6	134	12	08VO12	08VO12 hollyhock l
38	31	88.6	134	12	08OYV7	08OYV7 tomato leaf
39	31	88.6	134	12	08OL10	08OL10 tobacco cut
40	31	88.6	135	12	088943	088943 tomato yell
41	31	88.6	135	12	09YDX8	09YDX8 tomato yell
42	31	88.6	135	12	09Y128	09Y128 tomato yell
43	31	88.6	135	12	09WR18	09WR18 african cas
44	31	88.6	135	12	09JEB0	09JEB0 cassava gem
45	31	88.6	135	12	09JEA3	09JEA3 cassava gem

## ALIGNMENTS

## RESULT 1

P72919	PRELIMINARY;	PRT;	136 AA.
AC P72919;			
DT 01-FEB-1997 (TRENBLREL. 02, Created)			
DT 01-FEB-1997 (TRENBLREL. 02, Last sequence update)			
DT 01-MAR-2002 (TRENBLREL. 20, Last annotation update)			
DE Hypothetical protein Slr1082.			
GN SLR1082.			
OS Synchocystis sp. (strain PCC 6803).			
OC Bacteria; Cyanobacteria; Chroococcales; Synchocystis.			
OX NCBI_TaxID:1148;			
RN [1]			
RP SEQUENCE FROM N.A.			
RX MEDLINE=97061201; PubMed=8905231;			
RA Kaneo T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,			
RA Miyajima N., Hirosewa M., Sugiyura M., Sasamoto S., Kimura T.,			
RA Hosonouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S.,			
RA Shimo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,			
RA Tabata S.,			
RT "Sequence analysis of the genome of the unicellular cyanobacterium			
RT Synchocystis sp. strain PCC6803. II. Sequence determination of the			
RT entire genome and assignment of potential protein-coding regions."			
RL DNA Res. 3:109-136(1996).			
DR EMBL: D90901; BAA16936.1; -			
KW Hypothetical protein; Complete proteome.			
SC SEQUENCE 136 AA; 15774 MW; E80414D06029605E CRC64;			
Query Match	100.0%;	Score 35;	DB 16; Length 136;
Best Local Similarity	100.0%;	Pred. No. 41;	
Matches	6;	Conservative	0; Mismatches 0; Indels 0; Gaps 0;
OY	1 LDMSFL 6		
DB	42 LDMSFL 47		

## RESULT 2

044634

ID 044634 PRELIMINARY; PRT; 362 AA.  
 AC 044634;  
 DT 01-JUN-1998 (TREMBlrel. 06, Created)  
 DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE Hypothetical 42.3 kDa protein.  
 GN Fl684.2.  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Chromadorea; Rhabditida; Rhabditidae;  
 OC Rhabditidae; Peloderinae; Caenorhabditis.  
 OX NCBI\_TaxID=6239;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BRISTOL N2;  
 RX MEDLINE=99069613; PubMed=9851916;  
 RA None;  
 RT "Genome sequence of the nematode C. elegans: a platform for  
 investigating biology. The C. elegans Sequencing Consortium.";  
 RT Science 282:2012-2018(1998).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BRISTOL N2;  
 RA Davidson S., Wohldmann P., Bauer C., O'Neal D.;  
 RT "The sequence of C. elegans cosmid Fl684.";  
 RT Submitted (JAN-1998) to the EMBL/Genbank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BRISTOL N2;  
 RA Waterston R.;  
 RT "Direct Submission.";  
 RT Submitted (JUN-2001) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: AF035048; AAB94233.1; -;  
 DR InterPro: IPR001810; F-box.  
 DR Pfam: PF00646; F-box; 1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 362 AA; 42255 MW; 33D99EF0FD14006 CRC64;  
 QY Query Match 100.0%; Score 35; DB 5; Length 362;  
 Best Local Similarity 100.0%; Pred. No. 1e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 DB 26 LDMsFL 31  
 OY 1 LDMsFL 6  
 DB 26 LDMsFL 31  
 RESULT 3  
 O8YXB1 PRELIMINARY; PRT; 573 AA.  
 ID O8YXB1  
 AC O8YXB1  
 DT 01-MAR-2002 (TREMBlrel. 20, Created)  
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)  
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)  
 DE Sulfate permease family protein.  
 GN AL1304.  
 OS Anabaena sp. (strain PCC 7120).  
 OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.  
 OX NCBI\_TaxID=103690;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE=21595285; PubMed=11759840;  
 RA Kareko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,  
 RA Watanabe A., Iriyuchi M., Ishikawa A., Kawashima K., Kimura T.,  
 RA Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,  
 RA Nakazaki N., Shimo S., Sugimoto M., Takazawa M., Yamada M.,  
 RA Yasuda M., Tabata S.;  
 RT "Complete genomic sequence of the filamentous nitrogen-fixing  
 cyanobacterium Anabaena sp. strain PCC 7120.";  
 RT DNA Res. 8:205-213(2001).  
 DR EMBL: AP003585; BAB73261.1; -;  
 DR InterPro: IPR002645; STAS.  
 DR InterPro: IPR001902; Sulfate\_transp.  
 DR Pfam: PF01740; STAS; 1.

DR Pfam: PF00916; Sulfate\_transp; 1.  
 KW Complete proteome.  
 SQ SEQUENCE 573 AA; 60239 MW; F2D1C2F6A8E36CC CRC64;  
 QY Query Match 100.0%; Score 35; DB 16; Length 573;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 DB 357 LDMsFL 362  
 OY 1 LDMsFL 6  
 DB 357 LDMsFL 362  
 RESULT 4  
 Q9LMZ3 PRELIMINARY; PRT; 2621 AA.  
 ID Q9LMZ3  
 AC Q9LMZ3  
 DT 01-OCT-2000 (TREMBlrel. 15, Created)  
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)  
 DE T6D22.24.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eucosids II; Brassicales; Brassicaceae; Arabidopsis.  
 OX NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Shin P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Khan S.,  
 RA Kim C., Altafi H., Bel O., Chin C., Chou J., Choi E., Conn L.,  
 RA Conway A., Gonzales A., Hansen N., Howling B., Koo T., Lam B., Lee J.,  
 RA Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N., Nguyen M.,  
 RA Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A.,  
 RA Toriumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A.,  
 RA Ecker J.R.;  
 RT "Genomic sequence for Arabidopsis thaliana BAC T6D22 from chromosome  
 I.";  
 RT Submitted (MAR-2000) to the EMBL/Genbank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Ecker J.R.;  
 RT Submitted (MAR-2000) to the EMBL/Genbank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Ecker J.R.;  
 RT Submitted (APR-2000) to the EMBL/Genbank/DBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RA Cheuk R., Shin P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C.,  
 RA Khan S., Kim C., Altafi H., Bel B., Chin C., Chou J., Choi E., Conn L.,  
 RA Conn L., Conway A., Gonzales A., Hansen N., Howling B., Koo T., Lam B.,  
 RA Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsky N.,  
 RA Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A.,  
 RA Thaveri A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N.,  
 RA Theologis A., Ecker J.;  
 RT Submitted (JUN-2000) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: AC026875; AAF79832.1; -;  
 DR InterPro: IPR000676; NaH\_Exchange.  
 DR Pfam: PF00999; Na\_H\_Exchange; 1.  
 SQ SEQUENCE 2621 AA; 297067 MW; E3534EL16F2370M4 CRC64;  
 QY Query Match 100.0%; Score 35; DB 10; Length 2621;  
 Best Local Similarity 100.0%; Pred. No. 6.9e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 DB 2184 LDMsFL 2189  
 OY 1 LDMsFL 6  
 DB 2184 LDMsFL 2189  
 RESULT 5  
 Q9SGE4 PRELIMINARY; PRT; 2658 AA.  
 ID Q9SGE4

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AC 09SGE4;
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DE 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE T23G18.2.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OC NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Khan S.,
RA Kim C., Altif H., Bel O., Chin C., Chlou J., Choi E., Conn L.,
RA Conway A., Gonzales A., Hansen N., Howing B., Koo T., Lam B., Lee J.,
RA Lanz C., Li J., Liu A., Liu K., Liu S., Mukharsky N., Nguyen M.,
RA Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thayerl A.,
RA Toriumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A.,
RA Ecker J.R.;
RT "Genomic sequence for Arabidopsis thaliana BAC T23G18 from chromosome
RT 1."
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AC011438; AAF18257.1;
DR InterPro: IPR000676; Nsh_Exchange.
DR Pfam: PF00999; Na_H_Exchange; 1. 77ECF93667B4293F CRC64;
SQ SEQUENCE 2658 AA; 301850 MW; 77ECF93667B4293F CRC64;

Query Match 100.0%; Score 35; DB 10; Length 2658;
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSFL 6
Db 2221 LDMSFL 2226

RESULT 6
ID 061565 PRELIMINARY; PRT; 732 AA.
AC 061565;
DT 01-AUG-1998 (TREMblrel. 07, Created)
DT 01-AUG-1998 (TREMblrel. 07, Last sequence update)
DE 01-MAR-2002 (TREMblrel. 20, Last annotation update)
DE T-kappa-B kinase.
GN IKK.
OS Crassostrea gigas (Pacific oyster).
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pleuromorpha; Ostreida;
OC Ostroidea; Ostreidae; Crassostrea.
OX NCBI_TaxID=29159;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=9932074; Pubmed=10405163;
RA Escoubas J.M., Briant L., Montagnan C., Hez S., Devaux C., Roch P.;
RT "Oyster IKK-like protein shares structural and functional properties
RT with its mammalian homologues."
RL FBS Lett. 453:293-298(1999).
CC - SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DE EMBL: AF051320; AAC05683.1;
DR InterPro: IPR000719; Ser_thr_kinase.
DR InterPro: IPR002290; Ser_thr_kinase.
DR Pfam: PF00069; kinase.1.
DR ProDom: PD000001; Euk_kinase.1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 732 AA; 84215 MW; 871EB8D1CA3E39AF CRC64;

Query Match 94.3%; Score 33; DB 5; Length 732;
Best Local Similarity 83.3%; Pred. No. 4.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSFL 6

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Db 719 MDMSFL 724

RESULT 7
ID 09VXS9 PRELIMINARY; PRT; 788 AA.
AC 09VXS9;
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DE 01-MAY-2000 (TREMblrel. 13, Last annotation update)
DE CG9220 protein.
GN CG9220.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=BERKELEY;
RC MEDLINE=20196006; Pubmed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazey R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abell J.F., Aghayani A., An H.-J., Andrews-Pfankoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borokva D., Botchan M.R., Bouck J., Brockstein P., Brothier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cavley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwan C.,
RA Jaisli M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodaira C.D., Kraft C., Kravitz S., Kulp D., Lal Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Maltel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yen R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zhang X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
DR EMBL: AE003489; AAF48479.1;
DR FlyBase: FBgn0030662; CG9220.
SQ SEQUENCE 788 AA; 91141 MW; E74F314C987B7A1 CRC64;

Query Match 94.3%; Score 33; DB 5; Length 788;
Best Local Similarity 83.3%; Pred. No. 5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSFL 6
Db 331 LDMSFL 336

RESULT 8

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09SVS7
ID 09SVS7 PRELIMINARY; PRT; 962 AA.
AC 09SVS7;
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
DE Hypothetical 108.9 kDa protein.
GN F17122.160 OR AT4G21700.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC euroside II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Bevan M., Van Der Schueren J., Chuang Y.-J., Voet M., Robben J.,
RA Volckaert G., Bancroft I., Mewes H.W., Mayer K.F.X., Schueller C.;
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Van Der Schueren J., Vandenbusche F., Chuang Y.-J., Braeken M.,
RA Robben J., Volckaert G., Mewes H.W., Lemcke R., Mayer K.F.X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AT035527; CAB36814.1; -
DR EMBL: AL161555; CAB81277.1; -
DR InterPro: IPR000269; CUNH_oxidase.
DR PROSITE: PS01164; COPPER_AMINE_OXID_1; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 962 AA; 108894 MW; 5F48A94647488927 CRC64;

Query Match 94.3%; Score 33; DB 10; Length 962;
Best Local Similarity 83.3%; Pred. No. 6.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDMSFL 6
DB 889 LDMSFL 894

RESULT 9
044486 PRELIMINARY; PRT; 176 AA.
AC 044486;
DT 01-JUN-1998 (TREMblrel. 06, Created)
DT 01-JUN-1998 (TREMblrel. 06, Last sequence update)
DE 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE Hypothetical 20.6 kDa protein.
GN F42A6.5.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-BRISTOL N2;
RX MEDLINE=99069613; PubMed=9851916;
RA None;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology. The C. elegans Sequencing Consortium.";
RL Science 287:2012-2018(1998).
[2]
RP SEQUENCE FROM N.A.
RA STRAIN-BRISTOL N2;
RA Du Z., Scheet P., Andrews S.;
RT "The sequence of C. elegans cosmid F42A6.";
```

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RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA STRAIN-BRISTOL N2;
RA Waterston R.;
RT "Direct Submission.";
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF038613; AB592050.1; -
DR InterPro: IPR001357; BRCT.
DR Pfam: PF00533; BRCT; 1.
DR SMART: SM00292; BRCT; 1.
DR PROSITE: PS50172; BRCT; 1.
KW Hypothetical protein.
SQ SEQUENCE 176 AA; 20612 MW; 1F8E5E23AF3E25BD CRC64;

Query Match 91.4%; Score 32; DB 5; Length 176;
Best Local Similarity 83.3%; Pred. No. 1.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDMSFL 6
DB 37 LDMSFL 42

RESULT 10
098GAT PRELIMINARY; PRT; 203 AA.
AC 098GAT;
DT 01-OCT-2001 (TREMblrel. 18, Created)
DT 01-OCT-2001 (TREMblrel. 18, Last sequence update)
DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
DE Hypothetical protein ml13416.
GN ML13416.
OS Rhizobium loti (Mesorhizobium loti).
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Phyllobacteriaceae; Mesorhizobium.
OX NCBI_TaxID=381;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-MAFE30309;
RX MEDLINE=21082930; PubMed=11214968;
RA Kaneo T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
RA Watanabe A., Igesawa K., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kiyokawa C., Kohara M., Matsunoto K., Matsuno A.,
RA Wochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
RA Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
RT Mesorhizobium loti.";
RL DNA Res. 7:331-338(2000).
DR EMBL: AF003001; BAB50309.1; -
DR InterPro: IPR000534; Semialdehyde.
DR Pfam: PF01118; Semialdehyde; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 203 AA; 21716 MW; FC61A9883F2E3EEF CRC64;

Query Match 91.4%; Score 32; DB 16; Length 203;
Best Local Similarity 83.3%; Pred. No. 2.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDMSFL 6
DB 140 LDMSFL 145

RESULT 11
08UDW9 PRELIMINARY; PRT; 203 AA.
AC 08UDW9;
DT 01-JUN-2002 (TREMblrel. 21, Created)
DT 01-JUN-2002 (TREMblrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE Hypothetical protein Atu1999.
GN ATU1999 OR AGR_C_3633.
```

OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).  
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;  
 OC Rhizobiaceae; Rhizobium.  
 OX NCBI\_TaxID=176299;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21608550; PubMed=11743193;  
 RA Wood D.W., Selubal J.C., Kaul R., Monks D.E., Kitajima J.P.,  
 RA Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F., Jr., Woo L.,  
 RA Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Boyce D., Sr.,  
 RA Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,  
 RA Kutayian T., Levy R., Li M.-J., McCelland E., Palmeri A.,  
 RA Raymond C., Rouse G., Saenphimachak C., Wu Z., Romero P., Gordon D.,  
 RA Zhang S., Ioo H., Tao Y., Bliddle P., Jung M., Krespan W., Perry M.,  
 RA Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,  
 RA Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,  
 RA Nester E.W.;  
 RT "The genome of the natural genetic engineer Agrobacterium tumefaciens  
 RT C58.";  
 RL Science 294:2317-2323(2001).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21608551; PubMed=11743194;  
 RA Goodner B., Hinkle G., Gelling S., Miller N., Blanchard M.,  
 RA Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,  
 RA Houmel K., Gordon J., Vaudin M., Tarchoux O., Epp A., Liu F.,  
 RA Wollam C., Allinger M., Doughy D., Scott C., Lappas C., Markelz B.,  
 RA Flanagan C., Crowell C., Gursion J., Lomo C., Sear C., Strub G.,  
 RA Cleo C., Slater S.;  
 RT "Genome sequence of the plant pathogen and biotechnology agent  
 RT Agrobacterium tumefaciens C58.";  
 RL Science 294:2323-2328(2001).  
 DR EMBL: AE009151; AAL4292.1; -  
 DR EMBL: AE008117; AAK87755.1; -  
 KW Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 203 AA; 21846 MW; D5BF6AC4E3C6B7CB CRC64;  
 QY 1 LDMSFL 6  
 Db 140 LDWTF 145  
 Query Match 91.4%; Score 32; DB 16; Length 203;  
 Best Local Similarity 83.3%; Pred. No. 2.1e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RESULT 12  
 086850  
 ID 086850 PRELIMINARY; PRT; 284 AA.  
 AC 086850;  
 DT 01-NOV-1998 (TREMblrel. 08, Created)  
 DT 01-NOV-1998 (TREMblrel. 08, last sequence update)  
 DT 01-DEC-2001 (TREMblrel. 19, last annotation update)  
 DE Hypothetical 31.0 kDa protein.  
 GN ORF.  
 OS Streptomyces coelicolor.  
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;  
 OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.  
 OX NCBI\_TaxID=1902;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX STRAIN=M145;  
 RA Takano E., Chakraborty R., Nihira T., Yamada Y., Bibb M.;  
 RT "Characterisation of scbr, and scba genes involved in gamma-  
 RT butyrolactone binding and synthesis in Streptomyces coelicolor.";  
 RL Submitted (Aug-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: A3007331; CA07626.1; -  
 KW Hypothetical protein.  
 SQ SEQUENCE 284 AA; 30969 MW; 38DE00712A09BE7D CRC64;  
 QY 1 LDMSFL 6  
 Db 140 LDWTF 145  
 Query Match 91.4%; Score 32; DB 2; Length 284;  
 Best Local Similarity 83.3%; Pred. No. 2.9e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSFL 6  
 Db 125 LDWTF 130  
 Query Match 91.4%; Score 32; DB 16; Length 284;  
 Best Local Similarity 83.3%; Pred. No. 2.9e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RESULT 13  
 09RKS7  
 ID 09RKS7 PRELIMINARY; PRT; 284 AA.  
 AC 09RKS7;  
 DT 01-MAY-2000 (TREMblrel. 13, Created)  
 DT 01-MAY-2000 (TREMblrel. 13, last sequence update)  
 DT 01-JUN-2002 (TREMblrel. 21, last annotation update)  
 DE Hypothetical protein SC06267.  
 GN SC06267 OR SC06267.  
 OS Streptomyces coelicolor.  
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;  
 OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.  
 OX NCBI\_TaxID=1902;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX STRAIN=A3(2) / M145;  
 RA Bentley S.D., Chater K.F., Cerdano-Tarraga A.-M., Challis G.L.,  
 RA Thomson N.R., James K.D., Harris D.F., Quail M.A., Kieser H.,  
 RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,  
 RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,  
 RA Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neill S.,  
 RA Rabinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,  
 RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,  
 RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,  
 RA Hopwood D.A.;  
 RT "Complete genome sequence of the model actinomyce Streptomyces  
 RT coelicolor A3(2)."  
 RL Nature 417:141-147(2002).  
 DR EMBL: AL132824; CAB60186.1; -  
 KW Hypothetical protein.  
 SQ SEQUENCE 284 AA; 30951 MW; 38DE01702A08B7FD CRC64;  
 QY 1 LDMSFL 6  
 Db 125 LDWTF 130  
 Query Match 91.4%; Score 32; DB 16; Length 284;  
 Best Local Similarity 83.3%; Pred. No. 2.9e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RESULT 14  
 09CE52  
 ID 09CE52 PRELIMINARY; PRT; 339 AA.  
 AC 09CE52;  
 DT 01-JUN-2001 (TREMblrel. 17, Created)  
 DT 01-JUN-2001 (TREMblrel. 17, last sequence update)  
 DT 01-MAR-2002 (TREMblrel. 20, last annotation update)  
 DE ABC transporter permease protein.  
 GN EC5B OR IL1195.  
 OS Lactococcus lactis (subsp. lactis) (Streptococcus lactis).  
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;  
 OC Streptococcaceae; Lactococcus.  
 OX NCBI\_TaxID=1360;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX STRAIN=IL1403;  
 RA Boletín A., Wincker P., Mauger S., Jallion O., Malarne K.,  
 RA Weissenbach J., Ehrlich S.D., Sorokin A.;  
 RT "The complete genome sequence of the lactic acid bacterium Lactococcus  
 RT lactis ssp. lactis IL1403.";  
 RL Genome Res. 11:731-753(2001).  
 DR EMBL: AE006429; AAK06093.1; -  
 DR InterPro: IPR000005; HTHARAC.  
 DR PROSITE: PS00041; HTH\_ARAC\_FAMILY\_1; UNKNOWN\_1.  
 KW Complete proteome.

SO SEQUENCE 339 AA: 39765 MW: 0027676552F6F3E7 CRC64;

## Query Match

Best Local Similarity 91.4%; Score 32; DB 16; Length 339;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Search completed: May 30, 2003, 14:39:04  
Job time: 16.7632 secs

OY 1 LDMSFL 6  
DB 158 LDMAFL 163

## RESULT 15

0924X8 PRELIMINARY; PRT; 377 AA.  
AC 0924X8;  
DT 01-MAY-1999 (TREMUREL. 10, Created)  
DT 01-MAY-1999 (TREMUREL. 10, Last sequence update)  
DT 01-JUN-2002 (TREMUREL. 21, Last annotation update)  
DE Putative glycolate oxidase.  
GN SC03228 OR SCE53.05.  
OS Streptomyces coelicolor.  
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;  
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.  
OX NCBI\_TaxID-1902;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-A3(2);  
RA Saunderson D.C., Harris D.;  
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN-A3(2);  
RA Bentley S.D., Parkhill J., Barrett B.G., Rajandream M.A.;  
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RC MEDLINE-9700351; PubMed-8843436;  
RX Redenbach M., Kleser H.M., Denapalate D., Eichner A., Cullum J.,  
RA Kinashi H., Hopwood D.A.;  
RT "A set of ordered cosmids and a detailed genetic and physical map for  
the 8 Mb Streptomyces coelicolor A3(2) chromosome.";  
RL Mol. Microbiol. 21:77-96(1996).  
RN [4]  
RP SEQUENCE FROM N.A.  
RC STRAIN-A3(2) / M145;  
RA Bentley S.D., Chater K.F., Cerdano-Tarraga A.-M., Challis G.L.,  
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kleser H.,  
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,  
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,  
RA Huang C.-H., Kleser T., Latke U., Murphy L., Oliver K., O'Neill S.,  
RA Rabinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,  
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,  
RA Warren T., Wietzorrek A., Woodward J., Barrett B.G., Parkhill J.,  
RA Hopwood D.A.;  
RT "Complete genome sequence of the model actinomycete Streptomyces  
coelicolor A3(2).";  
RL Nature 417:141-147(2002).  
DR EMBL: AL035640; CAB38520.1; -.  
DR HSRF: P05414; IGOX.  
DR InterPro: IPR003009; FMN\_enzyme.  
DR InterPro: IPR000262; FMN\_hydroxyc-dh.  
DR Pfam: PF01070; FMN\_dh; 1.  
DR PROSITE: PS00557; FMN\_HYDROXY-ACID-DH; 1.  
SQ SEQUENCE 377 AA: 38744 MW: 2E9F5F3CC2402CCA CRC64;

## Query Match

Best Local Similarity 91.4%; Score 32; DB 16; Length 377;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDMSFL 6  
DB 207 LDMSFL 212

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

# OM protein - protein search, using sw model

Run on: May 30, 2003, 14:32:12 ; Search time 6.5921 Seconds

(without alignments)  
87.500 Million cell updates/sec

Title: US-09-643-260-15

Perfect score: 36

Sequence: 1 LDMSYL 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 segs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	36	100.0	939	2 AE2275	hypothetical prote
2	36	100.0	1466	2 T39557	vacuolar protein s
3	34	94.4	98	2 H64885	ydas protein - Esc
4	34	94.4	389	2 H71152	hypothetical prote
5	33	91.7	330	1 H69798	conserved hypothet
6	33	91.7	542	2 T39474	amino acid permeas
7	32	88.9	136	2 S74785	hypothetical prote
8	32	88.9	153	2 S7187	hypothetical prote
9	32	88.9	172	2 A75592	hypothetical prote
10	32	88.9	221	2 H84781	hypothetical prote
11	32	88.9	265	2 T40878	probable FAD synth
12	32	88.9	308	2 S57377	probable membrane
13	32	88.9	362	2 T32659	hypothetical prote
14	32	88.9	392	2 T45032	hypothetical prote
15	32	88.9	393	2 B71857	probable lipopolys
16	32	88.9	445	2 S27492	hypothetical prote
17	32	88.9	450	2 D90047	hypothetical prote
18	32	88.9	476	2 T43863	hypothetical prote
19	32	88.9	480	2 B70446	cardiolipin syntha
20	32	88.9	497	2 T43867	hypothetical prote
21	32	88.9	542	2 A69261	hypothetical prote
22	32	88.9	561	2 B82975	probable acid-CoA
23	32	88.9	567	2 AC0143	chooline dehydrogen
24	32	88.9	573	2 AE1869	sulfate permease I
25	32	88.9	707	2 T40070	origin recognition
26	32	88.9	735	2 A33369	glycogen(starch) s
27	32	88.9	737	2 A33156	glycogen(starch) s
28	32	88.9	839	2 F85334	myosin heavy chain
29	32	88.9	1446	2 T04528	myosin heavy chain

30	32	88.9	1556	2 F96587	hypothetical prote
31	32	88.9	1583	2 T00727	myosin heavy chain
32	32	88.9	1611	2 A84743	probable myosin he
33	32	88.9	1643	2 T07961	myosin heavy chain
34	32	88.9	1736	2 F86178	hypothetical prote
35	32	88.9	2245	2 T18278	myosin heavy chain
36	32	88.9	2658	2 A86216	protein T23618.2 l
37	31	86.1	223	2 T24188	hypothetical prote
38	31	86.1	237	2 G81026	inositol monophosp
39	31	86.1	237	2 B82644	5-amino-6-(5-phosp
40	31	86.1	256	2 D81971	hypothetical prote
41	31	86.1	506	2 T50211	WD-repeat protein
42	31	86.1	703	2 S45686	glycogen(starch) s
43	31	86.1	703	2 A35362	glycogen(starch) s
44	31	86.1	745	1 I49101	conserved helix-10
45	31	86.1	757	2 A39283	gamma-glutamyl car

## ALIGNMENTS

### RESULT 1

AE2275 hypothetical protein alr3756 [imported] - Nostoc sp. (strain PCC 7120)

C:Species: Nostoc sp.

A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120

C:Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 30-Jun-2002

C:Accession: AE2275

R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriugu Nakazaki, N.; Shimo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata

DNA Res. 8, 205-213, 2001

A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium

A:Reference number: AB1807; MUID:21595285; PMID:11759840

A:Accession: AE2275

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-939 <KOR>

A:Cross-references: GB:BA000019; PIDN:BAF75455.1; PID:G17132890; GSPDB:GN00179

A:Experimental source: strain PCC 7120

C:Genetics:

A:Gene: alr3756

Query Match

Best Local Similarity

Matches

OY

DB

1 LDMSYL 6

|||||

648 LDMSYL 653

Query Match

Best Local Similarity

Matches

100.0%

Score 36;

DB 2;

Length 939;

Pred. No. 81;

0; Mismatches

0; Indels

0; Gaps

0;

0;

0;

0;

0;

0;

0;

0;

0;

0;

0;

0;

0;

0;

0;

0;

0;

0;

0;

0;

0;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LDMSTYL 6  
 |||||  
 Db 1046 LDMSTYL 1051

## RESULT 3

ydas protein - Escherichia coli (strain K-12)  
 H64885  
 C:Species: Escherichia coli  
 C:Date: 12-Sep-1997 #sequence\_revision 17-Sep-1997 #text\_change 01-Mar-2002  
 C:Accession: H64885  
 R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; C.  
 A.; Rose, D.J.; Mau, B.; Shao, Y.  
 Science 277, 1453-1462, 1997  
 A:Title: The complete genome sequence of Escherichia coli K-12.  
 A:Reference number: A64720; MUID:97426617; PMID:9278503  
 A:Accession: H64885  
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-98 <BLAT>  
 A:Cross-references: GB:AE000233; GB:000096; NID:g1787613; PID:AACT4439.1; PID:g1787620;  
 A:Experimental source: strain K-12, substrain MG1655  
 C:Genetics:  
 A:Gene: ydas

Query Match 94.4%; Score 34; DB 2; Length 98;  
 Best Local Similarity 83.3%; Pred. No. 19;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSTYL 6  
 |||||  
 Db 67 LDMSTYL 72

## RESULT 4

H71152  
 hypothetical protein PH0423 - Pyrococcus horikoshii  
 C:Species: Pyrococcus horikoshii  
 C:Date: 14-Aug-1998 #sequence\_revision 14-Aug-1998 #text\_change 20-Jun-2000  
 C:Accession: H71152  
 R:Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Halkawa, Y.; Hino, Y.; Yamamoto, S.; Seki  
 N.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kusida, N.; Oguchi  
 DNA Res. 5, 55-76, 1998  
 A:Title: Complete sequence and gene organization of the genome of a hyper-thermophilic  
 A:Reference number: A71000; MUID:98344137; PMID:9679194  
 A:Accession: H71152  
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-389 <KAP>  
 A:Cross-references: GB:AP000002; NID:g3236129; PIDN:BA29509.1; PID:g3256826  
 A:Experimental source: strain OT3  
 A:Note: this accession replaces an interim accession for a sequence replaced by GenBank  
 C:Genetics:  
 A:Gene: PH0423  
 C:Superfamily: Pyrococcus horikoshii hypothetical protein PH0423

Query Match 94.4%; Score 34; DB 2; Length 389;  
 Best Local Similarity 83.3%; Pred. No. 76;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSTYL 6  
 |||||  
 Db 139 LDMSTYL 144

## RESULT 5

H69798  
 conserved hypothetical protein yetk - Bacillus subtilis  
 C:Species: Bacillus subtilis  
 C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 21-Jul-2000  
 C:Accession: H69798

R.Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Ber  
 C.; Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.;  
 A.; Ehrlich, S.D.; Emmer, P.T.; Ertling, K.D.; Errington, J.; Fabbet, C.; Ferrari,  
 Nature 390, 249-256, 1997

A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Gallizzi, A.; Gal  
 lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M  
 Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardino  
 A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mau  
 Y., M.; Ogawa, K.; Ogihara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portete  
 Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadate, Y.; Sato, T.; Scagl  
 A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Se  
 akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchida  
 T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida  
 A:Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.  
 A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis  
 A:Reference number: A69580; MUID:98044033; PMID:9384377

A:Accession: H69798  
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-330 <RUN>

A:Cross-references: GB:299107; GB:AL009126; NID:g2632866; PIDN:CAB12540.1; PID:g26330  
 A:Experimental source: strain 168  
 C:Genetics:  
 A:Gene: yetk

C:Superfamily: hypothetical protein ydek

Query Match 91.7%; Score 33; DB 1; Length 330;  
 Best Local Similarity 83.3%; Pred. No. 97;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSTYL 6  
 |||||  
 Db 239 LDMSTYL 244

## RESULT 6

T39474  
 amino acid permease - fission yeast (Schizosaccharomyces pombe)  
 C:Species: Schizosaccharomyces pombe  
 C:Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 21-Jan-2000  
 C:Accession: T39474  
 R:Livny, M.; Rajandream, M.A.; Barrell, B.G.; Xiang, Z.; Aves, S.  
 submitted to the EMBL Data Library, May 1998  
 A:Reference number: Z21857  
 A:Accession: T39474  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-542 <LYN>  
 A:Cross-references: EMBL:AL023290; PIDN:CA118895.1; GSPDB:GN00067; SPDB:SPBC1504.04c  
 A:Experimental source: strain 972h-; cosmid c1504  
 C:Genetics:  
 A:Gene: SPDB:SPBC1504.04c  
 A:Map position: 2  
 C:Superfamily: choline transport protein

Query Match 91.7%; Score 33; DB 2; Length 542;  
 Best Local Similarity 83.3%; Pred. No. 1.6e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSTYL 6  
 |||||  
 Db 436 LDMSTYL 441

## RESULT 7

S74785  
 hypothetical protein slr1082 - Synechocystis sp. (strain PCC 6803)  
 C:Species: Synechocystis sp.  
 A:Variety: PCC 6803  
 C:Date: 25-Apr-1997 #sequence\_revision 25-Apr-1997 #text\_change 21-Jul-2000  
 C:Accession: S74785  
 R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asanuma, E.; Nakamura, Y.; Miyajima,  
 O., K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yas

DNA Res. 3, 109-136, 1996

A:Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis* sp.

A:Reference number: S74322; MUID:97061201; PMID:8905231

A:Accession: S74785

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-136 <KAN>

A:Cross-references: EMBL:D90901; GB:AB001339; NID:g1651897; PIDN:BAAL6936.1; PID:g165201

A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

C:Superfamily: *Synechocystis* hypothetical protein slr0489

#### Query Match

Best Local Similarity 88.9%; Score 32; DB 2; Length 136;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDMSTL 6  
|||||  
DB 42 LDMSTL 47

#### RESULT 8

S7187  
hypothetical protein slr1813 - *Synechocystis* sp. (strain PCC 6803)

C:Species: *Synechocystis* sp.

A:Variety: PCC 6803

C:Date: 25-Apr-1997 #sequence\_revision 25-Apr-1997 #text\_change 20-Jun-2000

C:Accession: S77187

R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;

O. K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda

DNA Res. 3, 109-136, 1996

A:Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis* sp.

A:Reference number: S74322; MUID:97061201; PMID:8905231

A:Accession: S77187

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-153 <KAN>

A:Cross-references: EMBL:D90908; GB:AB001339; NID:g1652725; PIDN:BAAL7745.1; PID:g165282

A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

C:Superfamily: hypothetical protein slr1203

#### Query Match

Best Local Similarity 88.9%; Score 32; DB 2; Length 153;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 LDMSTL 6  
|||||  
DB 36 LDMSTL 41

#### RESULT 9

A75592  
hypothetical protein - *Deinococcus radiodurans* (strain R1)

C:Species: *Deinococcus radiodurans*

C:Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 28-Jul-2000

C:Accession: A75592

R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;

M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Uterback, T.; Zalewski, C.; Ma

S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.

Science 286, 1571-1577, 1999

A:Title: Genome sequence of the radioresistant bacterium *Deinococcus radiodurans* R1

A:Reference number: A75250; MUID:20036896; PMID:10567266

A:Accession: A75592

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-172 <WHI>

A:Cross-references: GB:AE001663; GB:AE001825; NID:g6460670; PIDN:AAFL2501.1; PID:g646079

A:Experimental source: strain R1

C:Genetics:

A:Gene: DRA0366

A:Map position: 2

C:Superfamily: *Deinococcus radiodurans* hypothetical protein DRA0366

Query Match 88.9%; Score 32; DB 2; Length 172;  
Best Local Similarity 100.0%; Pred. No. 76;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDMSTL 5  
|||||  
DB 96 LDMSTL 100

#### RESULT 10

H84781  
hypothetical protein At2g36550 [Imported] - *Arabidopsis thaliana*

C:Species: *Arabidopsis thaliana* (mouse-ear cress)

C:Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 02-Feb-2001

C:Accession: H84781

R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.T.; Town, C.D.; Fujii, C.Y.

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umeyam, L.; Tallon,

euss, D.; Nlerman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter

Nature 402, 761-768, 1999

A:Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.

A:Reference number: A84420; MUID:20083487; PMID:10617197

A:Accession: H84781

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-221 <STO>

A:Cross-references: GB:AE002093; NID:g4581153; PIDN:AMD24637.1; GSPDB:GN00139

C:Genetics:

A:Gene: At2g36550

A:Map position: 2

#### Query Match

Best Local Similarity 88.9%; Score 32; DB 2; Length 221;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDMSTL 5  
|||||  
DB 208 LDMSTL 212

#### RESULT 11

T40878  
probable FAD synthetase - fission yeast (*Schizosaccharomyces pombe*)

C:Species: *Schizosaccharomyces pombe*

C:Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 03-Dec-1999

C:Accession: T40878

R:Wood, V.; Rajandream, M.A.; Barrell, B.G.; Murphy, L.; Harris, D.

submitted to the EMBL Data Library, September 1998

A:Reference number: Z21954

A:Accession: T40878

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-265 <WOO>

A:Cross-references: EMBL:AL031764; PIDN:CAA21108.1; GSPDB:GN00068; SPDB:SPCC1235.04c

A:Experimental source: strain 972h-; cosmid c1235

C:Genetics:

A:Gene: SPDB:SPCC1235.04c

A:Map position: 3

A:Introns: 46/2; 182/3

#### Query Match

Best Local Similarity 88.9%; Score 32; DB 2; Length 265;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDMSTL 5  
|||||  
DB 173 LDMSTL 177

#### RESULT 12

S57377  
probable membrane protein YOL092w - yeast (*Saccharomyces cerevisiae*)

N:Alternate names: hypothetical protein O0929; protein YHRI47w homolog

C.Species: *Saccharomyces cerevisiae*  
 C.Date: 28-Oct-1995 #sequence\_revision 03-Nov-1995 #text\_change 19-Apr-2002  
 C.Accession: S57377; S66786; S50413  
 R.Zumstede, E.; Pearson, B.M.; Kalogeropoulos, A.; Schweizer, M.  
 Yeast 11, 975-986, 1995  
 A.Title: A 29.425 kb segment on the left arm of yeast chromosome XV contains more than  
 A.Reference number: S57374; MUID:96021609; PMID:8533473  
 A.Accession: S57377  
 A>Status: nucleic acid sequence not shown  
 A.Molecule type: DNA  
 A.Residues: 1-308 <ZUN>  
 A.Cross-references: EMBL:X83121; NID:9600461; PIDN:CA58187.1; PID:9600466  
 R.Zumstede, E.; Pearson, B.M.; Kalogeropoulos, A.; Schweizer, M.  
 Submitted to the Protein Sequence Database, July 1996  
 A.Reference number: S66775  
 A.Accession: S66786  
 A.Molecule type: DNA  
 A.Residues: 1-308 <ZUN>  
 A.Cross-references: EMBL:X74834; NID:91419937; PID:91419938; MIPS:XOL092W  
 A.Experimental source: strain S288C  
 C.Genetics:  
 A.Cross-references: SGD:S0005452  
 A.Map position: 15L  
 C.Superfamily: *Saccharomyces* probable membrane protein YBR147W  
 C.Keywords: transmembrane protein  
 F.14-30/Domain: transmembrane #status predicted <TM1>  
 F.45-61/Domain: transmembrane #status predicted <TM2>  
 F.73-89/Domain: transmembrane #status predicted <TM3>  
 F.168-184/Domain: transmembrane #status predicted <TM4>  
 F.249-265/Domain: transmembrane #status predicted <TM5>  
 F.278-294/Domain: transmembrane #status predicted <TM6>

Query Match 88.9%; Score 32; DB 2; Length 308;  
 Best Local Similarity 83.3%; Pred. No. 1.4e+02;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 LDMSYL 6  
 |||||  
 DB 267 LDMSYL 272

RESULT 13  
 T32669  
 hypothetical protein F16B4.2 - *Caenorhabditis elegans*  
 C.Species: *Caenorhabditis elegans*  
 C.Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 29-Oct-1999  
 C.Accession: T32669  
 R.Davidson, S.; Wohlmann, P.; Bauer, C.; O'Neal, D.  
 submitted to the EMBL Data Library, December 1997  
 A.Description: The sequence of *C. elegans* cosmid F16B4.  
 A.Reference number: Z21208  
 A.Accession: T32669  
 A>Status: Preliminary; translated from GB/EMBL/DBJ  
 A.Molecule type: DNA  
 A.Residues: 1-362 <DAV>  
 A.Cross-references: EMBL:AF039048; PIDN:AAB94233.1; GSPDB:GN00023; CESP:F16B4.2  
 C.Experimental source: strain Bristol N2; clone F16B4  
 C.Genetics:  
 A.Gene: CESP:F16B4.2  
 A.Map position: 5  
 A.Introns: 48/2; 112/2; 160/3; 255/3; 291/2; 333/3

Query Match 88.9%; Score 32; DB 2; Length 362;  
 Best Local Similarity 83.3%; Pred. No. 1.6e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDMSYL 6  
 |||||  
 DB 26 LDMSYL 31

RESULT 14  
 T45032

hypothetical protein Y39B6.f [imported] - *Caenorhabditis elegans*  
 C.Species: *Caenorhabditis elegans*  
 C.Date: 21-Jan-2000 #sequence\_revision 21-Jan-2000 #text\_change 21-Jul-2000  
 C.Accession: T45032  
 R.Wilson, R.; Almscough, R.; Anderson, K.; Baynes, C.; Berks, M.; Bonfield, J.; Burto  
 raser, A.; Fulton, L.; Gardner, A.; Green, P.; Hawkins, T.; Hillier, L.; Jier, M.; Jo  
 B.; O'Callaghan, M.; Parsons, J.; Percy, C.; Rinken, L.; Roopra, A.; Saunders, D.  
 Nature 368, 32-38, 1994  
 A.Authors: Showkhen, R.; Sims, M.; Smalton, N.; Smith, A.; Smith, M.; Sonhammer, E.  
 lock, L.; Wilkinson-Sproat, J.; Wohlmann, P.  
 A.Title: 2.2 Mb of contiguous nucleotide sequence from chromosome III of *C. elegans*.  
 A.Reference number: S43531; MUID:94150718; PMID:7906398  
 A.Accession: T45032  
 A>Status: preliminary; translated from GB/EMBL/DBJ  
 A.Molecule type: DNA  
 A.Residues: 1-392 <WIL>  
 A.Cross-references: EMBL:AL132896; NID:96434440; PIDN:CAB60911.1; PID:96434446  
 A.Experimental source: clone Y39B6  
 C.Genetics:  
 A.Map position: 3  
 A.Introns: 47/2; 82/2; 106/3; 151/1; 220/1; 260/3; 370/3  
 A.Note: Y39B6.f

Query Match 88.9%; Score 32; DB 2; Length 392;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 DMSYL 6  
 |||||  
 DB 289 DMSYL 293

RESULT 15  
 B71857  
 probable lipopolysaccharide biosynthesis protein - *Helicobacter pylori* (strain J99)  
 C.Species: *Helicobacter pylori*  
 A.Variety: strain J99  
 C.Date: 12-Feb-1999 #sequence\_revision 12-Feb-1999 #text\_change 08-Oct-1999  
 C.Accession: B71857  
 R.Alm, R.A.; Lang, L.S.L.; Molir, D.T.; King, B.L.; Brown, E.D.; Dolg, P.C.; Smith, D.  
 ; Ives, C.; Gibson, R.; Werberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.  
 Nature 397, 176-180, 1999  
 A.Title: Genomic sequence comparison of two unrelated isolates of the human gastric p  
 A.Reference number: A71800; MUID:99120557; PMID:9923682  
 A.Cross-references: B71857  
 A.Status: preliminary  
 A.Molecule type: DNA  
 A.Residues: 1-393 <ARN>  
 A.Cross-references: GB:AE001531; GB:AE001439; NID:94155617; PIDN:AAD06611.1; PID:9415  
 A.Experimental source: strain J99  
 C.Genetics:  
 A.Gene: jhp1031

Query Match 88.9%; Score 32; DB 2; Length 393;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 DMSYL 6  
 |||||  
 DB 284 DMSYL 288

Search completed: May 30, 2003, 14:52:58  
 Job time: 7.5921 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 30, 2003, 14:32:11 ; Search time 14.7632 Seconds

(without alignments)  
83.741 Million cell updates/sec

Title: US-09-643-260-15

Perfect score: 36

Sequence: 1 LDMSTL 6

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 segs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPREML\_21: \*  
1: sp.archaea: \*  
2: sp.bacteria: \*  
3: sp.fungi: \*  
4: sp.human: \*  
5: sp.invertebrate: \*  
6: sp.mammal: \*  
7: sp.mhc: \*  
8: sp.organelle: \*  
9: sp.phage: \*  
10: sp.plant: \*  
11: sp.potent: \*  
12: sp.virus: \*  
13: sp.vertibrate: \*  
14: sp.unclassified: \*  
15: sp.virus: \*  
16: sp.bacteriophage: \*  
17: sp.archaea: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	36	100.0	939	16	Q8YGR3	Q8YGR3 anaabaena sp
2	36	100.0	1466	3	Q42930	Q42930 schizosacch
3	34	94.4	389	17	O58160	O58160 pyrococcus
4	33	91.7	542	3	O60113	O60113 schizosacch
5	32	88.9	75	10	Q94HM4	Q94HM4 arabidopsis
6	32	88.9	136	16	P72919	P72919 synchocyst
7	32	88.9	153	16	P73698	P73698 synchocyst
8	32	88.9	172	16	O9RYF2	O9RYF2 delnococtus
9	32	88.9	221	10	O9S103	O9S103 arabidopsis
10	32	88.9	229	17	O82Y11	O82Y11 pyrobaculum
11	32	88.9	262	10	O9FNJ0	O9FNJ0 arabidopsis
12	32	88.9	278	10	O9LUT6	O9LUT6 saccharomyc
13	32	88.9	308	3	Q12010	Q12010 saccharomyc
14	32	88.9	337	4	O96RE6	O96RE6 homo sapien
15	32	88.9	362	5	O44634	O44634 caenorhabdi
16	32	88.9	392	5	O9NEV3	O9NEV3 caenorhabdi

17	32	88.9	393	16	Q9ZKA8	Q9ZKA8 helicobacte
18	32	88.9	412	10	Q8RY17	Q8RY17 oryza sativ
19	32	88.9	429	12	O65111	O65111 adelaide ri
20	32	88.9	438	16	O8RMH5	O8RMH5 fusobacteri
21	32	88.9	450	16	O99R10	O99R10 staphylococ
22	32	88.9	451	16	O91151	O91151 streptomyce
23	32	88.9	480	16	O67595	O67595 aquilex aeo
24	32	88.9	497	10	Q9LZE4	Q9LZE4 arabidopsis
25	32	88.9	497	10	Q94EY8	Q94EY8 arabidopsis
26	32	88.9	542	17	O30147	O30147 archaeoglob
27	32	88.9	561	16	O9HRT2	O9HRT2 pseudomonas
28	32	88.9	561	16	O8ZGWO	O8ZGWO yersinia pe
29	32	88.9	573	16	O81XB1	O81XB1 anaabaena sp
30	32	88.9	599	10	O9FHV3	O9FHV3 arabidopsis
31	32	88.9	647	2	O8VDM5	O8VDM5 staphylococ
32	32	88.9	673	4	O9BT79	O9BT79 homo sapien
33	32	88.9	708	5	O9WDB1	O9WDB1 drosophila
34	32	88.9	738	11	O8VZB0	O8VZB0 mus musculu
35	32	88.9	793	5	O9VY70	O9VY70 drosophila
36	32	88.9	828	3	O74240	O74240 thielavia h
37	32	88.9	839	10	O9M0G3	O9M0G3 arabidopsis
38	32	88.9	902	2	O9JMX0	O9JMX0 bradyrhizob
39	32	88.9	903	16	O987X1	O987X1 rhizobium l
40	32	88.9	913	11	O8VE73	O8VE73 mus musculu
41	32	88.9	937	5	O9VK32	O9VK32 drosophila
42	32	88.9	952	16	O988M2	O988M2 rhizobium l
43	32	88.9	1005	3	O8TFE6	O8TFE6 aspergillus
44	32	88.9	1114	5	O9N1A1	O9N1A1 drosophila
45	32	88.9	1446	10	O9SVT9	O9SVT9 arabidopsis

## ALIGNMENTS

### RESULT 1

ID	Q8YGR3	PRELIMINARY;	PRT;	939 AA.
AC	Q8YGR3			
DT	01-MAR-2002 (TREMBLrel. 20, Created)			
DT	01-MAR-2002 (TREMBLrel. 20, Last sequence update)			
DT	01-MAR-2002 (TREMBLrel. 20, Last annotation update)			
DE	Hypothetical protein A1R3756.			
GN	A1R3756.			
OS	Anabaena sp. (strain PCC 7120).			
OC	Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.			
OX	NCBI Taxid:103690;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=21595285; PubMed=11759840;			
RA	Kaneke T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,			
RA	Matsumoto M., Ishikawa A., Kawashima K., Kimura T.,			
RA	Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,			
RA	Nakazaki N., Shimp S., Sugimoto M., Takazawa M., Yamada M.,			
RA	Yasuda M., Tabata S.,			
RT	"Complete genomic sequence of the filamentous nitrogen-fixing			
RT	cyanobacterium Anabaena sp. strain PCC 7120."			
RL	DNA Res. 8:205-213(2001).			
DR	EMBL; AP003594; BAB75455.1;			
KW	Hypothetical protein; Complete proteome.			
SO	SEQUENCE 939 AA; 104233 MW; 8F80A7CA6C1759A5 CRC64;			

Query Match 100.0%; Score 36; DB 16; Length 939;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSTL 6  
Db 648 LDMSTL 653

### RESULT 2

ID Q42930 PRELIMINARY; PRT; 1466 AA.

AC 042930;  
 DT 01-JUN-1998 (TREMBLrel. 06, Created)  
 DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE Putative membrane glycoprotein, possible vacuolar protein sorting /targeting.  
 GN SPIC166.06.  
 OS Schizosaccharomyces pombe (fission yeast).  
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;  
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;  
 OC Schizosaccharomycetes.  
 NCBI\_TaxID=4896;  
 [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-972H-;  
 RA Furelle B., Goffeau A., Wood V., Lyne M., Barrell B.G.,  
 RA Rajandream M.A.;  
 RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AL021767; CNA16914.1; -  
 DR InterPro: IPR002860; GH\_BNR.  
 DR Pfam: PF02012; BNR; 12;  
 SQ SEQUENCE 1466 AA; 165061 MW; CEB315E0F768BD79 CRC64;

Query Match 100.0%; Score 36; DB 3; Length 1466;  
 Best Local Similarity 100.0%; Pred. No. 3e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDWSTL 6  
 DB 1046 LDWSTL 1051

RESULT 3  
 ID 058160 PRELIMINARY; PRT; 389 AA.  
 AC 058160;  
 DT 01-AUG-1998 (TREMBLrel. 07, Created)  
 DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE Hypothetical protein PH0423.  
 GN PH0423.  
 OS Pyrococcus horikoshii.  
 OC Archaea; Euryarchaeota; Thermococci; Thermococcaceae;  
 OC Pyrococcus.  
 NCBI\_TaxID=53953;  
 [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-073;  
 RX MEDLINE-98344137; PubMed-9679194;  
 RA Kawarabayashi Y., Sawada M., Horikawa H., Hino Y.,  
 RA Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,  
 RA Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,  
 RA Funahashi T., Tanaka T., Kudo H., Yamazaki J., Kushida N., Oguchi A.,  
 RA Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,  
 RA Masuchi Y., Shizuya H., Kikuchi H.;  
 RT "Complete sequence and gene organization of the genome of a hyper-  
 thermophilic archaeobacterium, Pyrococcus horikoshii 073.",  
 RL DNA Res. 5:55-76(1998)  
 DR EMBL; AP000002; BAA29509.1; -  
 DR InterPro: IPR002934; NTP\_transf.  
 DR Pfam: PF01909; NTP\_transf. 2; 1.  
 KW Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 389 AA; 46335 MW; 81P32C817B1A53D4 CRC64;

Query Match 94.4%; Score 34; DB 17; Length 389;  
 Best Local Similarity 83.3%; Pred. No. 1.8e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDWSTL 6  
 DB 139 LDWSTL 144

RESULT 4  
 ID 060113 PRELIMINARY; PRT; 542 AA.  
 AC 060113;  
 DT 01-AUG-1998 (TREMBLrel. 07, Created)  
 DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE Hypothetical amino-acid permease C15C4.04C.  
 GN SPIC15C4.04C.  
 OS Schizosaccharomyces pombe (fission yeast).  
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;  
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;  
 OC Schizosaccharomycetes.  
 NCBI\_TaxID=4896;  
 [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-972;  
 RA Lyne M., Rajandream M.A., Barrell B.G., Xiang Z., Aves S.;  
 RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.  
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).  
 CC -1- SIMILARITY: BELONGS TO THE AMINO ACID PERMEASE FAMILY.  
 DR EMBL; AL023290; CNA1895.1; -  
 DR InterPro: IPR002293; AA/rel\_pmeasel.  
 DR InterPro: IPR004840; AAC\_permease.  
 DR InterPro: IPR004756; AAC\_permease.  
 DR Pfam: PF00324; aa\_permeases; 1.  
 DR TIGRfams: TIGR00907; 2A0304.1.  
 DR PROSITE: PS00218; AMINO\_ACID\_PERMEASE\_1; 1.  
 KW Hypothetical protein; Transport; Amino-acid transport; Transmembrane.  
 FT TRANSMEM 95 115 POTENTIAL.  
 FT TRANSMEM 217 237 POTENTIAL.  
 FT TRANSMEM 255 275 POTENTIAL.  
 FT TRANSMEM 298 318 POTENTIAL.  
 FT TRANSMEM 348 368 POTENTIAL.  
 FT TRANSMEM 402 422 POTENTIAL.  
 FT TRANSMEM 425 445 POTENTIAL.  
 FT TRANSMEM 469 489 POTENTIAL.  
 FT TRANSMEM 500 520 POTENTIAL.  
 FT DOMAIN 396 399 POLY-THR.  
 SQ SEQUENCE 542 AA; 59726 MW; 17D9B15C04299468 CRC64;

Query Match 91.7%; Score 33; DB 3; Length 542;  
 Best Local Similarity 83.3%; Pred. No. 3.9e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDWSTL 6  
 DB 436 LDWSTL 441

RESULT 5  
 ID 094HW4 PRELIMINARY; PRT; 75 AA.  
 AC 094HW4;  
 DT 01-DEC-2001 (TREMBLrel. 19, Created)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE Hypothetical 8.8 kDa protein.  
 GN T4M14.6.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 NCBI\_TaxID=3702;  
 [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-CV. COLUMBIA;  
 RA Town C.D., Haas B.J., Wu D., Maitl R., Hannick L.I., Chan A.P.,  
 RA Tallon L.J., Rooney T., Utterback T.R., Vannken S.E., Feldblum T.V.,  
 RA White O., Fraser C.M.;  
 RT "Arabidopsis thaliana chromosome 1 BAC T4M14 genomic sequence.",  
 Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL: AC027036; AAK62781.1; -  
 KW Hypothetical protein.  
 SQ SEQUENCE 75 AA; 8834 MW; B34EB28B5C41EBB5 CRC64;

Query Match  
 Best Local Similarity 100.0%; Score 32; DB 10; Length 75;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDMSY 5  
 |||||  
 DB 12 LDMSY 16

RESULT 6  
 P72919

PRELIMINARY; PRT; 136 AA.

AC P72919;  
 DT 01-FEB-1997 (TREMBLrel. 02, Created)  
 DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)  
 DE 01-MAR-2002 (TREMBLrel. 20, Last annotation update)  
 GN SLR1082.  
 OS Synecocystis sp. (strain PCC 6803)  
 OC Bacteria; Cyanobacteria; Chroococcales; Synecocystis.  
 OX NCBI\_TaxID=1148;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97061201; Pubmed=8905231;  
 RA Kaneo T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,  
 RA Miyajima N., Hirosewa M., Sugitara M., Sasamoto S., Kimura T.,  
 RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naito K., Okumura S.,  
 RA Shilpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,  
 RA Tabata S.;  
 RT "Sequence analysis of the genome of the unicellular cyanobacterium  
 RT Synecocystis sp. strain PCC6803. II. Sequence determination of the  
 RT entire genome and assignment of potential protein-coding regions.";  
 RL DNA Res. 3:109-136(1996).  
 DR EMBL: D90901; BAA16936.1; -  
 KW Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 136 AA; 15774 MW; E80414D06029605E CRC64;

Query Match  
 Best Local Similarity 83.3%; Score 32; DB 16; Length 136;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDMSYL 6  
 |||||  
 DB 42 LDMSYL 47

RESULT 7  
 P73698  
 ID P73698 PRELIMINARY; PRT; 153 AA.  
 AC P73698;  
 DT 01-FEB-1997 (TREMBLrel. 02, Created)  
 DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)  
 DE 01-MAR-2002 (TREMBLrel. 20, Last annotation update)  
 GN SLR1813.  
 OS Synecocystis sp. (strain PCC 6803).  
 OC Bacteria; Cyanobacteria; Chroococcales; Synecocystis.  
 OX NCBI\_TaxID=1148;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97061201; Pubmed=8905231;  
 RA Kaneo T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,  
 RA Miyajima N., Hirosewa M., Sugitara M., Sasamoto S., Kimura T.,  
 RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naito K., Okumura S.,  
 RA Shilpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,  
 RA Tabata S.;  
 RT "Sequence analysis of the genome of the unicellular cyanobacterium  
 RT Synecocystis sp. strain PCC6803. II. Sequence determination of the  
 RT entire genome and assignment of potential protein-coding regions.";

RL DNA Res. 3:109-136(1996).  
 DR EMBL: D90908; BAA17745.1; -  
 DR InterPro: IPR002636; DUF29.  
 DR Pfam: PF01724; DUF29; 1.  
 KW Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 153 AA; 18387 MW; 6E54EB36EDCB9AF1 CRC64;

Query Match  
 Best Local Similarity 83.3%; Score 32; DB 16; Length 153;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 LDMSYL 6  
 |||||  
 DB 36 LDMSYL 41

RESULT 8  
 Q9RYF2

PRELIMINARY; PRT; 172 AA.

AC Q9RYF2;  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)  
 GN DRA0366.  
 OS Deinococcus radiodurans.  
 OC Bacteria; Thermus/Deinococcus group; Deinococci; Deinococcales;  
 OX NCBI\_TaxID=1299;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20036896; Pubmed=10567266;  
 RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,  
 RA Dodson R.J., Hatt D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,  
 RA Morla K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,  
 RA Vamathevan J.J., Lam P., McDonald L., Utterback T., Zaleski C.,  
 RA Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,  
 RA Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,  
 RA Fraser C.M.;  
 RT "Genome sequence of the radioresistant bacterium Deinococcus  
 RT radiodurans R1.";  
 RL EMBL: AE001863; AAF12501.1; -  
 DR TIGR: DRA0366;  
 KW Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 172 AA; 19874 MW; CCF8D41A4DCF7DC0 CRC64;

Query Match  
 Best Local Similarity 100.0%; Score 32; DB 16; Length 172;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDMSY 5  
 |||||  
 DB 96 LDMSY 100

RESULT 9  
 Q9SJ03  
 ID Q9SJ03 PRELIMINARY; PRT; 221 AA.  
 AC Q9SJ03;  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 GN At2g36550 protein.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 OX NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RC STRAIN-CV. COLUMBIA;  
 RA MEDLINE-20083487; PubMed=10617197;  
 RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Bentio M.-I., Town C.D.,  
 RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblum T.V.,  
 RA Buell C.R., Ketchum K.A., Lee J.J., Renning C.M., Koo H., Moffat K.S.,  
 RA Cronin L.A., Shen M., Vanaken S.E., Umayam L., Tallon L.J., Gill J.E.,  
 RA Adams M.D., Carreira A.J., Creasy T.H., Goodman H.M., Somerville C.R.,  
 RA Copenhagen G.P., Preuss D., Niernan W.C., White O., Eisen J.A.,  
 RA Salzberg S.L., Fraser C.M., Venter J.C.;  
 RA "Sequence and analysis of chromosome 2 of the plant *Arabidopsis*  
 RA *thaliana*.";  
 RT thaliana.402:761-768(1999).  
 RN [2].  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-CV. COLUMBIA;  
 RA Lin X.;  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AC006919; AAD24637.1; -  
 SQ SEQUENCE 221 AA; 25043 MW; D3037BC4CC103990 CRC64;

Query Match 88.9%; Score 32; DB 10; Length 221;  
 Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDMSY 5  
 DB 208 LDMSY 212

## RESULT 10

O8ZYL1 PRELIMINARY; PRT; 229 AA.  
 AC O8ZYL1;  
 DT 01-MAR-2002 (TREMBlrel. 20, Created)  
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)  
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)  
 DE Molybdenum cofactor biosynthesis protein D/E.  
 GN PAE0722.  
 OS Pyrobaculum aerophilum.  
 OC Archaea; Crenarchaeota; Thermoprotei; Thermoproteales;  
 CC Thermoproteaceae; Pyrobaculum.  
 CX NCBI\_TaxID=13773;  
 RN [1].  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-IM2 / ATCC 51768 / DSM 7523;  
 RX PubMed=11792869;  
 RA Fitz-Gibbon S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I.,  
 RA Miller J.H.;  
 RT "Genome sequence of the hyperthermophilic crenarchaeon *Pyrobaculum*  
 RT *aerophilum*.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:984-989(2002).  
 DR EMBL: AE009782; AAL62982.1; -  
 DR InterPro: IPR003448; MB\_biosynth\_MoA.  
 DR InterPro: IPR003749; This.  
 DR Pfam: PF02597; DUF170; 1.  
 DR Pfam: PF02391; MoA; 1.  
 DR Complete proteome.  
 KW SEQUENCE 229 AA; 25544 MW; 111B06C8F85962EA CRC64;

Query Match 88.9%; Score 32; DB 17; Length 229;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDMSY 5  
 DB 60 LDMSY 64

## RESULT 11

O9FNJO PRELIMINARY; PRT; 262 AA.  
 ID O9FNJO;  
 AC O9FNJO;  
 DT 01-MAR-2001 (TREMBlrel. 16, Created)

DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)  
 DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)  
 DE Genomic DNA, chromosome 5, pl clone:MDJ22.  
 OS *Arabidopsis thaliana* (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC euroids II; Brassicales; Brassicaceae; Arabidopsis.  
 CX NCBI\_TaxID=3702;  
 RN [1].  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-COLUMBIA;  
 RX MEDLINE-98069011; PubMed=9405937;  
 RA Kotani H., Nakamura Y., Sato S., Kaneko T., Asamizu E., Miyajima N.,  
 RA Tabata S.;  
 RT "Structural analysis of *Arabidopsis thaliana* chromosome 5. II.  
 RT Sequence features of the regions of 1,044,065 bp covered by thirteen  
 RT physically assigned pl clones.";  
 RL DNA Res. 4:291-300(1997).  
 DR EMBL: AB006699; BAB1677.1; -  
 SQ SEQUENCE 262 AA; 30706 MW; CE15D9E2CD3C6B9 CRC64;

Query Match 88.9%; Score 32; DB 10; Length 262;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 DMSYL 6  
 DB 46 DMSYL 50

## RESULT 12

O9LUT6 PRELIMINARY; PRT; 278 AA.  
 ID O9LUT6;  
 DT 01-OCT-2000 (TREMBlrel. 15, Created)  
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
 DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)  
 DE Gb|AAD32889.1.  
 OS *Arabidopsis thaliana* (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;  
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC euroids II; Brassicales; Brassicaceae; Arabidopsis.  
 CX NCBI\_TaxID=3702;  
 RN [1].  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-COLUMBIA;  
 RA Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Tabata S.;  
 RT Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.  
 RN [2].  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-COLUMBIA;  
 RX MEDLINE-20277480; PubMed=10819329;  
 RA Nakamura Y.;  
 RT "Structural analysis of *Arabidopsis thaliana* chromosome 3. I. Sequence  
 RT features of the regions of 4,504,864 bp covered by sixty pl and TAC  
 RT clones.";  
 RL DNA Res. 7:131-135(2000).  
 DR EMBL: AB022216; BAB02739.1; -  
 SQ SEQUENCE 278 AA; 31217 MW; A16AE1E0910484B2 CRC64;

Query Match 88.9%; Score 32; DB 10; Length 278;  
 Best Local Similarity 100.0%; Pred. No. 3e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDMSY 5  
 DB 217 LDMSY 221

## RESULT 13

O12010 PRELIMINARY; PRT; 308 AA.  
 ID O12010;  
 AC O12010;

```

DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Chromosome XV reading frame ORF YOL092W.
GN YOL092W.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RA Zumbstein E., Pearson B.M., Kalogeropoulos A., Schweizer M.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA MIPS;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA STRAIN-FY1679;
RC MEDLINE=96021609; PubMed=8533473;
RX Zumbstein E., Pearson B.M., Kalogeropoulos A., Schweizer M.;
RT "A 29,425 kb segment on the left arm of yeast chromosome XV contains
RT more than twice as many unknown as known open reading frames.";
RL Yeast 11:975-986(1995).
DR EMBL; Z74834; CAA99104.1; -
DR EMBL; X83121; CAA58187.1; -
DR SGD; S0005452; YOL092W.
SQ SEQUENCE 308 AA; 34872 MW; 38EB1645FA034812 CRC64;

Query Match      88.9%; Score 32; DB 3; Length 308;
Best Local Similarity 83.3%; Pred. No. 3.3e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDWSYL 6
DB 267 LDWSYL 272

RESULT 14
096RE6
ID 096RE6 PRELIMINARY; PRT; 337 AA.
AC 096RE6;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Allantoicase (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Vignetti D., Monetti C., Rimoldi S., Prati M., Gornati R.,
RA Bernardini G.;
RT "Genomic organization of human and murine allantoicase gene.";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF395820; AAK72970.1; -
DR InterPro: IPR005164; Allantoicase.
DR Pfam; PF03561; Allantoicase; 2.
FT NON_TER 1
FT NON_TER 1
FT NON_TER 337
SQ SEQUENCE 337 AA; 37647 MW; 382DF694E8C904D CRC64;

Query Match      88.9%; Score 32; DB 4; Length 337;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWSYL 6
DB 116 DWSYL 120

```

```

RESULT 15
044634
ID 044634 PRELIMINARY; PRT; 362 AA.
AC 044634;
DT 01-JUN-1998 (TREMBlrel. 06, Created)
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Hypothetical 42.3 kDa protein.
GN F16B4.2.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-BRISTOL N2;
RC MEDLINE=99069613; PubMed=9851916;
RX None;
RA "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA STRAIN-BRISTOL N2;
RC Davidson S., Woldmann P., Bauer C., O'Neal D.;
RT "The sequence of C. elegans cosmid F16B4.";
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA STRAIN-BRISTOL N2;
RC Waterston R.;
RT "Direct Submission.";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF039048; AAB94233.1; -
DR InterPro: IPR001810; F-box.
DR Pfam; PF00646; F-box; 1.
RW Hypothetical protein.
SQ SEQUENCE 362 AA; 42255 MW; 33D99EF0FD114006 CRC64;

Query Match      88.9%; Score 32; DB 5; Length 362;
Best Local Similarity 83.3%; Pred. No. 3.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSYL 6
DB 26 LDWSYL 31

```

Search completed: May 30, 2003, 14:39:05  
 Job time : 15.7632 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 30, 2003, 14:32:11 ; Search time 14.7632 Seconds  
(without alignments)  
83.741 Million cell updates/sec

Title: US-09-643-260-16  
Perfect score: 40  
Sequence: 1 LDMAWL 6

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 segs, 206047115 residues  
Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0  
Maximum DB seq length: 200000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: SP archaea: \*  
2: SP bacteria: \*  
3: SP fungi: \*  
4: SP human: \*  
5: SP invertebrate: \*  
6: SP mammal: \*  
7: SP unc: \*  
8: SP organelle: \*  
9: SP phage: \*  
10: SP plant: \*  
11: SP rodent: \*  
12: SP virus: \*  
13: SP vertebrate: \*  
14: SP unclassified: \*  
15: SP virus: \*  
16: SP bacteriophage: \*  
17: SP archaea: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40	100.0	645	2	Q9X6C6
2	38	95.0	396	17	Q96XZ8
3	37	92.5	740	6	Q95KV1
4	37	92.5	756	6	Q95KV0
5	36	90.0	27	12	Q9GRU7
6	36	90.0	27	12	Q9GRU6
7	36	90.0	207	5	Q96ZU3
8	36	90.0	215	17	Q9V227
9	36	90.0	251	16	Q07806
10	36	90.0	304	16	Q91719
11	36	90.0	316	16	Q8UBG8
12	36	90.0	444	2	Q9XBD4
13	36	90.0	516	10	Q4Z701
14	36	90.0	524	10	Q4Z700
15	36	90.0	544	10	Q9FEEL
16	36	90.0	1083	13	Q9OW08

17	36	90.0	1100	13	Q9OW09	Q9OW09 oncorhynch
18	36	90.0	1127	13	Q9W615	Q9W615 oryzias lat
19	36	90.0	1212	16	Q9HX70	Q9HX70 pseudomonas
20	36	90.0	1575	2	P94904	P94904 lysobacter
21	35	87.5	162	16	O53756	O53756 mycobacteri
22	35	87.5	204	16	Q9KER2	Q9KER2 bacillus ha
23	35	87.5	288	2	Q8VTT4	Q8VTT4 pseudomonas
24	35	87.5	299	16	Q9H218	Q9H218 pseudomonas
25	35	87.5	311	16	Q92MU7	Q92MU7 rhizobium m
26	35	87.5	313	2	Q8VU06	Q8VU06 pseudomonas
27	35	87.5	318	16	Q8EC58	Q8EC58 yersinia pe
28	35	87.5	329	16	Q8XVB4	Q8XVB4 ralsomias s
29	35	87.5	331	16	Q91427	Q91427 pseudomonas
30	35	87.5	337	16	Q8UB44	Q8UB44 agrobacteri
31	35	87.5	344	16	Q8YEH7	Q8YEH7 brucella me
32	35	87.5	353	16	Q9A7F0	Q9A7F0 caulobacter
33	35	87.5	386	16	Q92U27	Q92U27 rhizobium m
34	35	87.5	393	16	Q987Z1	Q987Z1 rhizobium l
35	35	87.5	394	10	Q9M0Y3	Q9M0Y3 arabidopsis
36	35	87.5	418	10	Q944N8	Q944N8 arabidopsis
37	35	87.5	418	10	Q944N8	Q944N8 arabidopsis
38	35	87.5	439	2	Q93061	Q93061 klebsiella
39	35	87.5	443	16	Q8ZDM7	Q8ZDM7 yersinia pe
40	35	87.5	449	6	Q8ZC91	Q8ZC91 yersinia pe
41	34	85.0	49	6	O8SP16	O8SP16 equus cabal
42	34	85.0	161	11	Q921P9	Q921P9 rattus norv
43	34	85.0	230	17	Q8THD6	Q8THD6 metanosarc
44	34	85.0	238	5	P92050	P92050 periplaneta
45	34	85.0	246	16	Q98BE8	Q98BE8 rhizobium l

## ALIGNMENTS

## RESULT 1

ID	Q9X6C6	PRELIMINARY;	PRT;	645 AA.
AC	Q9X6C6;			
DT	01-NOV-1999 (TREMBL)	12, Created)		
DT	01-NOV-1999 (TREMBL)	12, Last sequence update)		
DT	01-JUN-2002 (TREMBL)	21, Last annotation update)		
DE	Beta-galactosidase.			
GN	BGAT.			
OS	Thermus brockianus.			
OC	Bacteria; Thermus/Deinococcus group; Deinococci; Thermates;			
OC	Thermaceae; Thermus.			
OX	NCBI_Taxid-56956;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-IT1360;			
RC	MEDLINE-99402735; PubMed-10473401;			
RA	Fridjonsson O., Matzlawick H., Gehweiler A., Rohrlirsch T., Mattes R.;			
RT	brockianus IT1360 and Thermus thermophilus TH125.";			
RT	from Thermus brockianus IT1360.";			
RT	from Thermus brockianus IT1360.";			
RL	Appl. Environ. Microbiol. 65:3955-3963(1999).			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-IT1360;			
RC	MEDLINE-20203878; PubMed-10741834;			
RA	"The structure of the alpha-galactosidase gene loci in Thermus			
RT	brockianus IT1360 and Thermus thermophilus TH125.";			
RL	Extremophiles 4:23-33(2000).			
DR	EMBL: AF135398; AAD33667.1; -			
DR	InterPro: IPR001554; GH_14.			
DR	InterPro: IPR003476; Glyco_hydro_42.			
DR	Pfam: PF01373; Glyco_hydro_14; 1.			
DR	Pfam: PF02449; Glyco_hydro_42; 1.			
SO	SEQUENCE 645 AA; 73420 MW; C79A9E1C0020EC40 CRC64;			

Query Match

Best Local Similarity 100.0%; Score 40; DB 2; Length 645;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDMAML 6  
DB 48 LDMAML 53

## RESULT 2

O96XZ8 PRELIMINARY; PRT; 396 AA.  
AC O96XZ8; 01-DEC-2001 (TREMBlrel. 19, Created)  
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
DE 01-JUN-2002 (TREMBlrel. 21, Last annotation update)  
GN Putative anaerobic glycerol-3-phosphate dehydrogenase subunit C.  
OS Sulfolobus tokodaii.  
OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;  
OX NCBI\_TaxID=111955;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-JCM 10545 / 7;  
RX PubMed-11572479;  
RA Kawarabayashi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,  
RA Sekine M., Baba S.-I., Ankal A., Kosugi H., Hosoyama A., Fukui S.,  
RA Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y.,  
RA Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kushiida N., Oguchi A.,  
RA Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A.,  
RA Oshima T., Kikuchi H.;  
RT \*Complete genome sequence of an aerobic thermoacidophilic  
RT Crenarchaeon, Sulfolobus tokodaii strain 7.\*;  
RL DNA Res. 8:123-140(2001).  
DR EMBL: AP000989; BAB67479.1;  
DR InterPro: IPR001450; 4Fe4S\_Ferredoxin.  
DR InterPro: IPR004017; DUF224.  
DR Pfam: PF02754; DUF224; 2.  
DR PROSITE: PS00198; 4Fe4S\_FERREDOXIN; UNKNOWN\_1.  
KW Hypothetical protein; Complete proteome.  
SQ SEQUENCE 396 AA; 45359 MW; 15301A2AF2DDC9F CRC64;

Query Match 95.0%; Score 38; DB 17; Length 396;  
Best Local Similarity 83.3%; Pred. No. 1.4e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDMAML 6  
DB 94 LDMAML 99

RESULT 3  
O95KV1 PRELIMINARY; PRT; 740 AA.  
AC O95KV1; 01-DEC-2001 (TREMBlrel. 19, Created)  
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
DE 01-MAR-2002 (TREMBlrel. 20, Last annotation update)  
GN Ikb kinase-alpha.  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OX NCBI\_TaxID=9913;  
RN [1]  
RP SEQUENCE FROM N.A.  
RT Rottenberg S., Dobbelaere D.A.E., Heussler V.T.;  
RT "Identification and characterisation of the bovine Ikb kinases (IKKs)  
RT alpha, beta and gamma.";  
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AJ144555; CAC93686.1;  
DR InterPro: IPR000719; Euk\_pkinase.  
DR InterPro: IPR002290; Ser\_thr\_pkinase.  
DR InterPro: IPR001245; Tyr\_pkinase.

DR Pfam: PF00069; pkinase; 1.  
DR ProDom: PD000001; Euk\_pkinase; 1.  
DR SMART: SM00219; TYRKC; 1.  
DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP; UNKNOWN\_1.  
DR PROSITE: PS50011; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE: PS00108; PROTEIN\_KINASE\_ST; UNKNOWN\_1.  
KW ATP-binding; kinase; transferase.  
SQ SEQUENCE 740 AA; 84343 MW; 01903BE11F44D176 CRC64;

Query Match 92.5%; Score 37; DB 6; Length 740;  
Best Local Similarity 83.3%; Pred. No. 3.8e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDMAML 6  
DB 733 LDMAML 738

## RESULT 4

O95KV0 PRELIMINARY; PRT; 756 AA.  
AC O95KV0; 01-DEC-2001 (TREMBlrel. 19, Created)  
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
DE 01-JUN-2002 (TREMBlrel. 21, Last annotation update)  
GN Ikb kinase-beta.  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OX NCBI\_TaxID=9913;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Rottenberg S., Dobbelaere D.A.E., Heussler V.T.;  
RT "Identification and characterisation of the bovine Ikb kinases (IKKs)  
RT alpha, beta and gamma.";  
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AJ144556; CAC93687.1;  
DR InterPro: IPR000719; Euk\_pkinase.  
DR InterPro: IPR002290; Ser\_thr\_pkinase.  
DR InterPro: IPR001245; Tyr\_pkinase.  
DR Pfam: PF00069; pkinase; 1.  
DR ProDom: PD000001; Euk\_pkinase; 1.  
DR SMART: SM00219; TYRKC; 1.  
DR PROSITE: PS50011; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE: PS00108; PROTEIN\_KINASE\_ST; UNKNOWN\_1.  
KW ATP-binding; kinase; transferase.  
SQ SEQUENCE 756 AA; 86647 MW; A072D1561A176E5 CRC64;

Query Match 92.5%; Score 37; DB 6; Length 756;  
Best Local Similarity 83.3%; Pred. No. 3.9e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDMAML 6  
DB 737 LDMAML 742

RESULT 5  
O90R07 PRELIMINARY; PRT; 27 AA.  
AC O90R07; 01-MAY-2000 (TREMBlrel. 13, Created)  
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
DE 01-MAY-2000 (TREMBlrel. 13, Last annotation update)  
GN E2 glycoprotein hypervariable region (Fragment).  
OS Hepatitis C virus.  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
OC Hepacivirus.  
OX NCBI\_TaxID=11103;  
RN [1]  
RP SEQUENCE FROM N.A.

```

RC STRAIN-B-AS;
RA Yeh C.-T.;
RT "Replication of hepatitis C virus in the ascitic mononuclear cells and
RT development of distinct quasispecies in the ascitic fluid.";
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF109742; AAD51573.1; -.
FT NON_TER 1
FT NON_TER 27
SQ SEQUENCE 27 AA; 2964 MW; 8A68DCDC25CE4FAB CRC64;

Query Match
Best Local Similarity 90.0%; Score 36; DB 12; Length 27;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DNAML 6
Db 12 DNAML 16

RESULT 6
Q962U3 PRELIMINARY; PRT; 207 AA.
ID 0962U3;
AC 0962U3;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, last annotation update)
DE Cathepsin B-like protease (Fragment).
OS Trypanosoma rangeli.
OC Eukaryota; Euzoenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
OX NCBI_TaxID=5698;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SC 58;
RA Nobrega O.T., Teixeira A.R.L., Campbell D.A., Santana J.M.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF400046; AAK85411.1; -.
DR MEROPS; C01.098; -.
DR InterPro; IPR000668; Peptidase.C1.
DR InterPro; IPR000169; SHprot_acsite.
DR Pfam; PF00112; Peptidase.C1; 1.

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DR ProDom; PD000168; Peptidase.C1; 1.
DR PROSITE; PS00139; THIOL_PROTEASE_CYS; UNKNOWN_1.
DR PROSITE; PS00139; THIOL_PROTEASE_HIS; UNKNOWN_1.
KW Protease.
FT NON_TER 1
FT NON_TER 27
SQ SEQUENCE 207 AA; 22968 MW; 7AF0D959D5F81C5B CRC64;

Query Match
Best Local Similarity 90.0%; Score 36; DB 5; Length 207;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DNAML 6
Db 71 DNAML 75

RESULT 8
Q9V227 PRELIMINARY; PRT; 215 AA.
ID 09V227;
AC 09V227;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, last annotation update)
DE Purine phosphoribosyltransferase.
GN GPYA OR PAB2405.
OS Pyrococcus abyssi.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Pyrococcus.
OX NCBI_TaxID=29292;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ORSAY;
RA Hellig R.;
RT "Pyrococcus abyssi genome sequence: Insights into archaeal chromosome
RT structure and evolution.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ248283; CAB49171.1; -.
DR HSSP; Q26997; 10K3.
DR InterPro; IPR000836; PRTtransferase.
DR Pfam; PF00156; Pribosyltran; 1.
KW Glycosyltransferase; Transferase; Complete proteome.
SQ SEQUENCE 215 AA; 24832 MW; A58D71EBD5FD73 CRC64;

Query Match
Best Local Similarity 90.0%; Score 36; DB 17; Length 215;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDNAML 6
Db 141 LDNAML 146

RESULT 9
O07806 PRELIMINARY; PRT; 251 AA.
ID 007806;
AC 007806;
DT 01-JUL-1997 (TREMBlrel. 04, Created)
DT 01-JUL-1997 (TREMBlrel. 04, last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, last annotation update)
DE Phosphotransferase (Aminoglycoside 3'-phosphotransferase).
GN RV3817 OR MTCY409.13C OR MT3925.1.
OS Mycobacterium tuberculosis.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-H37RV;
RA MEDLINE-98295987; PubMed-96344230;
RA Cole S.T., Broesch R., Parkhill J., Garner T., Churcher C., Harris D.,
RA Gordon S.V., Eigemeier K., Gas S., Barry C.E. III, Tekala F.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,

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RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,  
 RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,  
 RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,  
 RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,  
 RA Sulston J.E., Taylor K., Whitehead S., Barrett B.G.,  
 RT "Deciphering the biology of Mycobacterium tuberculosis from the  
 RT complete genome sequence.";  
 RL Nature 393:537-544 (1998).  
 RN [2]

RP SEQUENCE FROM N.A.  
 RC STRAIN-CDC 1551 / OSHKOSH;  
 RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,  
 RA Peterson J., Deboy R., Dodson R., Gwinn M.L., Hart D., Hickey E.,  
 RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,  
 RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,  
 RA Bishai W.;  
 RT "Whole genome comparison of Mycobacterium tuberculosis clinical and  
 RT laboratory strains." to the EMBL/GenBank/DBJ databases.  
 RL Submitted (Apr-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; 297188; CAB10016.1; -;  
 DR EMBL; AE007186; AAK48292.1; -;  
 DR TIGR; MT3925; -;  
 DR Tuberculist; RV3817; -;  
 DR InterPro; IPR002575; APH;  
 DR Pfam; PF01636; APH; 1.  
 DR Transferrase; Complete proteome.  
 KW SEQUENCE 251 AA; 27241 MW; 52807PDA006A21B3 CRC64;

Query Match 90.0%; Score 36; DB 16; Length 251;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 DWAWL 6  
 DB 86 DWAWL 90

## RESULT 10

O91719 PRELIMINARY; PRT; 304 AA.  
 AC O91719;  
 DT 01-MAR-2001 (TREMBLrel. 16, Created)  
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
 DT 01-OCT-2001 (TREMBLrel. 18, Last annotation update)  
 DE Probable cytochrome c oxidase assembly factor.  
 GN PA0113.  
 OS Pseudomonas aeruginosa.  
 OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;  
 CC Pseudomonas  
 OX NCBI\_TaxID=287;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-ATCC 15692 / PAOI;  
 RX MEDLINE=20437337; PubMed=10984043;  
 RA Storer C.K., Pham X.-Q.T., Ervin A.L., Mizoguchi S.D., Warren P.,  
 RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,  
 RA Gardner R.L., Goltzy L., Tolentino E., Westbrock-Wadman S., Yuan Y.,  
 RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Lardig K., Lim R.M.,  
 RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,  
 RA Reizer J., Sater M.H., Hancock R.E.W., Lory S., Olson M.V.;  
 RT "Complete genome sequence of Pseudomonas aeruginosa PAOI, an  
 RT opportunistic pathogen.";  
 RL Nature 406:959-964 (2000).  
 DR EMBL; AE004449; AAG03503.1; -;  
 DR InterPro; IPR000537; UblA.  
 DR Pfam; PF01040; UblA; 1.  
 DR PROSITE; PS00943; UblA; UNKNOWN\_1.  
 KW Complete proteome.  
 GN SEQUENCE 304 AA; 33430 MW; DC278071764B671C CRC64;

Query Match 90.0%; Score 36; DB 16; Length 304;  
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDMAW 5  
 DB 259 LDMAW 263

## RESULT 11

O8UBG8 PRELIMINARY; PRT; 316 AA.  
 AC O8UBG8;  
 DT 01-JUN-2002 (TREMBLrel. 21, Created)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE ABC transporter, membrane spanning protein.  
 GN ATU3048 OR AGR\_L\_3514.  
 OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).  
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;  
 CC Rhizobiaceae; Rhizobium.  
 OX NCBI\_TaxID=176299;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE=21608550; PubMed=11743193;  
 RA Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,  
 RA Okura Y.K., Zhou Y., Chen L., Wood G.E., Almeida N.F., Jr., Woo L.,  
 RA Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Hovee D., St.,  
 RA Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,  
 RA Kutayavin T., Levy R., Li M.-J., McClelland E., Palmeri A.,  
 RA Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.,  
 RA Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan M., Perry M.,  
 RA Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,  
 RA Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,  
 RA Nester E.W.;  
 RT "The genome of the natural genetic engineer Agrobacterium tumefaciens  
 RT C58.";  
 RL Science 294:2317-2323 (2001).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE=21608551; PubMed=11743194;  
 RA Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,  
 RA Quorillo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,  
 RA Hounel K., Gordon J., Vaudin M., Iarchouk O., Epp A., Liu F.,  
 RA Mollan C., Allinger M., Doughty D., Scott C., Lappas C., Martelz B.,  
 RA Flanagan C., Crowell C., Gursun J., Lomo C., Sear C., Strub G.,  
 RA Cleio C., Slater S.;  
 RT "Genome sequence of the plant pathogen and biotechnology agent  
 RT Agrobacterium tumefaciens C58.";  
 RL Science 294:2323-2328 (2001).  
 DR EMBL; AE009235; AAL43864.1; -;  
 DR EMBL; AE008379; AAK90334.1; -;  
 KW Complete proteome.  
 GN SEQUENCE 316 AA; 35079 MW; 7137741D79029267 CRC64;

Query Match 90.0%; Score 36; DB 16; Length 316;  
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDMAW 5  
 DB 67 LDMAW 71

## RESULT 12

O9XBDA PRELIMINARY; PRT; 444 AA.  
 AC O9XBDA;  
 DT 01-NOV-1999 (TREMBLrel. 12, Created)  
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)  
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)  
 DE Putative integral membrane sugar transporter.  
 GN CZA382.17C.  
 OS Amycolatopsis orientalis.  
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;  
 CC Actinomycetales; Pseudonocardineae; Pseudonocardaceae; Amycolatopsis.

OX NCHI\_TaxID=31958;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-A3(2);  
 RA Lennard N., Harris B.;  
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-A3(2);  
 RA Bentley S.D., Parkhill J., Barrell B.G., Rajandream M.A.;  
 RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-A3(2);  
 RA van Wageningen A., Kirkpatrick P., Williams D., Harris B., Kershaw J.,  
 RA Lennard N., Jones M., Jones S., Soleberg P.;  
 RT "Sequencing and analysis of genes involved in the biosynthesis of a  
 RT vancomycin group antibiotic."  
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).  
 DR EMBL: AL078635; CAB45038.1; -;  
 DR InterPro: IPR003662; sub.transporter.  
 DR Pfam: PF00083; sugar.tr.1.  
 DR Sugar transporter; Transmembrane.  
 KW SEQUENCE 444 AA; 48039 MW; 51ACE2D9EB121EDA CRC64;

Query Match 90.0%; Score 36; DB 2; Length 444;  
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDRAW 5  
 |||||  
 Db 194 LDRAW 198

RESULT 13  
 ID 042701 PRELIMINARY; PRT; 516 AA.  
 AC 042701;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)  
 DE Cytochrome P450 (Fragment).  
 GN CYP72C.  
 OS Catharanthus roseus (Rosa periwinkle) (Madagascar periwinkle).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Asteridae; easterids I; Gentianales; Apocynaceae; Rauvolfioideae;  
 OC Vincet; Catharanthus.  
 OX NCHI\_TaxID=4058;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-CP3;  
 RA Mangold U., Eichel J., Batschauer A., Lanz T., Kaiser T.,  
 RA Spangenberg G., Werck-Reichhart D., Schroeder J.;  
 RT "Gene and cDNA for plant cytochrome P450 proteins (CYP72 family) from  
 RT Catharanthus roseus, and transgenic expression in tobacco and  
 RT Arabidopsis thaliana."  
 RL Plant Sci. 96:129-136(1994).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-CP3;  
 RA Joachim Schroeder;  
 RL submitted (SEP-1993) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.  
 DE EMBL: L19075; AAA17746.1; -;  
 DR InterPro: IPR001128; Cytochrome\_P450.  
 DR Pfam: PF00067; P450.1.  
 DR PRINTS: PR00385; P450.  
 DR PROSITE: PS00086; CYTOCHROME\_P450; UNKNOWN\_1.  
 DR Heme; Monooxygenase; Oxidoreductase.  
 KW NCHI\_TaxID=4530;  
 FT NON TER 1  
 SO SEQUENCE 516 AA; 59720 MW; 02A7D9B0936D931F CRC64;

Query Match 90.0%; Score 36; DB 10; Length 516;  
 Best Local Similarity 100.0%; Pred. No. 3.8e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDRAW 5  
 |||||  
 Db 17 LDRAW 21

RESULT 14  
 ID 042700 PRELIMINARY; PRT; 524 AA.  
 AC 042700;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)  
 DE Cytochrome P450.  
 GN CYP72B.  
 OS Catharanthus roseus (Rosa periwinkle) (Madagascar periwinkle).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Asteridae; easterids I; Gentianales; Apocynaceae; Rauvolfioideae;  
 OC Vincet; Catharanthus.  
 OX NCHI\_TaxID=4058;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-CP3;  
 RA Mangold U., Eichel J., Batschauer A., Lanz T., Kaiser T.,  
 RA Spangenberg G., Werck-Reichhart D., Schroeder J.;  
 RT "Gene and cDNA for plant cytochrome P450 proteins (CYP72 family) from  
 RT Catharanthus roseus, and transgenic expression in tobacco and  
 RT Arabidopsis thaliana."  
 RL Plant Sci. 96:129-136(1994).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-CP3;  
 RA Schroeder J.;  
 RL submitted (SEP-1993) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.  
 DE EMBL: L19074; AAA17732.1; -;  
 DR InterPro: IPR001128; Cytochrome\_P450.  
 DR Pfam: PF00067; P450.1.  
 DR PRINTS: PR00385; P450.  
 DR PROSITE: PS00086; CYTOCHROME\_P450; UNKNOWN\_1.  
 DR Heme; Monooxygenase; Oxidoreductase.  
 KW NCHI\_TaxID=4058;  
 SO SEQUENCE 524 AA; 60414 MW; 08B8087FE663F929 CRC64;

Query Match 90.0%; Score 36; DB 10; Length 524;  
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDRAW 5  
 |||||  
 Db 28 LDRAW 32

RESULT 15  
 ID 09FEEL PRELIMINARY; PRT; 544 AA.  
 AC 09FEEL;  
 DT 01-MAR-2001 (TREMBLrel. 16, Created)  
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)  
 DE Putative cytochrome P450.  
 GN P0688A04.9 OR P0006C01.24.  
 OS Oryza sativa (Rice).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC Ehrharioideae; Oryzaceae; Oryza.  
 OX NCHI\_TaxID=4530;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RC STRAIN-CV. NIPPONBARE;  
 RA Sasaki T., Matsumoto T., Yamamoto K.;  
 RT "Oryza sativa nippondare(GA3) genomic DNA, chromosome 1, PAC  
 RT clone:P0688A04.";  
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-CV. NIPPONBARE;  
 RA Sasaki T., Matsumoto T., Yamamoto K.;  
 RT "Oryza sativa nippondare(GA3) genomic DNA, chromosome 1, PAC  
 RT clone:P0006C01.";  
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.  
 DR EMBL: AP002839; BAB19103.1; -;  
 DR EMBL: AP002744; BAB19082.1; -;  
 DR InterPro: IPR001128; Cytochrome\_P450.  
 DR Pfam: PF00067; P450; 1.  
 DR PRINTS: PR00385; P450.  
 DR PROSITE: PS00086; CYTOCHROME\_P450; UNKNOWN\_1.  
 KW Heme; Monooxygenase; Oxidoreductase.  
 SQ Heme; Monooxygenase; Oxidoreductase.  
 SQ SEQUENCE 544 AA; 60867 MW; 273EAF5968D1A024 CRC64;

Query Match

Best Local Similarity 90.0%; Score 36; DB 10; Length 544;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMAML 6  
 1:|||||  
 DB 48 LEMAML 53

Search completed: May 30, 2003, 14:39:06  
 Job time : 15.7632 secs



XX 02-MAY-2000; 2000US-201261P.  
 PR 22-AUG-2000; 2000US-0643260.  
 XX  
 PA (UYVA ) UNIV YALE.  
 XX May MJ, Ghosh S;  
 PI  
 XX WPI; 2002-179350/23.  
 DR  
 XX  
 PT Modulating NF-kappaB induction in a cell, useful for treating e.g.  
 PT inflammatory disorders, osteoporosis and cancer, comprises contacting a  
 PT cell with an anti-inflammatory compound comprising at least one NEMO  
 PT binding domain  
 XX  
 XX  
 PS Claim 23; Page 44; 82pp; English.

XX The invention relates to modulating NF-kappaB (NF- $\kappa$ B) induction in a cell  
 CC comprises contacting a cell with an anti-inflammatory compound  
 CC (ABB08725-ABB08742) comprising at least one NEMO binding domain  
 CC (AAB77313). The compound has acts through selective inhibition of  
 CC cytokine-mediated NF- $\kappa$ B activation by blocking the interaction of NEMO  
 CC with I $\kappa$ Beta at the NEMO binding domain. Blockage of I $\kappa$ Beta-NEMO  
 CC interaction results in inhibition of I $\kappa$ Beta kinase activation and  
 CC subsequent decreased phosphorylation of I $\kappa$ Beta. The compound may also  
 CC act (directly or indirectly) by blocking the recruitment of leukocytes  
 CC into sites of acute and chronic inflammation, by down-regulating the  
 CC expression of E-selectin on leukocytes or by blocking osteoclast  
 CC differentiation. The compound is useful in treating NF- $\kappa$ B mediated  
 CC conditions, where the condition is an inflammatory disorder, an  
 CC autoimmune disease, transplant rejection, osteoporosis, cancer,  
 CC Alzheimer's disease, atherosclerosis, a viral infection or ataxia  
 CC telangiectasia. The inflammatory disorder is asthma, allergies,  
 CC urticaria, anaphylaxis, cutaneous inflammation, sepsis, psoriasis,  
 CC rheumatoid arthritis, osteoarthritis, psoriatic arthritis, inflammatory  
 CC bowel disease, chronic obstructive pulmonary disease, vasculitis and  
 CC bursitis. The inflammatory disorder may also be dermatitis, eczema,  
 CC psoriasis, osteoarthritis, psoriatic arthritis, lupus and  
 CC spondylarthritis. Also for Crohn's disease, ulcerative colitis,  
 CC polyomyelitis, scleroderma, Wegner's granulomatosis, temporal arteritis,  
 CC cryoglobulinemia or multiple sclerosis. For chronic viral infections,  
 CC caused by Epstein-Barr, cytomegalovirus or herpes simplex. Other viral  
 CC diseases include HIV and Influenza. The compound may also be useful for  
 CC treating anaphylaxis, drug and food sensitivity, contact dermatitis,  
 CC sunburn or aging. The compound may be used to replace corticosteroids in  
 CC any application in which corticosteroids are used, including  
 CC immunosuppression in transplants and cancer therapy. Also for identifying  
 CC anti-inflammatory compounds and for diagnosis of an inflammatory disorder.  
 CC The compound may be administered alone or in combination with other known  
 CC anti-inflammatory agents. The present sequence is that of a mutated NEMO  
 CC binding domain of I $\kappa$ Beta.  
 XX  
 SQ Sequence 6 AA;

Query Match 100.0%; Score 40; DB 23; Length 6;  
 Best Local Similarity 100.0%; Pred. NO. 7.8e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSML 6  
 |||||  
 Db 1 ADMSML 6

RESULT 2  
 AAM48509  
 ID AAM48509 standard; Peptide: 6 AA.  
 XX  
 AC AAM48509;  
 XX  
 DT 20-MAR-2002 (first entry)  
 XX  
 DE NBD mutant peptide SEQ ID NO 4.  
 XX

KW Antiinflammatory; antiaesthetic; cytostatic; antipsoriatic; neutrophic;  
 KW antineumatic; antiarthritic; osteopathic; antibacterial; virucide;  
 KW immunosuppressive; dermatologic; neuroprotective; antiatherosclerotic;  
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;  
 KW cytokine; NF-kappaB; I $\kappa$ Beta kinase beta; I $\kappa$ Beta; cancer; psoriasis;  
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
 KW autoimmune disorder; multiple sclerosis; transplant rejection;  
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.

OS Synthetic.  
 XX  
 XX W0200183554-A2.  
 PN  
 XX 08-NOV-2001.  
 PD  
 XX 02-MAY-2001; 2001WO-US14346.  
 PF  
 XX 02-MAY-2000; 2000US-201261P.  
 PR  
 XX 22-AUG-2000; 2000US-0643260.  
 PA (PRAE-) PRAECIS PHARM INC.  
 PA (UYVA ) UNIV YALE.

XX May MJ, Ghosh S, Flindeis MA, Phillips K;  
 PI  
 XX WPI; 2002-121889/16.  
 DR  
 XX  
 XX Novel antiinflammatory compound comprising membrane translocation  
 PT domain fused to NEMO binding sequence, useful for blocking nuclear  
 PT factor kappaB activation, and for treating asthma, lung inflammation,  
 PT psoriasis  
 PT  
 XX Example 6; Page 47; 88pp; English.

PS The invention relates to an antiinflammatory compound (especially  
 XX (AAM48628-AAM48645), comprising a membrane translocation domain  
 CC (AAM48628-AAM48645) or (AAM48646-AAM48651) which comprises from 6-15  
 CC amino acid residues, fused to a NEMO binding sequence  
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiaesthetic,  
 CC cytostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,  
 CC antibacterial, immunosuppressive, dermatologic, neuroprotective,  
 CC neutrophic, antiatherosclerotic, virucide and antiallergic activity. The  
 CC compounds act as selective inhibitors of cytokine-mediated NF-kappaB  
 CC activation by blocking interaction of I $\kappa$ Beta kinase beta (I $\kappa$ Beta) at  
 CC the NEMO binding domain that results in inhibition of I $\kappa$ Beta kinase  
 CC activation and subsequent decreased phosphorylation of I $\kappa$ Beta. The  
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,  
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,  
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,  
 CC bursitis, autoimmune diseases such as lupus, polyomyelitis, scleroderma,  
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;  
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia  
 CC telangiectasia. The compounds are also useful for treating  
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,  
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and  
 CC arthritis.  
 CC  
 XX  
 XX

SQ Sequence 6 AA;

Query Match 100.0%; Score 40; DB 23; Length 6;  
 Best Local Similarity 100.0%; Pred. NO. 7.8e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSML 6  
 |||||  
 Db 1 ADMSML 6

RESULT 3  
 AAM48536  
 ID AAM48536 standard; Peptide: 6 AA.  
 XX

AC AAM48536;  
 XX 20-MAR-2002 (first entry)  
 XX  
 DE Anti-inflammatory peptide SEQ ID NO 39.  
 XX  
 KW Antiinflammatory; antiasthmatic; cytosstatic; antipsoriatic; noctropic;  
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;  
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;  
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;  
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;  
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
 KW autoimmune disorder; multiple sclerosis; transplant rejection;  
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.  
 OS Synthetic.  
 XX  
 XX WO200183554-A2.  
 XX  
 PD 08-NOV-2001.  
 XX  
 PF 02-MAY-2001; 2001WO-US14346.  
 XX  
 PR 02-MAY-2000; 2000US-201261P.  
 PR 22-AUG-2000; 2000US-0643260.  
 XX  
 PA (PRAE-) PRACIS PHARM INC.  
 PA (UYA) UNIV YALE.  
 XX  
 PI May MJ, Ghosh S, Findeis MA, Phillips K;  
 XX  
 DR WPI; 2002-121889/16.  
 XX  
 PT Novel antiinflammatory compound comprising membrane translocation  
 PT domain fused to NEMO binding sequence, useful for blocking nuclear  
 PT factor kappaB activation, and for treating asthma, lung inflammation,  
 PT psoriasis  
 XX  
 PS Claim 6; Page 61; 88pp; English.  
 XX  
 CC The invention relates to an antiinflammatory compound (especially  
 CC AAM48628-AAM48645), comprising a membrane translocation domain  
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15  
 CC amino acid residues, fused to a NEMO binding sequence  
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,  
 CC cytosstatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,  
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,  
 CC noctropic, antiatherosclerotic, virucide and antiallergic activity. The  
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB  
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at  
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase  
 CC activation and subsequent decreased phosphorylation of IkappaB. The  
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,  
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 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,  
 CC bursitis, autoimmune diseases such as lupus, polymyalgia, scleroderma,  
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;  
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia  
 CC telangiectasia. The compounds are also useful for treating  
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,  
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and  
 CC arthritis.  
 CC  
 CC Sequence 6 AA:  
 SO

Query Match 100.0%; Score 40; DB 23; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ADMSWL 6  
 DB 1 ADMSWL 6

RESULT 4  
 ID AAM48548  
 XX AAM48548 standard; Peptide: 6 AA.  
 XX  
 XX AAM48548;  
 XX  
 DE 20-MAR-2002 (first entry)  
 XX  
 DE Anti-inflammatory peptide SEQ ID NO 51.  
 XX  
 KW Antiinflammatory; antiasthmatic; cytosstatic; antipsoriatic; noctropic;  
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;  
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;  
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;  
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;  
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
 KW autoimmune disorder; multiple sclerosis; transplant rejection;  
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.  
 OS Synthetic.  
 XX  
 XX WO200183554-A2.  
 XX  
 PD 08-NOV-2001.  
 XX  
 PF 02-MAY-2001; 2001WO-US14346.  
 XX  
 PR 02-MAY-2000; 2000US-201261P.  
 PR 22-AUG-2000; 2000US-0643260.  
 XX  
 PA (PRAE-) PRACIS PHARM INC.  
 PA (UYA) UNIV YALE.  
 XX  
 PI May MJ, Ghosh S, Findeis MA, Phillips K;  
 XX  
 DR WPI; 2002-121889/16.  
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 PT Novel antiinflammatory compound comprising membrane translocation  
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 PT psoriasis  
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 PS Claim 6; Page 62; 88pp; English.  
 XX  
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 CC activation and subsequent decreased phosphorylation of IkappaB. The  
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 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,  
 CC bursitis, autoimmune diseases such as lupus, polymyalgia, scleroderma,  
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;  
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia  
 CC telangiectasia. The compounds are also useful for treating  
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,  
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and  
 CC arthritis.  
 CC  
 CC Sequence 6 AA:  
 SO

Query Match 100.0%; Score 40; DB 23; Length 6;

Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ADMSWL 6  
111111  
DB 1 ADMSWL 6

RESULT 5  
AAM48552  
ID AAM48552 standard; Peptide; 7 AA.

AC AAM48552;

DT 20-MAR-2002 (first entry)

DE Anti-inflammatory peptide SEQ ID NO 55.

XX Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; neutropic;  
XX antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;  
KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;  
KW anti-allergic; membrane translocation domain; NEMO binding domain; eczema;  
KW cytokine; NF-kappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;  
KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
KW autoimmune disorder; multiple sclerosis; transplant rejection;  
KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.

OS Synthetic.

PN WO200183554-A2.

PD 08-NOV-2001.

PF 02-MAY-2001; 2001WO-US14346.

PR 02-MAY-2000; 2000US-201261P.

PR 22-AUG-2000; 2000US-0643260.

PA (PRAE-) PRAECIS PHARM INC.

PA (UYVA) UNIV YALE.

PI May MJ, Ghosh S, Findels MA, Phillips K;

DR WPI; 2002-121889/16.

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PT domain fused to NEMO binding sequence, useful for blocking nuclear  
PT factor kappaB activation, and for treating asthma, lung inflammation,  
PT psoriasis

PS Claim 6; Page 62; 88pp; English.

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CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15  
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CC neutropic, antiatherosclerotic, virucide and anti-allergic activity. The  
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CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,  
CC dermatitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,  
CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;  
CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia  
CC telangiectasia. The compounds are also useful for treating  
CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,

CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and  
CC arthritis.

XX SQ Sequence 7 AA:

Query Match 100.0%; Score 40; DB 23; Length 7;  
Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ADMSWL 6  
111111  
DB 1 ADMSWL 6

RESULT 6  
AAM48545  
ID AAM48545 standard; Peptide; 8 AA.

AC AAM48545;

DT 20-MAR-2002 (first entry)

DE Anti-inflammatory peptide SEQ ID NO 48.

XX Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; neutropic;  
XX antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;  
KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;  
KW anti-allergic; membrane translocation domain; NEMO binding domain; eczema;  
KW cytokine; NF-kappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;  
KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
KW autoimmune disorder; multiple sclerosis; transplant rejection;  
KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.

OS Synthetic.

PN WO200183554-A2.

PD 08-NOV-2001.

PF 02-MAY-2001; 2001WO-US14346.

PR 02-MAY-2000; 2000US-201261P.

PR 22-AUG-2000; 2000US-0643260.

PA (PRAE-) PRAECIS PHARM INC.

PA (UYVA) UNIV YALE.

PI May MJ, Ghosh S, Findels MA, Phillips K;

DR WPI; 2002-121889/16.

XX Novel antiinflammatory compound comprising membrane translocation  
PT domain fused to NEMO binding sequence, useful for blocking nuclear  
PT factor kappaB activation, and for treating asthma, lung inflammation,  
PT psoriasis

PS Claim 6; Page 62; 88pp; English.

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CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15  
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 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;  
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia  
 CC telangiectasia. The compounds are also useful for treating  
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,  
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and  
 CC arthritis.  
 XX  
 SQ Sequence 8 AA;  
 Query Match 100.0%; Score 40; DB 23; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 ADMSWL 6  
 111111  
 DB 3 ADMSWL 8  
 RESULT 7  
 ID AAM48553 standard; Peptide: 8 AA.  
 AC AAM48553;  
 XX  
 DT 20-MAR-2002 (first entry)  
 XX  
 DE Anti-inflammatory peptide SEQ ID NO 56.  
 XX  
 KW Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;  
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;  
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;  
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;  
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;  
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
 KW autoimmune disorder; multiple sclerosis; transplant rejection;  
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200183554-A2.  
 PD 08-NOV-2001.  
 XX  
 PF 02-MAY-2001; 2001WO-US14346.  
 XX  
 PR 02-MAY-2000; 2000US-201261P.  
 PR 22-AUG-2000; 2000US-0643260.  
 XX  
 PA (PRAE-) PRAECIS PHARM INC.  
 PA (UYVA) UNIV YALE.  
 XX  
 PI May MJ, Ghosh S, Findeis MA, Phillips K;  
 DR WPI; 2002-121889/16.  
 XX  
 PT Novel antiinflammatory compound comprising membrane translocation  
 PT domain fused to NEMO binding sequence, useful for blocking nuclear  
 PT factor kappaB activation, and for treating asthma, lung inflammation,  
 PT psoriasis  
 XX  
 PS Claim 6; Page 62; 88pp; English.  
 XX  
 CC The invention relates to an antiinflammatory compound (especially  
 CC AAM48628-AAM48645) comprising a membrane translocation domain  
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15  
 CC amino acid residues, fused to a NEMO binding sequence  
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,  
 CC cytoskeletal, antipsoriatic, antirheumatic, antiallergic, osteopathic,  
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,  
 CC nootropic, antiatherosclerotic, virucide and antiallergic activity. The

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 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at  
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 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,  
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;  
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia  
 CC telangiectasia. The compounds are also useful for treating  
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,  
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and  
 CC arthritis.  
 XX  
 SQ Sequence 8 AA;  
 Query Match 100.0%; Score 40; DB 23; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 ADMSWL 6  
 111111  
 DB 1 ADMSWL 6  
 RESULT 8  
 ID AAM48544 standard; Peptide: 9 AA.  
 AC AAM48544;  
 XX  
 DT 20-MAR-2002 (first entry)  
 XX  
 DE Anti-inflammatory peptide SEQ ID NO 47.  
 XX  
 KW Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;  
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;  
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;  
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;  
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;  
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
 KW autoimmune disorder; multiple sclerosis; transplant rejection;  
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200183554-A2.  
 PD 08-NOV-2001.  
 XX  
 PF 02-MAY-2001; 2001WO-US14346.  
 XX  
 PR 02-MAY-2000; 2000US-201261P.  
 PR 22-AUG-2000; 2000US-0643260.  
 XX  
 PA (PRAE-) PRAECIS PHARM INC.  
 PA (UYVA) UNIV YALE.  
 XX  
 PI May MJ, Ghosh S, Findeis MA, Phillips K;  
 DR WPI; 2002-121889/16.  
 XX  
 PT Novel antiinflammatory compound comprising membrane translocation  
 PT domain fused to NEMO binding sequence, useful for blocking nuclear  
 PT factor kappaB activation, and for treating asthma, lung inflammation,  
 PT psoriasis  
 XX  
 PS Claim 6; Page 62; 88pp; English.  
 XX  
 CC The invention relates to an antiinflammatory compound (especially  
 CC AAM48628-AAM48645), comprising a membrane translocation domain

CC (AA48620-AA48627 or AA48646-AA48651) which comprises from 6-15  
 CC amino acid residues, fused to a NEMO binding sequence  
 CC (AA48525-AA48619). The antiinflammatory compounds have antiasthmatic,  
 CC cytoskeletal, antiapoptotic, antirheumatic, antiarthritic, osteopathic,  
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,  
 CC neurotropic, antiatherosclerotic, virucide and antiallergic activity. The  
 CC compounds act as selective inhibitors of cytokine-mediated NF-kappaB  
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 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;  
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia  
 CC telangiectasia. The compounds are also useful for treating  
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,  
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and  
 CC arthritis.

CC Sequence 9 AA;

Query Match 100.0%; Score 40; DB 23; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ADMSWL 6

DB 1 ADMSWL 6

RESULT 9  
 AA48547  
 ID AA48547 standard; Peptide; 9 AA.

AC AA48547;

DT 20-MAR-2002 (first entry)

DE Anti-inflammatory peptide SEQ ID NO 50.

XX Antinflammatory; antiasthmatic; cytoskeletal; antipapillary; neurotropic;  
 XX antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;  
 XX immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;  
 XX antiallergic; membrane translocation domain; NEMO binding domain; eczema;  
 XX cytokine; NF-kappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;  
 XX rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
 XX autoimmune disorder; multiple sclerosis; transplant rejection;  
 XX osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
 XX ataxia telangiectasia; allergy; anaphylaxis; arthritis.

OS Synthetic.

PN WO200183554-A2.

PD 08-NOV-2001.

PF 02-MAY-2001; 2001WO-US14346.

PR 02-MAY-2000; 2000US-201261P.

PR 22-AUG-2000; 2000US-0643260.

PA (PRAE-) PRAECIS PHARM INC.

PA (UYVA) UNIV YALE.

PI May MJ, Ghosh S, Findeis MA, Phillips K;

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 PT domain, fused to NEMO binding sequence, useful for blocking nuclear  
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CC Sequence 9 AA;

Query Match 100.0%; Score 40; DB 23; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ADMSWL 6

DB 1 ADMSWL 6

RESULT 10  
 AA48550  
 ID AA48550 standard; Peptide; 9 AA.

AC AA48550;

DT 20-MAR-2002 (first entry)

DE Anti-inflammatory peptide SEQ ID NO 53.

XX Antinflammatory; antiasthmatic; cytoskeletal; antipapillary; neurotropic;  
 XX antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;  
 XX immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;  
 XX antiallergic; membrane translocation domain; NEMO binding domain; eczema;  
 XX cytokine; NF-kappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;  
 XX rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
 XX autoimmune disorder; multiple sclerosis; transplant rejection;  
 XX osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
 XX ataxia telangiectasia; allergy; anaphylaxis; arthritis.

OS Synthetic.

PN WO200183554-A2.

PD 08-NOV-2001.

PF 02-MAY-2001; 2001WO-US14346.

PR 02-MAY-2000; 2000US-201261P.

PR 22-AUG-2000; 2000US-0643260.

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PA (UYVA) UNIV YALE.

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 CC arthritis.  
 CC  
 SQ Sequence 9 AA:  
 QY  
 DB 1 ADMSWL 6  
 3 ADMSWL 8  
 Query Match 100.0%; Score 40; DB 23; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 11  
 ID AAM48551 standard; Peptide; 9 AA.  
 AC AAM48551:  
 XX  
 XX 20-MAR-2002 (first entry)  
 DE Anti-inflammatory peptide SEQ ID NO 54.  
 XX  
 XX Antinflammatory; antiasthmatic; cytoskeletal; antipsoriatic; nootropic;  
 KW antirheumatic; antiarthritic; osteoprotective; antibacterial; virucide;  
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;  
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;  
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;  
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 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.  
 XX  
 XX Synthetic.  
 OS  
 XX  
 PN W0200183554-A2.  
 XX  
 PD 08-NOV-2001.  
 XX  
 XX 02-MAY-2001; 2001WO-0514346.  
 PF  
 XX  
 XX 02-MAY-2000; 2000US-201261P.  
 PR

PR 22-AUG-2000; 2000US-0643260.  
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 XX (PRAE-) PRAECIS PHARM INC.  
 PA (UYXA ) UNIV YALE.  
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 XX May M, Ghosh S, Findels MA, Phillips K;  
 PI WPI; 2002-121889/16.  
 XX  
 XX Claim 6; Page 62; 88pp; English.  
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 CC nootropic, antiatherosclerotic, virucide and antiallergic activity. The  
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB  
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at  
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase  
 CC activation and subsequent decreased phosphorylation of IkappaB. The  
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,  
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,  
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,  
 CC bursitis, autoimmune diseases such as lupus, polymyalgia, scleroderma,  
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;  
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia  
 CC telangiectasia. The compounds are also useful for treating  
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,  
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and  
 CC arthritis.  
 CC  
 SQ Sequence 9 AA:  
 QY  
 DB 1 ADMSWL 6  
 2 ADMSWL 7  
 Query Match 100.0%; Score 40; DB 23; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 12  
 ID AAM48546 standard; Peptide; 10 AA.  
 AC AAM48546:  
 XX  
 XX 20-MAR-2002 (first entry)  
 DE Anti-inflammatory peptide SEQ ID NO 49.  
 XX  
 XX Antinflammatory; antiasthmatic; cytoskeletal; antipsoriatic; nootropic;  
 KW antirheumatic; antiarthritic; osteoprotective; antibacterial; virucide;  
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;  
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;  
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;  
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
 KW autoimmune disorder; multiple sclerosis; transplant rejection;  
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.  
 XX  
 XX Synthetic.  
 OS  
 XX  
 PN W0200183554-A2.  
 PR

XX 08-NOV-2001.  
 PD  
 XX  
 PF 02-MAY-2001; 2001WO-US14346.  
 XX  
 PR 02-MAY-2000; 2000US-201261P.  
 XX 22-ADG-2000; 2000US-0643260.  
 PR  
 PA (PRAE-) PRAECIS PHARM INC.  
 PA (UYVA ) UNIV YALE.  
 PI May MJ, Ghosh S, Flindels MA, Phillips K;  
 PI WPI: 2002-121889/16.  
 DR  
 XX Novel antiinflammatory compound comprising membrane translocation  
 PT domain fused to NEMO binding sequence, useful for blocking nuclear  
 PT factor kappaB activation, and for treating asthma, lung inflammation,  
 PT psoriasis  
 XX  
 PS Claim 6; Page 62; 88pp; English.  
 CC The invention relates to an antiinflammatory compound (especially  
 CC (AAM48628-AAM48645), comprising a membrane translocation domain  
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15  
 CC amino acid residues, fused to a NEMO binding sequence  
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,  
 CC cytoskeletal, antipsoriatic, antirheumatic, antiarthritic, osteopathic,  
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,  
 CC neurotropic, antiatherosclerotic, virocidic and antiallergic activity. The  
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB  
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at  
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase  
 CC activation and subsequent decreased phosphorylation of IKKbeta. The  
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,  
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,  
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,  
 CC bursitis, autoimmune diseases such as lupus, polymyalgia, scleroderma,  
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;  
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia  
 CC telangiectasia. The compounds are also useful for treating  
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,  
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and  
 CC arthritis.  
 CC  
 SQ Sequence 10 AA;  
 QY Query Match 100.0%; Score 40; DB 23; Length 10;  
 DB Best Local Similarity 100.0%; Pred. No. 2.1;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 ADMSWL 6  
 DB 2 ADMSWL 7  
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 AAM48549  
 ID AAM48549 standard; Peptide; 10 AA.  
 AC AAM48549;  
 XX  
 XX 20-MAR-2002 (first entry)  
 DE Anti-inflammatory peptide SEQ ID NO 52.  
 XX  
 XX Antiinflammatory; antiasthmatic; cytoskeletal; antipsoriatic; neurotropic;  
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virocidic;  
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;  
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;  
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;  
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
 KW autoimmune disorder; multiple sclerosis; transplant rejection;

KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.  
 XX  
 XX Synthetic.  
 OS  
 XX WO200183554-A2.  
 PN  
 PD 08-NOV-2001.  
 PD  
 PF 02-MAY-2001; 2001WO-US14346.  
 PF  
 PR 02-MAY-2000; 2000US-201261P.  
 PR 22-ADG-2000; 2000US-0643260.  
 PR  
 PA (PRAE-) PRAECIS PHARM INC.  
 PA (UYVA ) UNIV YALE.  
 PI May MJ, Ghosh S, Flindels MA, Phillips K;  
 PI WPI: 2002-121889/16.  
 DR  
 XX Novel antiinflammatory compound comprising membrane translocation  
 PT domain fused to NEMO binding sequence, useful for blocking nuclear  
 PT factor kappaB activation, and for treating asthma, lung inflammation,  
 PT psoriasis  
 XX  
 PS Claim 6; Page 62; 88pp; English.  
 CC The invention relates to an antiinflammatory compound (especially  
 CC (AAM48628-AAM48645), comprising a membrane translocation domain  
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15  
 CC amino acid residues, fused to a NEMO binding sequence  
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,  
 CC cytoskeletal, antipsoriatic, antirheumatic, antiarthritic, osteopathic,  
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,  
 CC neurotropic, antiatherosclerotic, virocidic and antiallergic activity. The  
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 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at  
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 CC activation and subsequent decreased phosphorylation of IKKbeta. The  
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 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,  
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;  
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia  
 CC telangiectasia. The compounds are also useful for treating  
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,  
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and  
 CC arthritis.  
 CC  
 SQ Sequence 10 AA;  
 QY Query Match 100.0%; Score 40; DB 23; Length 10;  
 DB Best Local Similarity 100.0%; Pred. No. 2.1;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 ADMSWL 6  
 DB 3 ADMSWL 8  
 RESULT 14  
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 ID AAM48543 standard; Peptide; 11 AA.  
 AC AAM48543;  
 XX  
 XX 20-MAR-2002 (first entry)  
 DE Anti-inflammatory peptide SEQ ID NO 46.  
 XX  
 KW Antiinflammatory; antiasthmatic; cytoskeletal; antipsoriatic; neurotropic;

KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;  
 KW immunosuppressive; dermatological; neuroprotective; antithrombotic;  
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;  
 KW cytokine; NF-kappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;  
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
 KW autoimmune disorder; multiple sclerosis; transplant rejection;  
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.  
 OS Synthetic.  
 XX  
 PN WO200183554-A2.  
 XX  
 PD 08-NOV-2001.  
 XX  
 PF 02-MAY-2001; 2001WO-US14346.  
 XX  
 PR 02-MAY-2000; 2000US-201261P.  
 PR 22-AUG-2000; 2000US-0643260.  
 XX  
 PA (PRAE-) PRAECIS PHARM INC.  
 PA (UYA-) UNIV YALE.  
 PI May MJ, Ghosh S, Fludeis MA, Phillips K;  
 XX WPI; 2002-121889/16.  
 DR  
 XX  
 PT Novel antiinflammatory compound comprising membrane translocation  
 PT domain fused to NEMO binding sequence, useful for blocking nuclear  
 PT factor kappaB activation, and for treating asthma, lung inflammation,  
 PT psoriasis -  
 PS  
 XX Claim 6; Page 62; 88pp: English.  
 PS  
 CC The invention relates to an antiinflammatory compound (especially  
 CC (AAM48628-AAM48645), comprising a membrane translocation domain  
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15  
 CC amino acid residues, fused to a NEMO binding sequence  
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,  
 CC cytotactic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,  
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,  
 CC nootropic, antithrombotic, virucide and antiallergic activity. The  
 CC compounds act as selective inhibitors of cytokine-mediated NF-kappaB  
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at  
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase  
 CC activation and subsequent decreased phosphorylation of IkappaB. The  
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 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,  
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,  
 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,  
 CC granulomatosis; multiple sclerosis; transplant rejection; osteoporosis;  
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia  
 CC telangiectasia. The compounds are also useful for treating  
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,  
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and  
 CC arthritis.  
 CC  
 XX  
 SQ Sequence 11 AA;  
 Query Match 100.0%; Score 40; DB 23; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 2,3; Mismatches 0; Gaps 0;  
 Matches 6; Conservative 0; Indels 0; Gaps 0;  
 OY 1 ADMSWL 6  
 DB 3 ADMSWL 8  
 RESULT 15  
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 ID AAM39444 standard; Protein; 276 AA.  
 XX  
 AC AAM39444;

XX  
 DT 22-OCT-2001 (first entry)  
 XX  
 DE Human polypeptide SEQ ID NO 2589.  
 XX  
 KW Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;  
 KW peripheral nervous system; neuropathy; central nervous system; CNS;  
 KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;  
 KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;  
 KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;  
 KW leukaemia.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200153312-A1.  
 XX  
 PD 26-JUL-2001.  
 XX  
 PF 26-DEC-2000; 2000WO-US34263.  
 XX  
 PR 21-JAN-2000; 2000US-0488725.  
 PR 25-APR-2000; 2000US-0552317.  
 PR 09-JUL-2000; 2000US-0598042.  
 PR 19-JUL-2000; 2000US-0620312.  
 PR 03-AUG-2000; 2000US-0653450.  
 PR 14-SEP-2000; 2000US-0662191.  
 PR 19-OCT-2000; 2000US-0693036.  
 PR 29-NOV-2000; 2000US-0727344.  
 XX  
 PA (HYSE-) HYSEO INC.  
 XX  
 PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;  
 PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;  
 PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;  
 XX  
 DR WPI; 2001-442253/47.  
 DR N-PDB; AAI58600.  
 PT  
 PT Novel nucleic acids and polypeptides, useful for treating disorders  
 PT such as central nervous system injuries -  
 XX  
 PS Example 4: SEQ ID NO 2589; 10078pp: English.  
 XX  
 CC The invention relates to human nucleic acids (AA157798-AA161369) and  
 CC the encoded polypeptides (AAM38642-AAM42213) with nootropic,  
 CC immunosuppressant and cytostatic activity. The polynucleotides are useful  
 CC in gene therapy. A composition containing a polypeptide or polynucleotide  
 CC of the invention may be used to treat diseases of the peripheral nervous  
 CC system, such as peripheral nervous injuries, peripheral neuropathy and  
 CC localized neuropathies and central nervous system diseases, such as  
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic  
 CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the  
 CC utilisation of the activities such as: Immune system suppression,  
 CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic  
 CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,  
 CC assays for receptor activity, arthritis and inflammation, leukaemias and  
 CC C.N.S disorders.  
 CC Note: The sequence data for this patent did not form part of the printed  
 CC specification.  
 CC  
 XX  
 SQ Sequence 276 AA;  
 Query Match 100.0%; Score 40; DB 22; Length 276;  
 Best Local Similarity 100.0%; Pred. No. 69; Mismatches 0; Gaps 0;  
 Matches 6; Conservative 0; Indels 0; Gaps 0;  
 OY 1 ADMSWL 6  
 DB 162 ADMSWL 167  
 Search completed: May 30, 2003, 14:49:42  
 Job time : 20.7529 secs

\_\_\_\_\_

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 30, 2003, 14:32:12 ; Search time 19.6974 Seconds

(without alignments)  
40.589 Million cell updates/sec

Title: US-09-643-260-5

Perfect score: 40

Sequence: 1 LDMSWA 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 08

Maximum Match 100%

Listing first 45 summaries

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21: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:\*  
22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:\*  
23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40	100.0	6	23	AB08728
2	40	100.0	6	23	AA048510
3	40	100.0	6	23	AA048537
4	40	100.0	6	23	AA048559
5	40	100.0	7	23	AA048563
6	40	100.0	8	23	AA048556
7	40	100.0	8	23	AA048564
8	40	100.0	9	23	AA048555
9	40	100.0	9	23	AA048558
10	40	100.0	9	23	AA048561

11	40	100.0	9	23	AA048562	Anti-inflammatory
12	40	100.0	10	23	AA048554	Anti-inflammatory
13	40	100.0	10	23	AA048557	Anti-inflammatory
14	40	100.0	10	23	AA048560	Anti-inflammatory
15	40	100.0	745	23	AB077292	Human IKKalpha mut
16	40	100.0	756	23	AB077309	Human IKKbeta muta
17	36	90.0	6	23	AB08725	IKKbeta NEMO bindi
18	36	90.0	6	23	AA048530	Anti-inflammatory
19	36	90.0	6	23	AA048538	Anti-inflammatory
20	36	90.0	6	23	AA048570	NBD mutant peptide
21	36	90.0	7	23	AA048555	Anti-inflammatory
22	36	90.0	7	23	AA048534	Anti-inflammatory
23	36	90.0	7	23	AA048574	Anti-inflammatory
24	36	90.0	8	23	AA048527	Anti-inflammatory
25	36	90.0	8	23	AA048535	Anti-inflammatory
26	36	90.0	8	23	AA048567	Anti-inflammatory
27	36	90.0	8	23	AA048575	Anti-inflammatory
28	36	90.0	9	20	AA06152	IKK-alpha polypept
29	36	90.0	9	23	AA048526	Anti-inflammatory
30	36	90.0	9	23	AA048529	Anti-inflammatory
31	36	90.0	9	23	AA048532	Anti-inflammatory
32	36	90.0	9	23	AA048533	Anti-inflammatory
33	36	90.0	9	23	AA048566	Anti-inflammatory
34	36	90.0	9	23	AA048559	Anti-inflammatory
35	36	90.0	9	23	AA048572	Anti-inflammatory
36	36	90.0	9	23	AA048573	Anti-inflammatory
37	36	90.0	10	23	AB077313	IKKbeta NEMO bindi
38	36	90.0	10	23	AA048528	Anti-inflammatory
39	36	90.0	10	23	AA048531	Anti-inflammatory
40	36	90.0	10	23	AA048568	Anti-inflammatory
41	36	90.0	10	23	AA048571	Anti-inflammatory
42	36	90.0	11	23	AB077311	Human NBD peptide
43	36	90.0	11	23	AA048506	Human IKKbeta pept
44	36	90.0	11	23	AA048525	Anti-inflammatory
45	36	90.0	11	23	AA048565	Anti-inflammatory

#### ALIGNMENTS

RESULT 1	AB08728	standard; peptide: 6 AA.
ID	AB08728	
AC	AB08728	
XX	14-JUN-2002	(first entry)
DE	Mutated IKKbeta NEMO binding domain peptide SEQ ID NO 5.	
XX	IKKbeat; IKKalpha; NEMO; NEMO binding domain; NBD; NF-kappaB; NF-KB;	
KW	kinase activation; leukocyte; inflammation; E-selectin; osteoclast;	
KW	autoimmune disease; transplant rejection; osteoporosis; cancer;	
KW	Alzheimer's disease; viral; infection; asthma; anaphylaxis; psoriasis;	
KW	rheumatoid arthritis; Crohn's disease; multiple sclerosis; HIV;	
KW	corticosteroid; immunosuppression; anti-inflammatory; immunosuppressive;	
KW	osteopathic; cytosolic; nootropic; neuroprotective; anti-HIV; human;	
KW	antiartherosclerotic; virucide; antiaspartic; antiallergic;	
KW	dermatological; antibacterial; antipruritic; antihemmatic;	
KW	antiarthritic; osteopathic; antitumor; mutant; muten.	
XX		
OS	Homo sapiens.	
XX	Synthetic.	
FT	Key	Location/Qualifiers
FT	Misc-difference 6	/note- "Wildtype Leu substituted by Ala"
XX		
PN	W0200183547-A2.	
XX		
XX	08-NOV-2001.	
PD		
XX		
PF	02-MAY-2001; 2001WO-US40654.	



AC	AA48537;
XX	
DT	20-MAR-2002 (first entry)
XX	
DE	Anti-inflammatory peptide SEQ ID NO 40.
XX	
KW	Antiinflammatory; antiasthmatic; cyostatic; antipsoriatic; nootropic;
KM	antirheumatic; antithritic; osteoporotic; antibacterial; virucide;
XX	immunosuppressive; dermatologic; neuroprotective; antithrombotic;
KM	antiallergic; membrane translocation domain; NEMO binding domain; eczema;
KM	cystokine; NFkappaB; Ikappab kinase beta; IKKbeta; cancer; psoriasis;
KM	rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
KM	autoimmune disorder; multiple sclerosis; transplant rejection;
KM	osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
KM	ataxia telangiectasia; allergy; anaphylaxis; arthritis.
XX	
OS	Synthetic.
XX	
PN	WO200183554-A2.
XX	
PD	08-NOV-2001;
XX	
PE	02-MAY-2001; 2001WO-US14346.
XX	
PR	02-MAY-2000; 2000US-201261P.
PR	22-AUG-2000; 2000US-0643260.
XX	
PA	(PRAE-) PRAECIS PHARM INC.
XX	(UYVA ) UNITIV YALE.
PI	May MJ, Ghosh S, Flindels MA, Phillips K;
DR	WPI; 2002-121889/16.
XX	
PT	Novel antiinflammatory compound comprising membrane translocation
PT	domain fused to NEMO binding sequence, useful for blocking nuclear
PT	factor kappaB activation, and for treating asthma, lung inflammation,
PT	psoriasis -
XX	
PS	Claim 6; Page 61; 88pp; English.
XX	
CC	The invention relates to an antiinflammatory compound (especially
CC	AA48628-AA48645), comprising a membrane translocation domain
CC	(AA48620-AA48627 or AA48646-AA48651) which comprises from 6-15
CC	amino acid residues, fused to a NEMO binding sequence
CC	(AA48625-AA48619). The antiinflammatory compounds have antiasthmatic,
CC	cyostatic, antipsoriatic, antirheumatic, antithritic, osteopathic,
CC	antibacterial, immunosuppressive, dermatological, neuroprotective,
CC	nootropic, antithrombotic, virucide and antiallergic activity. The
CC	compounds act as selective inhibitors of cytokine-mediated NFkappaB
CC	activation by blocking interaction of Ikappab kinase beta (IKKbeta) at
CC	the NEMO binding domain that results in inhibition of IKKbeta kinase
CC	activation and subsequent decreased phosphorylation of Ikappab. The
CC	compounds are useful for treating inflammatory disorders, e.g. asthma,
CC	lung inflammation or cancer, psoriasis, rheumatoid arthritis,
CC	osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
CC	bursitis; autoimmune diseases such as lupus, polyaragia, scleroderma,
CC	granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
CC	Alzheimer's disease; atherosclerosis; viral infections; and ataxia
CC	telangiectasia. The compounds are also useful for treating
CC	pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
CC	drug or food sensitivity, eczema, dermatitis, sunburn, aging and
CC	arthritis.
XX	
SO	Sequence 6 AA;
QY	Query Match 100.0%; Score 40; DB 23; Length 6;
	Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches	6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB	1 LDWSMA 6
DB	1 LDWSMA 6

XX	AA048559	standard; peptide; 6 AA.
XX	AA048559;	
XX	20-MAR-2002	(first entry)
XX	Anti-inflammatory peptide SEQ ID NO 62.	
XX	Anti-inflammatory; antiasthmatic; cyostatic; antipsoriatic; neutrotropic;	
XX	antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;	
XX	immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;	
XX	antiallergic; membrane translocation domain; NEMO binding domain; eczema;	
XX	cytokine; NF-kappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;	
XX	rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;	
XX	autoimmune disorder; multiple sclerosis; transplant rejection;	
XX	osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;	
XX	ataxia telangiectasia; allergy; anaphylaxis; arthritis.	
XX	Synthetic.	
XX	WO200183554-A2.	
XX	08-NOV-2001.	
XX	02-MAY-2001; 2001WO-US14346.	
XX	02-MAY-2000; 2000US-201261P.	
XX	22-AUG-2000; 2000US-0643260.	
XX	(PRAE ) PRAECIS PHARM INC.	
XX	(UYVA ) UNIV YALE.	
XX	May MJ, Ghosh S, Findeis MA, Phillips K;	
XX	WPI: 2002-121889/16.	
XX	Novel antiinflammatory compound comprising membrane translocation	
XX	domain fused to NEMO binding sequence, useful for blocking nuclear	
XX	factor kappaB activation, and for treating asthma, lung inflammation,	
XX	psoriasis	
XX	Claim 6; Page 62; 88pp; English.	
XX	The invention relates to an antiinflammatory compound (especially	
XX	AA048528-AA048645), comprising a membrane translocation domain	
XX	(AA048620-AA048637 or AA048646-AA048651) which comprises from 6-15	
XX	amino acid residues, fused to a NEMO binding sequence	
XX	(AA048525-AA048619). The antiinflammatory compounds have antasthmatic,	
XX	cyostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,	
XX	antibacterial, immunosuppressive, dermatological, neuroprotective,	
XX	neutrotropic, antiatherosclerotic, virucide and antiallergic activity. The	
XX	compounds act as selective inhibitors of cytokine-mediated NF-kappaB	
XX	activation by blocking interaction of IkappaB kinase beta (IKKbeta) at	
XX	the NEMO binding domain that results in inhibition of IkappaB kinase	
XX	activation and subsequent decreased phosphorylation of IkappaB. The	
XX	compounds are useful for treating inflammatory disorders, e.g. asthma,	
XX	lung inflammation or cancer, psoriasis, rheumatoid arthritis,	
XX	osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,	
XX	bursts; autoimmune diseases such as lupus, polyarthritis, scleroderma,	
XX	granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;	
XX	Alzheimer's disease; atherosclerosis; viral infections; and ataxia	
XX	telangiectasia. The compounds are also useful for treating	
XX	pro-inflammatory responses such as allergies, urticaria, anaphylaxis,	
XX	drug or food sensitivity, eczema, dermatitis, sunburn, aging and	
XX	arthritis.	
XX	Sequence 6 AA;	

Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDMSMA 6  
111111  
Db 1 LDMSMA 6

RESULT 5  
AAM48563  
ID AAM48563 standard; Peptide; 7 AA.

AC AAM48563;

DT 20-MAR-2002 (first entry)

DE Anti-inflammatory peptide SEQ ID NO 66.

XX Anti-inflammatory; antialasthmatic; cytosolic; antipsoriatic; neutrotropic;  
XX antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;  
XX immunosuppressive; dermatological; neutrotropic; antiatherosclerotic;  
XX antiallergic; membrane translocation domain; NEMO binding domain; eczema;  
XX cytokine; NF-kappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;  
XX rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
XX autoimmune disorder; multiple sclerosis; transplant rejection;  
XX osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
XX ataxia telangiectasia; allergy; anaphylaxis; arthritis.

OS Synthetic.

PN WO200183554-A2.

PD 08-NOV-2001.

PF 02-MAY-2001; 2001WO-US14346.

PR 02-MAY-2000; 2000US-201261P.

PR 22-AUG-2000; 2000US-0643260.

PA (PRAE-) PRAECIS PHARM INC.

PA (UYVA) UNIV YALE.

PI May MJ, Ghosh S, Findeis MA, Phillips K;

XX WPI; 2002-121889/16.

XX Novel anti-inflammatory compound comprising membrane translocation  
PT domain fused to NEMO binding sequence, useful for blocking nuclear  
PT factor kappaB activation, and for treating asthma, lung inflammation,  
PT psoriasis

PS Claim 6; Page 62; 88pp; English.

XX The invention relates to an anti-inflammatory compound (especially  
CC AAM48563-AAM48645), comprising a membrane translocation domain  
CC (AAM48620-AAM48637 or AAM48646-AAM48651) which comprises from 6-15  
CC amino acid residues, fused to a NEMO binding sequence  
CC (AAM48525-AAM48619). The anti-inflammatory compounds have antialasthmatic,  
CC cytosolic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,  
CC antibacterial, immunosuppressive, dermatological, neutrotropic,  
CC neutrotropic, antiatherosclerotic, virucide and antiallergic activity. The  
CC compounds act as selective inhibitors of cytokine-mediated NF-kappaB  
CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at  
CC the NEMO binding domain that results in inhibition of IKKbeta kinase  
CC activation and subsequent decreased phosphorylation of IkappaB. The  
CC compounds are useful for treating inflammatory disorders, e.g. asthma,  
CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,  
CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,  
CC bursts; autoimmune diseases such as lupus, polymyalgia, scleroderma,  
CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;  
CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia  
CC telangiectasia. The compounds are also useful for treating  
CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,

CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and  
CC arthritis.

XX SO Sequence 7 AA;

Query Match 100.0%; Score 40; DB 23; Length 7;  
Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDMSMA 6  
111111  
Db 1 LDMSMA 6

RESULT 6  
AAM48556  
ID AAM48556 standard; Peptide; 8 AA.

AC AAM48556;

DT 20-MAR-2002 (first entry)

DE Anti-inflammatory peptide SEQ ID NO 59.

XX Anti-inflammatory; antialasthmatic; cytosolic; antipsoriatic; neutrotropic;  
XX antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;  
XX immunosuppressive; dermatological; neutrotropic; antiatherosclerotic;  
XX antiallergic; membrane translocation domain; NEMO binding domain; eczema;  
XX cytokine; NF-kappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;  
XX rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
XX autoimmune disorder; multiple sclerosis; transplant rejection;  
XX osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
XX ataxia telangiectasia; allergy; anaphylaxis; arthritis.

OS Synthetic.

PN WO200183554-A2.

PD 08-NOV-2001.

PF 02-MAY-2001; 2001WO-US14346.

PR 02-MAY-2000; 2000US-201261P.

PR 22-AUG-2000; 2000US-0643260.

PA (PRAE-) PRAECIS PHARM INC.

PA (UYVA) UNIV YALE.

PI May MJ, Ghosh S, Findeis MA, Phillips K;

XX WPI; 2002-121889/16.

XX Novel anti-inflammatory compound comprising membrane translocation  
PT domain fused to NEMO binding sequence, useful for blocking nuclear  
PT factor kappaB activation, and for treating asthma, lung inflammation,  
PT psoriasis

PS Claim 6; Page 62; 88pp; English.

XX The invention relates to an anti-inflammatory compound (especially  
CC AAM48563-AAM48645), comprising a membrane translocation domain  
CC (AAM48620-AAM48637 or AAM48646-AAM48651) which comprises from 6-15  
CC amino acid residues, fused to a NEMO binding sequence  
CC (AAM48525-AAM48619). The anti-inflammatory compounds have antialasthmatic,  
CC cytosolic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,  
CC antibacterial, immunosuppressive, dermatological, neutrotropic,  
CC neutrotropic, antiatherosclerotic, virucide and antiallergic activity. The  
CC compounds act as selective inhibitors of cytokine-mediated NF-kappaB  
CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at  
CC the NEMO binding domain that results in inhibition of IKKbeta kinase  
CC activation and subsequent decreased phosphorylation of IkappaB. The  
CC compounds are useful for treating inflammatory disorders, e.g. asthma,  
CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,

CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,  
 CC burstitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,  
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;  
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia  
 CC telangiectasia. The compounds are also useful for treating  
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,  
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and  
 CC arthritis.  
 CC Sequence 8 AA:  
 SO  
 Query Match 100.0%; Score 40; DB 23; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 LDMSMA 6  
 Db 3 LDMSMA 8  
 RESULT 7  
 ID AAM48564 standard; Peptide: 8 AA.  
 AC AAM48564:  
 XX  
 DT 20-MAR-2002 (first entry)  
 XX  
 DE Anti-inflammatory peptide SEQ ID NO 67.  
 XX  
 KW Anti-inflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;  
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;  
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;  
 KW anti-allergic; membrane translocation domain; NEMO binding domain; eczema;  
 KW cytokine; NF-kappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;  
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
 KW autoimmune disorder; multiple sclerosis; transplant rejection;  
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200183554-A2.  
 PN  
 PD 08-NOV-2001.  
 XX  
 XX 02-MAY-2001; 2001WO-US14346.  
 PF  
 PR 02-MAY-2000; 2000US-201261P.  
 PR 22-AUG-2000; 2000US-0643260.  
 XX  
 PA (PRAE-) PRAECIS PHARM INC.  
 PA (UYVA ) UNIV YALE.  
 XX  
 PI May MJ, Ghosh S, Findeis MA, Phillips K;  
 DR WPI; 2002-121889/16.  
 XX  
 PT Novel anti-inflammatory compound comprising membrane translocation  
 PT domain fused to NEMO binding sequence, useful for blocking nuclear  
 PT factor kappaB activation, and for treating asthma, lung inflammation,  
 PT psoriasis  
 XX  
 XX Claim 6; Page 62; 88pp; English.  
 PS  
 CC The invention relates to an anti-inflammatory compound (especially  
 CC AAM48628-AAM48645), comprising a membrane translocation domain  
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15  
 CC amino acid residues, fused to a NEMO binding sequence  
 CC (AAM48525-AAM48619). The anti-inflammatory compounds have antiasthmatic,  
 CC cytoskeletal, antipsoriatic, antirheumatic, antiarthritic, osteopathic,  
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,  
 CC nootropic, antiatherosclerotic, virucide and anti-allergic activity. The

CC compounds act as selective inhibitors of cytokine-mediated NF-kappaB  
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at  
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase  
 CC activation and subsequent decreased phosphorylation of IkappaB. The  
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,  
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,  
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,  
 CC burstitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,  
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;  
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia  
 CC telangiectasia. The compounds are also useful for treating  
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,  
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and  
 CC arthritis.  
 CC Sequence 8 AA:  
 SO  
 Query Match 100.0%; Score 40; DB 23; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 LDMSMA 6  
 Db 1 LDMSMA 6  
 RESULT 8  
 ID AAM48555 standard; Peptide: 9 AA.  
 AC AAM48555:  
 XX  
 DT 20-MAR-2002 (first entry)  
 XX  
 DE Anti-inflammatory peptide SEQ ID NO 58.  
 XX  
 KW Anti-inflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;  
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;  
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;  
 KW anti-allergic; membrane translocation domain; NEMO binding domain; eczema;  
 KW cytokine; NF-kappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;  
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
 KW autoimmune disorder; multiple sclerosis; transplant rejection;  
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200183554-A2.  
 PN  
 PD 08-NOV-2001.  
 XX  
 XX 02-MAY-2001; 2001WO-US14346.  
 PF  
 PR 02-MAY-2000; 2000US-201261P.  
 PR 22-AUG-2000; 2000US-0643260.  
 XX  
 PA (PRAE-) PRAECIS PHARM INC.  
 PA (UYVA ) UNIV YALE.  
 XX  
 PI May MJ, Ghosh S, Findeis MA, Phillips K;  
 DR WPI; 2002-121889/16.  
 XX  
 PT Novel anti-inflammatory compound comprising membrane translocation  
 PT domain fused to NEMO binding sequence, useful for blocking nuclear  
 PT factor kappaB activation, and for treating asthma, lung inflammation,  
 PT psoriasis  
 XX  
 XX Claim 6; Page 62; 88pp; English.  
 PS  
 CC The invention relates to an anti-inflammatory compound (especially  
 CC AAM48628-AAM48645), comprising a membrane translocation domain

CC (AA48620-AA48627 or AA48646-AA48651) which comprises from 6-15  
 CC amino acid residues, fused to a NEMO binding sequence  
 CC (AA48525-AA48619). The antiinflammatory compounds have antiasthmatic,  
 CC cytoskeletal, antiproliferative, antirheumatic, antiarthritic, osteopathic,  
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,  
 CC neurotropic, antitumor, antiparasitic, antiviral and antiallergic activity. The  
 CC compounds act as selective inhibitors of cytokine-mediated NF-kappaB  
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at  
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase  
 CC activation and subsequent decreased phosphorylation of IkappaB. The  
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,  
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,  
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,  
 CC bursitis, autoimmune diseases such as lupus, polymyalgia, scleroderma,  
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;  
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia  
 CC telangiectasia. The compounds are also useful for treating  
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,  
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and  
 CC arthritis.

SO Sequence 9 AA;  
 Query Match 100.0%; Score 40; DB 23; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDMSWA 6  
 DB 1 LDMSWA 6

RESULT 9  
 ID AA48558  
 AA48558 standard; Peptide; 9 AA.

AC AA48558;  
 DT 20-MAR-2002 (first entry)  
 DE Anti-inflammatory peptide SEQ ID NO 61.

XX Antiinflammatory; antiasthmatic; cytoskeletal; antiproliferative; neurotropic;  
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; antiviral;  
 KW immunosuppressive; dermatological; neuroprotective; antitumor; antiparasitic;  
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;  
 KW cytokine; NF-kappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;  
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
 KW autoimmune disorder; multiple sclerosis; transplant rejection;  
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.

OS Synthetic.  
 XX  
 PN WO200183554-A2.  
 PD 08-NOV-2001.  
 PE 02-MAY-2001; 2001WO-US14346.  
 PR 02-MAY-2000; 2000US-201261P.  
 PR 22-AUG-2000; 2000US-0643260.  
 PA (PRAE-) PRAECIS PHARM INC.  
 PA (UYVA ) UNIV YALE.  
 PI May MJ, Ghosh S, Flindels MA, Phillips K;  
 DR WPI; 2002-121889/16.  
 XX Novel antiinflammatory compound comprising membrane translocation  
 PT domain fused to NEMO binding sequence, useful for blocking nuclear  
 PT factor kappaB activation, and for treating asthma, lung inflammation,

PT psoriasis  
 XX Claim 6; Page 62; 88pp; English.

XX The invention relates to an antiinflammatory compound (especially  
 PS AA48628-AA48645), comprising a membrane translocation domain  
 CC (AA48620-AA48627 or AA48646-AA48651) which comprises from 6-15  
 CC amino acid residues, fused to a NEMO binding sequence  
 CC (AA48525-AA48619). The antiinflammatory compounds have antiasthmatic,  
 CC cytoskeletal, antiproliferative, antirheumatic, antiarthritic, osteopathic,  
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,  
 CC neurotropic, antitumor, antiparasitic, antiviral and antiallergic activity. The  
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 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at  
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 CC activation and subsequent decreased phosphorylation of IkappaB. The  
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 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,  
 CC bursitis, autoimmune diseases such as lupus, polymyalgia, scleroderma,  
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;  
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia  
 CC telangiectasia. The compounds are also useful for treating  
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,  
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and  
 CC arthritis.

SO Sequence 9 AA;  
 Query Match 100.0%; Score 40; DB 23; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDMSWA 6  
 DB 1 LDMSWA 6

RESULT 10  
 ID AA48561  
 AA48561 standard; Peptide; 9 AA.

AC AA48561;  
 DT 20-MAR-2002 (first entry)  
 DE Anti-inflammatory peptide SEQ ID NO 64.

XX Antiinflammatory; antiasthmatic; cytoskeletal; antiproliferative; neurotropic;  
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; antiviral;  
 KW immunosuppressive; dermatological; neuroprotective; antitumor; antiparasitic;  
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;  
 KW cytokine; NF-kappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;  
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
 KW autoimmune disorder; multiple sclerosis; transplant rejection;  
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.

OS Synthetic.  
 XX  
 PN WO200183554-A2.  
 PD 08-NOV-2001.  
 PE 02-MAY-2001; 2001WO-US14346.  
 PR 02-MAY-2000; 2000US-201261P.  
 PR 22-AUG-2000; 2000US-0643260.  
 PA (PRAE-) PRAECIS PHARM INC.  
 PA (UYVA ) UNIV YALE.  
 PI May MJ, Ghosh S, Flindels MA, Phillips K;

XX WPI; 2002-121889/16.  
 DR Novel antiinflammatory compound comprising membrane translocation  
 XX domain fused to NEMO binding sequence, useful for blocking nuclear  
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 PT psoriasis  
 PS Claim 6; Page 62; 88pp; English.  
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 CC The invention relates to an antiinflammatory compound (especially  
 CC AAM48628-AAM48645), comprising a membrane translocation domain  
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15  
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 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,  
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 CC  
 SQ Sequence 9 AA;  
 OY  
 Query Match 100.0%; Score 40; DB 23; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 1 LDMSWA 6  
 3 LDMSWA 8  
 RESULT 11  
 ID AAM48562 standard; Peptide; 9 AA.  
 XX  
 AC AAM48562;  
 XX  
 DT 20-MAR-2002 (first entry)  
 XX  
 DE Anti-inflammatory peptide SEQ ID NO 65.  
 XX  
 KM Antiinflammatory; antiasthmatic; cytoskeletal; antipsoriatic; neurotropic;  
 KM antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;  
 KM immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;  
 KM antiallergic; membrane translocation domain; NEMO binding domain; eczema;  
 KM cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;  
 KM rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
 KM autoimmune disorder; multiple sclerosis; transplant rejection;  
 KM osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
 KM ataxia telangiectasia; allergy; anaphylaxis; arthritis.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200183554-A2.  
 XX  
 PD 08-NOV-2001.  
 XX  
 PF 02-MAY-2001; 2001WO-US14346.  
 XX  
 PR 02-MAY-2000; 2000US-201261P.

PR 22-AUG-2000; 2000US-0643260.  
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 PA (PRAE-) PRACIS PHARM INC.  
 PA (UYVA ) UNIV YALE.  
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 PI May MJ, Ghosh S, Flindeis MA, Phillips K;  
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 DR WPI; 2002-121889/16.  
 XX  
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 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;  
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia  
 CC telangiectasia. The compounds are also useful for treating  
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,  
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and  
 CC arthritis.  
 CC  
 SQ Sequence 9 AA;  
 OY  
 Query Match 100.0%; Score 40; DB 23; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 1 LDMSWA 6  
 2 LDMSWA 7  
 RESULT 12  
 ID AAM48554 standard; Peptide; 10 AA.  
 XX  
 AC AAM48554;  
 XX  
 DT 20-MAR-2002 (first entry)  
 XX  
 DE Anti-inflammatory peptide SEQ ID NO 57.  
 XX  
 KM Antiinflammatory; antiasthmatic; cytoskeletal; antipsoriatic; neurotropic;  
 KM antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;  
 KM immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;  
 KM antiallergic; membrane translocation domain; NEMO binding domain; eczema;  
 KM cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;  
 KM rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
 KM autoimmune disorder; multiple sclerosis; transplant rejection;  
 KM osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
 KM ataxia telangiectasia; allergy; anaphylaxis; arthritis.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200183554-A2.



KM antihemetic; antiarthritic; osteopathic; antibacterial; virucide;  
 KM immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;  
 KM anti-allergic; membrane translocation domain; NEMO binding domain; eczema;  
 KM cytokine; NF-kappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;  
 KM rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
 KM autoimmune disorder; multiple sclerosis; transplant rejection;  
 KM osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
 KM ataxia telangiectasia; allergy; anaphylaxis; arthritis.  
 OS Synthetic.  
 XX WO200183554-A2.  
 XX 08-NOV-2001.  
 XX 02-MAY-2001; 2001WO-US14346.  
 XX 02-MAY-2000; 2000US-201261P.  
 PR 22-AUG-2000; 2000US-0643260.  
 XX (PRAE-) PRACIS PHARM INC.  
 PA (UYVA) UNIV YALE.  
 XX May MJ, Ghosh S, Finkel MA, Phillips K;  
 DR WPI; 2002-121889/16.  
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 PT domain fused to NEMO binding sequence, useful for blocking nuclear  
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 PT psoriasis.  
 XX Claim 6; Page 62; 88pp; English.  
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 CC nootropic, antiatherosclerotic, virucide and anti-allergic activity. The  
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 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at  
 CC the NEMO binding domain that results in inhibition of IkappaB kinase  
 CC activation and subsequent decreased phosphorylation of IkappaB. The  
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,  
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,  
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,  
 CC dermatitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,  
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;  
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia  
 CC telangiectasia. The compounds are also useful for treating  
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,  
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and  
 CC arthritis.  
 CC Sequence 10 AA;  
 SO

Query Match 100.0%; Score 40; DB 23; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 2.2; Indels 0; Gaps 0;  
 Matches 6; Conservative 0; Mismatches 0;

QY 1 LDMSMA 6  
 111111  
 Db 3 LDMSMA 8

RESULT 15  
 ABB77292  
 ID ABB77292 standard; protein; 745 AA.  
 XX ABB77292;  
 AC

XX 14-JUN-2002 (first entry)  
 DT Human IKKalpha mutant L743A.  
 XX IKKbeta; IKKalpha; NEMO; NEMO binding domain; NBD; NF-kappaB; NF-kB;  
 KM kinase activation; leukocyte; inflammation; E-selectin; osteoclast;  
 KM autoimmune disease; transplant rejection; osteoporosis; cancer;  
 KM Alzheimer's disease; viral infection; asthma; anaphylaxis; psoriasis;  
 KM rheumatoid arthritis; Crohn's disease; multiple sclerosis; HIV;  
 KM corticosteroid; immunosuppression; antiinflammatory; immunosuppressive;  
 KM osteopathic; cytoskeletal; nootropic; neuroprotective; anti-HIV; human;  
 KM antiatherosclerotic; virucide; antiasthmatic; anti-allergic;  
 KM dermatological; antibacterial; antipsoriatic; antihemetic;  
 KM antiarthritic; osteopathic; antitumor; mutant; mutagen.  
 XX Homo sapiens.  
 OS Synthetic.  
 XX Key Location/Qualifiers  
 FH Misc-difference 743 /note="Wildtype Leu substituted by Ala"  
 FT  
 XX WO200183547-A2.  
 XX 08-NOV-2001.  
 XX 02-MAY-2001; 2001WO-US40654.  
 XX 02-MAY-2000; 2000US-201261P.  
 PR 22-AUG-2000; 2000US-0643260.  
 XX (UYVA) UNIV YALE.  
 PA May MJ, Ghosh S;  
 PI WPI; 2002-179350/23.  
 XX Modulating NF-kappaB induction in a cell, useful for treating e.g.  
 PT inflammatory disorders, osteoporosis and cancer, comprises contacting a  
 PT cell with an anti-inflammatory compound comprising at least one NEMO  
 PT binding domain.  
 XX Example 11; Page -; 82pp; English.  
 PS The invention relates to modulating NF-kappaB (NF-kB) induction in a cell  
 CC comprises contacting a cell with an anti-inflammatory compound  
 CC (ABB08725-ABB08742) comprising at least one NEMO binding domain  
 CC (ABB77313). The compound has acts through selective inhibition of  
 CC cytokine-mediated NF-kB activation by blocking the interaction of NEMO  
 CC with IKKbeta at the NEMO binding domain. Blockage of IKKbeta-NEMO  
 CC interaction results in inhibition of IKKbeta kinase activation and  
 CC subsequent decreased phosphorylation of IkappaB. The compound may also  
 CC act (directly or indirectly) by blocking the recruitment of leukocytes  
 CC into sites of acute and chronic inflammation, by down-regulating the  
 CC expression of E-selectin on leukocytes or by blocking osteoclast  
 CC differentiation. The compound is useful in treating NF-kB mediated  
 CC conditions, where the condition is an inflammatory disorder, an  
 CC autoimmune disease, transplant rejection, osteoporosis, cancer,  
 CC Alzheimer's disease, atherosclerosis, a viral infection or ataxia  
 CC telangiectasia. The inflammatory disorder is asthma, allergies,  
 CC urticaria, anaphylaxis, cutaneous inflammation, sepsis, psoriasis,  
 CC rheumatoid arthritis, osteoarthritis, psoriatic arthritis, inflammatory  
 CC bowel disease, chronic obstructive pulmonary disease, vasculitis and  
 CC bursitis. The inflammatory disorder may also be dermatitis, eczema,  
 CC psoriasis, osteoarthritis, psoriatic arthritis, lupus and  
 CC spondylarthritis. Also for Crohn's disease, ulcerative colitis,  
 CC polymyalgia, scleroderma, Wegner's granulomatosis, temporal arteritis,  
 CC cryoglobulinemia or multiple sclerosis. For chronic viral infections  
 CC caused by Epstein-Barr, cytomegalovirus or herpes simplex. Other viral  
 CC diseases include HIV and influenza. The compound may also be useful for  
 CC treating anaphylaxis, drug and food sensitivity, contact dermatitis, in  
 CC sunburn or aging. The compound may be used to replace corticosteroids in

CC any application in which corticosteroids are used, including  
 CC immunosuppression in transplants and cancer therapy. Also for identifying  
 CC antiinflammatory compounds and for diagnosis of an inflammatory disorder.  
 CC The compound may be administered alone or in combination with other known  
 CC anti-inflammatory agents. The present sequence is that of an IKKalpha  
 CC mutant, useful in examples of the invention.  
 CC Note: The present sequence is not given in the specification but is  
 CC derived from GenBank Accession No. 015111 (AB077290).

XX  
 SQ Sequence 745 AA;

Query Match 100.0%; Score 40; DB 23; Length 745;  
 Best Local Similarity 100.0%; Pred. No. 2e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDMSWA 6  
 |||||  
 DB 738 LDMSWA 743

Search completed: May 30, 2003, 14:49:42  
 Job time : 19.7529 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 30, 2003, 14:41:40 ; Search time 3.11842 Seconds  
(without alignments)  
79.803 Million cell updates/sec

Title: US-09-643-260-10  
Perfect score: 33  
Sequence: 1 IDASWL 6

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues  
Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_40.\*  
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	30	90.9	290 1	BLA1_XANMA P52700 xanthomonas
2	30	90.9	648 1	Y084_HUMAN Q14699 homo sapien
3	30	90.9	918 1	CAPP_CORGL P12880 corynebacte
4	29	87.9	177 1	CYCL_PARDE P29899 paracoccus
5	29	87.9	277 1	YHT1_CAEEL P91247 caenorhabdi
6	29	87.9	286 1	YDBC_ECOLI P25006 escherichia
7	29	87.9	289 1	THMR_CHICK P25324 gallus gall
8	29	87.9	295 1	THMR_RAT P24329 rattus norv
9	29	87.9	296 1	RECO_ANASP Q8Y519 anabaena sp
10	29	87.9	296 1	THRM_HUMAN P25325 homo sapien
11	29	87.9	296 1	THRM_HUMAN P97532 rattus norv
12	29	87.9	296 1	THMR_BOVIN P00586 bos taurus
13	29	87.9	296 1	THMR_CRIGR P46635 cricetus
14	29	87.9	296 1	THMR_HUMAN Q16762 homo sapien
15	29	87.9	296 1	THMR_MOUSE P52196 mus musculi
16	29	87.9	359 1	FRBG_SALTY P26397 salmonella
17	29	87.9	360 1	YMT2_CAEEL P34889 caenorhabdi
18	29	87.9	424 1	Y826_METH P02614 methanobact
19	29	87.9	430 1	PUCK_BACSU Q32140 bacillus su
20	29	87.9	459 1	NUAK_MOUSE P03511 mus musculi
21	29	87.9	464 1	YTI3_CAEEL Q10917 caenorhabdi
22	29	87.9	477 1	RP54_ECOLI P24255 escherichia
23	29	87.9	477 1	RP54_KLEPN P06223 klebsiella
24	29	87.9	477 1	RP54_SALTY P26979 salmonella
25	29	87.9	481 1	CBE5_EMENT Q43100 emeticella
26	29	87.9	491 1	XYLE_ECOLI P09098 escherichia
27	29	87.9	508 1	TDT_HUMAN P04053 homo sapien
28	29	87.9	510 1	G6PD_ASPNG P48826 aspergillus
29	29	87.9	511 1	G6PD_EMENT P41764 emeticella
30	29	87.9	514 1	DKCL_HUMAN P06032 homo sapien
31	29	87.9	520 1	TDT_BOVIN P06526 bos taurus
32	29	87.9	854 1	DIS1_HUMAN Q9N115 homo sapien
33	29	87.9	1034 1	BGAL_BACME O52847 bacillus me

34	29	87.9	1043 1	RRPO_NODAV Q91m4 nodamura vi
35	29	87.9	3770 1	ACVS_EMENT P27742 emeticella
36	28	84.8	225 1	ALKD_PSEPU P00885 pseudomonas
37	28	84.8	325 1	IRRL_HUMAN P10914 homo sapien
38	28	84.8	401 1	HISL_STYR3 P74592 synecocyst
39	28	84.8	494 1	DPOK_HUMAN Q9np87 homo sapien
40	28	84.8	502 1	NU2C_MESVI Q9muq6 mesosigma
41	28	84.8	506 1	TDT_CHICK P36195 gallus gall
42	28	84.8	508 1	N060_DROME Q44081 drosophila
43	28	84.8	518 1	TDT_MONDO Q02789 monodelphis
44	28	84.8	522 1	CPH4_RAT P51869 rattus norv
45	28	84.8	529 1	TKM_ECOLI P08957 escherichia

## ALIGNMENTS

RESULT 1  
BLA1\_XANMA STANDARD; PRT; 290 AA.  
ID BLA1\_XANMA  
AC P52700;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Metallo-beta-lactamase LI precursor (Beta-lactamase, type II)  
DE (EC 3.5.2.6) (penicillinase).  
OS Xanthomonas maltophilia (Pseudomonas maltophilia) (Stenotrophomonas maltophilia).  
OC Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;  
OC Stenotrophomonas.  
OX NCBI\_TaxID=40324;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=IID 1275;  
RX MEDLINE=94289479; PubMed=8018721;  
RA Walsh T.R., Hall L., Assinder S.J., Nichols W.W., Cartwright S.J., Macgowan A.P., Bennett P.M.;  
RT "Sequence analysis of the LI metallo-beta-lactamase from Xanthomonas maltophilia."  
RL Biochim. Biophys. Acta 1218:199-201(1994).  
RN [2]  
RP SEQUENCE OF 34-65.  
RC STRAIN=IID 1275;  
RX MEDLINE=86025393; PubMed=3931629;  
RA Bicknell R., Emanuel E.L., Gagnon J., Waley S.G.;  
RT "The production and molecular properties of the zinc beta-lactamase of Pseudomonas maltophilia IID 1275."  
RL Biochem. J. 229:791-797(1985).  
RN [3]  
RP X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS).  
RX MEDLINE=99030465; PubMed=9811546;  
RA Ullah J.H., Walsh T.R., Taylor I.A., Emery D.C., Verma C.S., Gambhira S.J., Spencer J.;  
RT "The crystal structure of the LI metallo-beta-lactamase from Stenotrophomonas maltophilia at 1.7 A resolution."  
RL J. Mol. Biol. 284:125-136(1998).  
CC - FUNCTION: HAS A HIGH ACTIVITY AGAINST IMIPENEM. UNSTABLE BELOW PH 8. UNLESS ZINC IS PRESENT.  
CC - CATALYTIC ACTIVITY: A beta-lactam + H(2)O = a substituted beta-amino acid.  
CC - COFACTOR: BINDS TWO ZINC IONS PER MOLECULE.  
CC - ENZYME REGULATION: INHIBITED BY HG2+ OR CU2+. REDUCED ENZYMATIC ACTIVITY IN PRESENCE OF CO2+, NI2+, CU2+, AND MN2+.  
CC - SUBUNIT: HOMOTETRAMER.  
CC - SUBCELLULAR LOCATION: Periplasmic (Potential).  
CC - SIMILARITY: BELONGS TO THE CLASS-B BETA-LACTAMASE FAMILY.  
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CC      or send an email to license@lsb-sib.ch).
CC
DR      EMBL: X75074; CA552968.1; -.
DR      PDB: 1SMU; 20-SEP-99.
DR      InterPro: IPR001018; Beta_lactamase_B.
DR      InterPro: IPR001279; Bactamase-like.
DR      Pfam: PF00753; Lactamase_B; 1.
DR      PROSITE: PS00743; BETA_LACTAMASE_B_1; 1.
DR      PROSITE: PS00744; BETA_LACTAMASE_B_2; FALSE_NEG.
KW      Hydroxylase; Zinc; Antibiotic resistance; Periplasmic; Signal;
KW      3D-structure.
FT      SIGNAL          1          21          POTENTIAL.
FT      PROPEP         22          33
FT      CHAIN          34          290          METALLO-BETA-LACTAMASE IL.
FT      DISULFID       239          267
FT      METAL          105          105          ZINC 1.
FT      METAL          107          107          ZINC 1.
FT      METAL          109          109          ZINC 2.
FT      METAL          181          181          ZINC 1.
FT      METAL          205          205          ZINC 2.
FT      METAL          217          217          ZINC 2.
FT      CONFLICT       36          37          AS -> OR (IN REF. 2).
FT      CONFLICT       40          40          O -> A (IN REF. 2).
FT      CONFLICT       56          58          TED -> ROH (IN REF. 2).
FT      CONFLICT       63          63          L -> H (IN REF. 2).
FT      CONFLICT
SO      SEQUENCE       290 AA; 38081 MW; 0B34CAB5451B9C1E CRC64;

Query Match          90.9%; Score 30; DB 1; Length 290;
Best Local Similarity 83.3%; Pred. No. 62;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 IDIASML 6
Db      34 VDAASML 39

RESULT 2
Y084_HUMAN STANDARD; PRT; 648 AA.
ID      Y084_HUMAN
AC      014699;
DT      01-NOV-1997 (Rel. 35, Created)
DT      01-NOV-1997 (Rel. 35, Last sequence update)
DT      15-JUN-2002 (Rel. 41, Last annotation update)
DE      Hypothetical protein KIAA0084 (HA2022) (Fragment).
GN      KIAA0084.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI TaxID:9606;
OX      [1]
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Bone marrow.
RX      MEDLINE=95308325; PubMed=7788527;
RA      Nagase T., Miyajima N., Tanaka A., Sazuka T., Seki N., Sato S.,
RA      Tabata S., Ishiyawa K.-I., Kawarayashi Y., Kotani H., Nomura N.;
RA      "Prediction of the coding sequences of unidentified human genes. III.
RT      The coding sequences of 40 new genes (KIAA0081-KIAA0120) deduced by
RT      analysis of cDNA clones from human cell line KG-1.";
RT      DNA Res. 2:37-43(1995).
CC      -----
CC      THIS SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
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CC      or send an email to license@lsb-sib.ch).
CC      -----
DR      EMBL: DA2043; BAA07644.1; -.
KW      Hypothetical protein.
FT      NON_TER        1
SQ      SEQUENCE       648 AA; 70463 MW; 88F6A6A2D6C1CDA1 CRC64;

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Query Match Similarity      90.9%; Score 30; DB 1; Length 648;
Best Local Similarity      83.3%; Pred No. 1.4e+02;
Matches      5; Conservative      1; Mismatches      0; Indels      0; Gaps      0;

OY      1 LDASWL 6
      |||:|
Db      384 LDANWL 389

RESULT 3
CAPL_CORGL      STANDARD;      PRG;      918 AA.
AC      P12880;
DT      01-OCT-1989 (Rel. 12, Created)
DT      15-JUN-2002 (Rel. 41, Last sequence update)
DT      15-JUN-2002 (Rel. 41, Last annotation update)
DE      Phosphoenolpyruvate carboxylase (EC 4.1.1.31) (PEPCASE) (PEPC).
GN      PPC OR CG11585.
OS      Corynebacterium glutamicum (Brevibacterium flavum).
OC      Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
OC      Actinomycetales; Corynebacterineae; Corynebacteriaceae;
OC      Corynebacterium;
OX      NCBI_TaxID=1718;
RN      [1]
RP      SEQUENCE FROM N.A. /
RC      STRAIN-ATCC 13059 / AS019;
RX      MEDLINE=89384460; Pubmed=2779518;
RA      Elkmanns B.J., Follettie M.T., Griot M.O., Sinskey A.J.
RT      "The phosphoenolpyruvate carboxylase gene of Corynebacterium
RT      glutamicum: molecular cloning, nucleotide sequence, and expression.";
RL      Mol. Gen. Genet. 218:330-339(1989).
RN      [2]
RP      SEQUENCE FROM N.A. AND SEQUENCE OF 1-15.
RC      STRAIN-ATCC 13032 / DSM 20300 / NCIB 10025;
RX      MEDLINE=89326141; Pubmed=2666264;
RA      O'Regan M., Thierbach G., Bachmann B., Villevall D., Lepage P.,
RT      Viret J.F., Lemoine Y.;
RT      "Cloning and nucleotide sequence of the phosphoenolpyruvate
RT      carboxylase-coding gene of Corynebacterium glutamicum ATCC13032.";
RL      Gene 77:237-251(1989).
RN      [3]
RP      SEQUENCE FROM N.A.
RC      STRAIN-ATCC 13032 / DSM 20300 / NCIB 10025;
RA      Nakagawa S.;
RL      "Complete genomic sequence of Corynebacterium glutamicum ATCC 13032.";
RT      Submitted (May-2002) to the EMBL/Genbank/DBJ databases.
CC      -1- FUNCTION: TO FORM OXALOACETATE, A FOUR-CARBON DICARBOXYLIC ACID
CC      SOURCE FOR THE TRICARBOXYLIC ACID CYCLE.
CC      -1- CATALYTIC ACTIVITY: Phosphate + oxaloacetate -> H(2)O +
CC      phosphoenolpyruvate + CO(2)
CC      -1- ENZYME REGULATION: ACTIVITY NOT STIMULATED BY ACETYL-COA IN THE
CC      ABSENCE OF ANY ALLOSTERIC INHIBITOR, WHILE THE CORRESPONDING
CC      PROTEIN FROM E. COLI IS STRONGLY STIMULATED.
CC      -1- PATHWAY: Tricarboxylic acid cycle.
CC      -1- SIMILARITY: BELONGS TO THE PEPCASE FAMILY.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC      use by non-profit institutions as long as its content is in no way
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CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/or\_send\_an\_email\_to\_licens@isb-sib.ch).
CC      -----
DR      EMBL; X14234; CA932450.1; -
DR      EMBL; M25819; AA833537.1; -
DR      EMBL; A09073; CA00827.1; -
DR      EMBL; AP005279; BAB8978.1; -
DR      PIR; S05512; OYFGK.
DR      HSSP; P00864; IRFG.
DR      InterPro; IPR001449; PEPCase.
DR      Pfam; PF00311; PEPCase; 1.
DR      PRINTS; PR00150; PEPCARBLASE.

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DR PROSITE; PS00393; PEPCase\_2; 1.  
 DR PROSITE; PS00781; PEPCase\_1; 1.  
 KM Lyase; Carbon dioxide fixation; Allosteric enzyme;  
 FT Tricarboxylic acid cycle.  
 FT INIT\_MER 0  
 FT ACT\_SITE 137 137 BY SIMILARITY.  
 FT ACT\_SITE 579 579 BY SIMILARITY.  
 FT CONFLICT 606 607 KL -> NV (IN REF. 1).  
 FT CONFLICT 799 800 FT -> LP (IN REF. 1).  
 FT CONFLICT 914 914 L -> V (IN REF. 1).  
 SQ SEQUENCE 918 AA; 103066 MW; A56C2703169D0698 CRC64;

Query Match 90.9%; Score 30; DB 1; Length 918;  
 Best Local Similarity 83.3%; Pred. No. 2e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDASWL 6  
 DB 104 LDATWL 109

RESULT 4  
 CYCL\_PARDE STANDARD; PRT; 177 AA.  
 AC P29899;  
 DT 01-APR-1993 (Rel. 25, Created)  
 DT 01-APR-1993 (Rel. 25, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Cytochrome c-L precursor (Cytochrome C511) (C552).  
 GN MOXG.  
 OS Paracoccus denitrificans.  
 OC Bacteria; Proteobacteria; alpha subdivision; Rhodobacter group;  
 OC Paracoccus.  
 NC NCB1\_TaxID=266;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-Pd 1222;  
 RX MEDLINE-92041581; PubMed-1657871;  
 RA van Spanning R.J.M., Wansell C.W., de Boer T., Hazelaar M.J.,  
 RA Anazawa H., Harms N., Olmann L.F., Stouthamer A.H.;  
 RT Isolation and characterization of the mox, moxg, moxi, and moxr  
 RT genes of Paracoccus denitrificans: Inactivation of mox, moxg, and  
 RT moxr and the resultant effect on methylotrophic growth.\*;  
 RL J. Bacteriol. 173:6948-6961(1991).  
 RN [2]  
 RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS).  
 RX MEDLINE-94188715; PubMed-8140419;  
 RA Chen L., Durlay R., Mathews F.S., Davidson V.L.;  
 RT Structure of an electron transfer complex: methylamine  
 RT dehydrogenase, amicyanin, and cytochrome c511.\*;  
 RL Science 264:86-90(1994).  
 CC -1- FUNCTION: ELECTRON ACCEPTOR FOR MDH. ACTS IN METHANOL OXIDATION.  
 CC THIS CYTOCHROME HAS A REDOX POTENTIAL OF ABOUT +190 MV.  
 CC -1- SUBCELLULAR LOCATION: Periplasmic (Potential).  
 CC -1- INDUCTION: DURING GROWTH ON METHANOL.  
 CC  
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 CC  
 CC EMBL; M57684; AAA25583.1; -.  
 DR PIR; BA1377; BA1377.  
 DR PDB; 2MTA; 31-JAN-94.  
 DR InterPro; IPR000345; Cyt\_c\_heme\_bind.  
 DR PROSITE; PS00190; CYTOCHROME\_C\_1.  
 KM Electron transport; Heme; Signal; Methanol utilization; Periplasmic;  
 FT 3D-structure. 1 22 POTENTIAL.  
 FT CHAIN 23 177 CYTOCHROME C-L.

FT BINDING 79 79 HEME (COVALENT) (BY SIMILARITY).  
 FT BINDING 82 82 HEME (COVALENT) (BY SIMILARITY).  
 FT METAL 83 83 HEME (COVALENT) (BY SIMILARITY).  
 FT STRAND 27 27 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).  
 FT STRAND 34 34  
 FT HELIX 37 39  
 FT HELIX 42 44  
 FT HELIX 48 44  
 FT HELIX 56 56  
 FT TURN 60 63  
 FT TURN 65 67  
 FT HELIX 68 78  
 FT TURN 79 79  
 FT HELIX 80 83  
 FT TURN 85 86  
 FT HELIX 103 106  
 FT HELIX 108 117  
 FT TURN 121 122  
 FT TURN 127 129  
 FT HELIX 132 144  
 FT TURN 145 145  
 FT TURN 150 151  
 FT TURN 154 155  
 FT HELIX 158 162  
 FT TURN 163 163  
 SQ SEQUENCE 177 AA; 19396 MW; 6949PDC8B2C056E CRC64;

Query Match 87.9%; Score 29; DB 1; Length 177;  
 Best Local Similarity 100.0%; Pred. No. 59;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 DASWL 6  
 DB 152 DASWL 156

RESULT 5  
 THTL\_CAEEL STANDARD; PRT; 277 AA.  
 ID THTL\_CAEEL  
 AC P91247;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 15-JUL-1998 (Rel. 36, Last annotation update)  
 DE Putative thiosulfate sulfotransferase Flig11.9 (EC 2.8.1.1).  
 GN Flig11.9.  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;  
 OC Rhabditidae; Peloderinae; Caenorhabditis.  
 NC NCB1\_TaxID=6239;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-Bristol N2;  
 RA Lettelle P., Deadman R.;  
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.  
 CC -1- CATALYTIC ACTIVITY: Thiosulfate + cyanide -> sulfite + thiocyanate.  
 CC -1- SIMILARITY: BELONGS TO THE RHODANSE FAMILY.  
 CC  
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 CC  
 CC EMBL; U80451; AAB37840.1; -.  
 DR HSP; P00586; IRRS.  
 DR WormPep; Flig11.9; CE09351.  
 DR InterPro; IPR001763; Rhodanese-like.  
 DR InterPro; IPR001307; Rhodanese.  
 DR Pfam; PF00581; Rhodanese; 1.  
 DR SMART; SM00450; RHOD; 1.  
 DR PROSITE; PS00683; RHODANSE\_2; FALSE\_NEG.  
 KM Hypothetical protein; Transferase.

FT ACT\_SITE 258 258 BY SIMILARITY.  
SQ SEQUENCE 277 AA; 30699 MW; 25EDF66CE12824C CRC64;  
Query Match  
Best Local Similarity 100.0%; Pred. No. 93;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LDASW 5  
DB 22 LDASW 26  
RESULT 6  
YBRC\_ECOLI  
ID YBRC\_ECOLI STANDARD; PRT; 286 AA.  
AC P25906;  
DT 01-MAY-1992 (Rel. 22, Created)  
DT 01-MAY-1992 (Rel. 22, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Hypothetical oxidoreductase ybdc (EC 1.-.-.-).  
GN Ybdc OR B1406.  
OS Escherichia coli.  
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
OC Escherichia.  
OX NCBI\_Taxid=562;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-K12;  
RX MEDLINE=92190338; PubMed=1665988;  
RA Moser I., Glaser P., Danchin A.;  
RT "Multiple IS insertion sequences near the replication terminus in  
RL Escherichia coli K-12."  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN-K12 / MG1655;  
RX MEDLINE=97426617; PubMed=9278503;  
RA Blatner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,  
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,  
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,  
RA Mau B., Shao Y.;  
RT "The complete genome sequence of Escherichia coli K-12."  
RL Science 277:1453-1474(1997).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN-K12;  
RX MEDLINE=9751357; PubMed=9097039;  
RA Alba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K.,  
RA Itoh T., Kasai H., Kashimoto K., Kimura S., Kitakawa M.,  
RA Kitagawa M., Makino K., Miki T., Mizobuchi K., Mori H., Mori T.,  
RA Motomura K., Nakade S., Nakamura Y., Nashimoto H., Nishio Y.,  
RA Oshima T., Saito N., Sampei G., Seki Y., Sivasubraman S.,  
RA Tagami H., Takeda J., Takemoto K., Takeuchi Y., Wada C.,  
RA Yamamoto Y., Horiiuchi T.;  
RT "A 570-kb DNA sequence of the Escherichia coli K-12 genome  
corresponding to the 28.0-40.1 min region on the linkage map."  
RL DNA Res. 3:363-377(1996).  
RN [4]  
RP SEQUENCE OF 1-69 FROM N.A.  
RC STRAIN-W / ATCC 11105;  
RX MEDLINE=98421522; PubMed=9748275;  
RA Ferrandez A., Mhambres B., Garcia B., Olivera E.R., Luengo J.M.,  
RA Garcia J.L., Diaz E.;  
RT "Catabolism of phenylacetic acid in Escherichia coli. Characterization  
of a new aerobic hybrid pathway."  
RL J. Biol. Chem. 273:25974-25986(1998).  
CC -1- SIMILARITY: BELONGS TO THE ALDO/KETO REDUCTASE 2 FAMILY.  
CC -----  
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CC -----  
CC EMBL: X62680; CAA44553.1; -  
CC DR EMBL: AE000238; AAC74488.1; -  
CC DR EMBL: D90779; BA15021.1; -  
CC DR EMBL: X87452; CAA6103.1; -  
CC DR PIR: S22111; S22111.  
CC DR PIR: A48399; A48399.  
CC DR HSSP: P06632; 1HW6.  
CC DR Ecogene: EG11309; Ybdc.  
CC DR InterPro: IPR001395; Aldo\_ket\_red.  
CC DR Pfam: PF00248; Aldo\_ket\_red; 1.  
CC DR ProDom: PD000288; Aldo\_ket\_red; 1.  
CC KW Hypothetical protein; Oxidoreductase; Complete proteome.  
SQ SEQUENCE 286 AA; 30706 MW; 82B587AEAD3115BF9 CRC64;  
Query Match  
Best Local Similarity 100.0%; Pred. No. 96;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 DASWL 6  
DB 92 DASWL 96  
RESULT 7  
THTR\_CHICK  
ID THTR\_CHICK STANDARD; PRT; 289 AA.  
AC P25324;  
DT 01-MAY-1992 (Rel. 22, Created)  
DT 01-MAY-1992 (Rel. 22, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE Thiosulfate sulfotransferase (EC 2.8.1.1) (Rhodanese).  
GN Gallus gallus (Chicken).  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
OC Gallus.  
OX NCBI\_Taxid=9031;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Liver;  
RX MEDLINE=91113289; PubMed=2275748;  
RA Kohanski R.A., Heinrichson R.L.;  
RT "Primary structure of avian hepatic rhodanese."  
RL J. Protein Chem. 9:369-377(1990).  
CC -1- FUNCTION: FORMATION OF IRON-SULFUR COMPLEXES AND CYANIDE  
CC DETOXIFICATION.  
CC -1- CATALYTIC ACTIVITY: Thiosulfate + cyanide = sulfite + thiocyanate.  
CC -1- SUBUNIT: MONOMER.  
CC -1- SUBCELLULAR LOCATION: Mitochondrial matrix.  
CC -1- TISSUE SPECIFICITY: FOUND IN NUMEROUS TISSUES.  
CC -1- DOMAIN: THE STRUCTURE CONSISTS OF 2 DOMAINS OF VERY SIMILAR  
CC CONFORMATION, SUGGESTING A COMMON EVOLUTIONARY ORIGIN. HOWEVER,  
CC THE SEQUENCES OF THE 2 DOMAINS ARE VERY DIFFERENT.  
CC -1- SIMILARITY: BELONGS TO THE RHODANESE FAMILY.  
CC -----  
CC PIR: A37209; A37209.  
CC DR HSSP: P00586; 1RHS.  
CC DR InterPro: IPR001763; Rhodanese-like.  
CC DR InterPro: IPR001307; Rhodanese.  
CC DR Pfam: PF00581; Rhodanese; 2.  
CC DR SMART: SM00450; RHOD; 2.  
CC DR PROSITE: PS00380; RHODANESE\_1; 1.  
CC DR PROSITE: PS00683; RHODANESE\_2; 1.  
CC KW Transferrase; Mitochondrion.  
CC FT DOMAIN 1 142 A DOMAIN.  
FT 143 158 HINGE.  
FT DOMAIN 159 289 B DOMAIN.  
FT ACT\_SITE 186 186 MAY PLAY A ROLE IN SUBSTRATE BINDING (BY  
FT ACT\_SITE 244 244 SIMILARITY).  
FT ACT\_SITE 245 245 SUBSTRATE (THIOSULFATE) BINDING

FT ACT\_SITE 246 246 (BY SIMILARITY).  
 FT SEQUENCE 289 AA; 32286 MW; 8BPCF671DE0B2B44 CRC64;  
 SQ SEQUENCE 289 AA; 32286 MW; 8BPCF671DE0B2B44 CRC64;  
 Query Match 87.9%; Score 29; DB 1; Length 289;  
 Best Local Similarity 100.0%; Pred. No. 97;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 LDASM 5  
 31 LDASM 35

RESULT 8  
 ID THTR\_RAT STANDARD; PRT; 295 AA.  
 AC P24329;  
 DT 01-MAR-1992 (Rel. 21, Created)  
 DT 01-MAR-1992 (Rel. 21, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Thiosulfate sulfurtransferase (EC 2.8.1.1) (Rhodanese) (Fragment).  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Sprague-Dawley; TISSUE=Liver;  
 RX MEDLINE=91207296; PubMed=2018478;  
 RA Weiland K.T., Dooley T.P.;  
 RT "Molecular cloning, sequencing and characterization of cDNA to rat  
 RT liver rhodanese, a thiosulfate sulphurtransferase.";  
 RT Biochem. J. 275:227-231(1991).  
 RL [2]  
 RN [2]  
 RP MORGANESIS.  
 RC TISSUE=Liver;  
 RX MEDLINE=95332330; PubMed=7608189;  
 RA Nagahara N., Okazaki T., Nishino T.;  
 RT "Cytosolic mercaptopyruvate sulfurtransferase is evolutionarily  
 RT related to mitochondrial rhodanese. Striking similarity in active site  
 RT amino acid sequence and the increase in the mercaptopyruvate  
 RT sulfurtransferase activity of rhodanese by site-directed  
 RT mutagenesis.";  
 RL J. Biol. Chem. 270:16230-16235(1995).  
 CC -1- FUNCTION: INVOLVED IN THE FORMATION OF IRON-SULFUR COMPLEXES,  
 CC CYANIDE DETOXIFICATION OR MODIFICATION OF SULFUR-CONTAINING  
 CC ENZYMES. OTHER THIOL COMPOUNDS, BESIDES CYANIDE, CAN ACT AS SULFUR  
 CC ION ACCEPTORS. ALSO HAS WEAK MERCAPTOPYRUVATE SULFURTRANSFERASE  
 CC (MST) ACTIVITY.  
 CC -1- CATALYTIC ACTIVITY: Thiosulfate + cyanide = sulfite + thiocyanate.  
 CC -1- SUBUNIT: MONOMER.  
 CC -1- SUBCELLULAR LOCATION: Mitochondrial matrix.  
 CC -1- TISSUE SPECIFICITY: FOUND IN NUMEROUS TISSUES.  
 CC -1- DOMAIN: THE STRUCTURE CONSISTS OF 2 DOMAINS OF VERY SIMILAR  
 CC CONFORMATION, SUGGESTING A COMMON EVOLUTIONARY ORIGIN. HOWEVER,  
 CC THE SEQUENCES OF THE 2 DOMAINS ARE VERY DIFFERENT.  
 CC -1- SIMILARITY: BELONGS TO THE RHODANESE FAMILY.  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC EMBL: X56228; CAA39677.1; -  
 DR PIR: S15081; S15081.  
 DR HSSP: P00586; IRHS.  
 DR InterPro: IPR001763; Rhodanese-1like.  
 DR InterPro: IPR001307; Rhodanese.

DR Pfam: PF00561; Rhodanese; 2.  
 DR SMART: SM00450; RHOD; 2.  
 DR PROSITE: PS00380; RHODANESE\_1; 1.  
 DR PROSITE: PS00683; RHODANESE\_2; 1.  
 KW Transferase; Mitochondrion.  
 FT NON\_TER 1  
 FT DOMAIN 1 141  
 FT DOMAIN 142 157  
 FT DOMAIN 158 295  
 FT ACT\_SITE 185 185  
 FT ACT\_SITE 246 246  
 FT ACT\_SITE 247 247  
 FT ACT\_SITE 248 248  
 FT ACT\_SITE 247 247  
 FT MOTAGEN 248 248  
 FT MOTAGEN 248 248  
 FT SEQUENCE 295 AA; 33176 MW; 24C5B35690934E1 CRC64;  
 SQ SEQUENCE 295 AA; 33176 MW; 24C5B35690934E1 CRC64;  
 Query Match 87.9%; Score 29; DB 1; Length 295;  
 Best Local Similarity 100.0%; Pred. No. 99;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 LDASM 5  
 30 LDASM 34

RESULT 9  
 ID RECO\_ANASP STANDARD; PRT; 296 AA.  
 AC 08YPL9;  
 DT 15-JUN-2002 (Rel. 41, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE DNA repair protein reco (Recombination protein O).  
 DE RECO OR ALR4175.  
 GN Anabaena sp. (strain PCC 7120).  
 OS Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.  
 OX NCBI\_TaxID=103690;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21595285; PubMed=11759840;  
 RA Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Saseamoto S.,  
 RA Watanabe A., Irliguchi M., Ishikawa A., Kawashima K., Kimura T.,  
 RA Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,  
 RA Nakazaki N., Shimp S., Sugimoto K., Takazawa M., Yamada M.,  
 RA Yasuda M., Tabata S.;  
 RT "Complete genomic sequence of the filamentous nitrogen-fixing  
 RT cyanobacterium Anabaena sp. strain PCC 7120.";  
 RL DNA Res. 8:205-213(2001).  
 CC -1- FUNCTION: Involved in DNA repair and recf pathway recombination  
 CC (By similarity).  
 CC -1- SIMILARITY: BELONGS TO THE RECO FAMILY.  
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 CC EMBL: AP003595; BAB75874.1; -  
 DR InterPro: IPR003717; Reco.  
 DR Pfam: PF02365; Reco; 1.  
 DR DNA repair; DNA recombination; Complete proteome.  
 SQ SEQUENCE 296 AA; 32728 MW; A5B3D540F162BE72 CRC64;  
 Query Match 87.9%; Score 29; DB 1; Length 296;  
 Best Local Similarity 100.0%; Pred. No. 99;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DASWL 6  
DB 256 DASWL 260

RESULT 10  
THRM\_HUMAN STANDARD: PRT; 296 AA.

AC P25325; 075750;  
DT 01-MAY-1992 (Rel. 22, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE 3-mercaptopyruvate sulfinyltransferase (EC 2.8.1.2) (MST).  
GN MST OR TST2.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Liver;  
RX MEDLINE=20057165; PubMed=10591208;  
RT PubMed=92062122; PubMed=1953758;  
RT Pallini R., Guazzi G.C., Cannello C., Cacace M.G.;  
RT Cloning and sequence analysis of the human liver rhodanese;  
RT comparison with the bovine and chicken enzymes;  
RL Biochem. Biophys. Res. Commun. 180:887-893(1991).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20057165; PubMed=10591208;  
RT PubMed=92062122; PubMed=1953758;  
RT Dunham I., Hunt A.R., Collins J.E., Bruskewich R., Beare D.M.,  
RT Clamp M., Smink L.J., Alnscough R., Almeida J.P., Babbage A.K.,  
RT Baguley C., Bailey J., Barlow K.F., Bates K.N., Beasley O.P.,  
RT Bird C.P., Blakey S.E., Bridgeman A.M., Buck D., Burgess J.,  
RT Burdill W.D., Burton J., Carder C., Carter N.P., Chen Y., Clark G.,  
RT Clegg S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R.,  
RT Conroy D., Corby N.R., Coville G.J., Cox A.V., Davis J., Dawson E.,  
RT Dhanl P.D., Dockree C., Dodsworth S.J., Durbin R.M., Ellington A.G.,  
RT Evans K.L., Fey J.M., Fleming K., French L., Garner A.A.,  
RT Gilbert J.G.R., Goward M.E., Graffam D.V., Griffiths M.N.D., Hall C.,  
RT Hall R.E., Hall-Tamlyn G., Heathcott R.W., Ho S., Holmes S.,  
RT Hunt S.E., Jones M.C., Kershaw J., Kimberley A.M., King J.,  
RT Laird G.K., Langford C.F., Leverisha M.A., Lloyd C., Lloyd D.M.,  
RT Martin I.D., Mashreghi-Mohammadi M., Matthews L.H., Mccann O.T.,  
RT Mcclay J., McLaren S., McMurray A.A., Milne S.A., Mortimore B.J.,  
RT Odell C.N., Pavitt R., Pearce A.V., Pearson D., Phillimore B.J.C.T.,  
RT Phillips S.H., Plumb R.W., Ramsay H., Ramsey Y., Rogers L., Ross M.T.,  
RT Scott C.E., Sehra H.K., Skuce C.D., Smalley S., Smith M.L.,  
RT Soderlund C., Spraggon L., Steward C.A., Sulston J.E., Swann R.M.,  
RT Vaudin M., Wall M., Wallis J.M., Whiteley M.N., Willey D.L.,  
RT Williams L., Williams S.A., Williamson H., Wilmer T.E., Wilming L.,  
RT Wright C.L., Hubbard T., Bentley D.R., Beck S., Rogers J., Shimizu N.,  
RT Minoshima S., Kawasaki K., Sasaki T., Asakawa S., Kudoh J.,  
RT Shintani A., Shibuya K., Yoshizaki Y., Aoki N., Mitsuama S.,  
RA Roe B.A., Chen F., Chu L., Crabtree J., Deschamps S., Do A., Do T.,  
RA Dorman A., Fang F., Fu Y., Hu P., Hua A., Kenton S., Lai H., Lao H.T.,  
RA Lewis J., Lewis S., Lin S.-P., Lon P., Malay E., Nguyen T., Pan H.,  
RA Phan S., Qi S., Qian Y., Ray L., Ren Q., Shaull S., Sloan D., Song L.,  
RA Wang Q., Wang Y., Wang Z., White J., Willingham D., Wu H., Yao Z.,  
RA Zhan M., Zhang G., Chissoe S., Murray J., Miller N., Minx P.,  
RA Fulton R., Johnson D., Bemis G., Bentley D., Bradshaw H., Bourne S.,  
RA Cordes M., Du Z., Fulton L., Goela D., Graves T., Hawkins J.,  
RA Hinds K., Kemp K., Latreille P., Layman D., Ozesky P., Rohlfing T.,  
RA Scheet P., Walker C., Wamsley A., Woldmann P., Pepin K., Nelson R.,  
RA Korf I., Bedell J.A., Hillier L., Mardis E., Waterston R., Wilson R.,  
RA Emanuel B.S., Shaikh T., Kurahashi H., Salita S., Budarf M.L.,  
RA Mcdermid H.E., Johnson A., Wong A.C.C., Morrow B.E., Edelmann L.,  
RA Kim U.J., Shizuya H., Simon M.I., Dumanaki J.P., Peyzard M., Kedra D.,  
RA Seconssi E., Ericsson I., Tapia I., Bruder C.E., O'Brien K.P.,  
RA Wilkison P., Bodenteich A., Hartman K., Hu X., Khan A.S., Lane L.,  
RA Tiliahun Y., Wright H.;  
RT "The DNA sequence of human chromosome 22.";  
RL Nature 402:489-495(1999).

RN [3]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Bone marrow, Muscle, and Pancreas;  
RA Strausberg R.;  
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.  
CC -1- FUNCTION: TRANSFER OF A SULFUR ION TO CYANIDE OR TO OTHER THIOL  
CC COMPOUNDS. ALSO HAS WEAK RHODANASE ACTIVITY. MAY HAVE A ROLE IN  
CC CYANIDE DEGRADATION OR IN THIOSULFATE BIOSYNTHESIS.  
CC -1- CATALYTIC ACTIVITY: 3-mercaptopyruvate + cyanide = pyruvate +  
CC thioacetate.  
CC -1- SUBUNIT: MONOMER OR DISULFIDE-LINKED HOMODIMER (BY SIMILARITY).  
CC -1- SUBCELLULAR LOCATION: CYTOSOL.  
CC -1- DOMAIN: THE STRUCTURE CONSISTS OF 2 DOMAINS OF VERY SIMILAR  
CC CONFORMATION, SUGGESTING A COMMON EVOLUTIONARY ORIGIN. HOWEVER,  
CC THE SEQUENCES OF THE 2 DOMAINS ARE VERY DIFFERENT.  
CC -1- SIMILARITY: BELONGS TO THE RHODANASE FAMILY.  
CC -1- CAUTION: WAS ORIGINALLY (REF.1) THOUGHT TO BE RHODANASE.  
CC -----  
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CC -----  
DR EMBL: X59434; CAA42060.1; -;  
DR EMBL: 273420; CAA9763.1; -;  
DR EMBL: BC003508; AAH03508.1; -;  
DR EMBL: BC016737; AAH16737.1; -;  
DR EMBL: BC018717; AAH18717.1; -;  
DR PIR: JH0461; JH0461.  
DR HSSP: P00586; IRHS.  
DR Genew: HGNC:7223; MST.  
DR MIM: 602496; -;  
DR InterPro: IPR001763; Rhodanese-like.  
DR InterPro: IPR001307; Rhodanese.  
DR Pfam: PF00581; Rhodanese.  
DR SMART: SM00450; RHOD. 2.  
DR PROSITE: PS00380; RHODANASE\_1; 1.  
DR PROSITE: PS00683; RHODANASE\_2; 1.  
KW Transferase.  
FT INIT\_MER 0 0 BY SIMILARITY.  
FT DOMAIN 1 143 A DOMAIN.  
FT DOMAIN 144 159 HINGE.  
FT DOMAIN 160 236 B DOMAIN.  
FT ACT\_SITE 187 187 SUBSTRATE (MERCAPTOPYRUVATE) BINDING  
FT ACT\_SITE 187 187 (BY SIMILARITY).  
FT ACT\_SITE 196 196 SUBSTRATE (MERCAPTOPYRUVATE) BINDING  
FT ACT\_SITE 196 196 (BY SIMILARITY).  
FT ACT\_SITE 247 247 BY SIMILARITY.  
FT CONFLICT 45 47 RRE -> TO (IN REF. 1).  
SQ SEQUENCE 296 AA; 33047 MW; 1991F0F1CAE8C8E1 CRC64;  
Query Match 87.9%; Score 29; DB 1; Length 296;  
Best Local Similarity 100.0%; Pred. NO. 99;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IDASW 5  
DB 31 IDASW 35

RESULT 11  
THRM\_RAT STANDARD: PRT; 296 AA.

AC P97532;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE 3-mercaptopyruvate sulfinyltransferase (EC 2.8.1.2) (MST).  
GN MST.  
OS Rattus norvegicus (Rat).

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 CC NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A., PARTIAL SEQUENCE, AND MUTAGENESIS.  
 RC STRAIN=Histar; TISSUE=Liver;  
 RX MEDLINE=97066916; PubMed=8910318;  
 RA Nagahara N., Nishino T.;  
 RT "Role of amino acid residues in the active site of rat liver  
 RT mercaptopyruvate sulfurtransferase. cDNA cloning, overexpression, and  
 RT site-directed mutagenesis.";  
 RL J. Biol. Chem. 271:27395-27401(1996).  
 RN [2]  
 RP SEQUENCE OF 8-76 AND 146-284, AND CHARACTERIZATION.  
 RC STRAIN=Histar; TISSUE=Liver;  
 RX MEDLINE=95332330; PubMed=7608189;  
 RA Nagahara N., Okazaki T., Nishino T.;  
 RT "Cytosolic mercaptopyruvate sulfurtransferase is evolutionarily  
 RT related to mitochondrial rhodanese. Striking similarity in active site  
 RT amino acid sequence and the increase in the mercaptopyruvate  
 RT sulfurtransferase activity of rhodanese by site-directed  
 RT mutagenesis.";  
 RL J. Biol. Chem. 270:16230-16235(1995).  
 CC -1- FUNCTION: TRANSFERS A SULFUR ION TO CYANIDE OR TO OTHER THIOL  
 CC COMPOUNDS. ALSO HAS WEAK RHODANES ACTIVITY. MAY HAVE A ROLE IN  
 CC CYANIDE DEGRADATION OR IN THIOSULFATE BIOSYNTHESIS.  
 CC -1- CATALYTIC ACTIVITY: 3-mercaptopyruvate + cyanide = pyruvate +  
 CC thiocyanate.  
 CC -1- SUBUNIT: MONOMER OR DISULFIDE-LINKED HOMODIMER.  
 CC -1- SUBCELLULAR LOCATION: CYTOSOL (MOSTLY) AND MITOCHONDRIAL.  
 CC -1- DOMAIN: THE STRUCTURE CONSISTS OF 2 DOMAINS OF VERY SIMILAR  
 CC CONFORMATION, SUGGESTING A COMMON EVOLUTIONARY ORIGIN. HOWEVER,  
 CC THE SEQUENCES OF THE 2 DOMAINS ARE VERY DIFFERENT.  
 CC -1- PTM: THE N-TERMINAL IS BLOCKED.  
 CC -1- SIMILARITY: BELONGS TO THE RHODANES FAMILY.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL; D50564; BAA09127.1; -  
 DR HSP; P00586; IRHS.  
 DR InterPro: IPR001763; Rhodanese-like.  
 DR InterPro: IPR001307; Rhodanese.  
 DR Pfam: PF00581; Rhodanese; 2.  
 DR SMART: SM00450; RHOD; 2.  
 DR PROSITE: PS00380; RHODANES\_1; 1.  
 DR PROSITE: PS00683; RHODANES\_2; 1.  
 DR Transferrase; Mitochondrion.  
 KM TRANSFERASE; Mitochondrion.  
 FT INIT MET 0  
 FT DOMAIN 1 143 A DOMAIN.  
 FT DOMAIN 144 139 HINGE.  
 FT DOMAIN 160 296 B DOMAIN.  
 FT ACT\_SITE 187 187 SUBSTRATE (MERCAPTOPYRUVATE) BINDING.  
 FT ACT\_SITE 196 196 SUBSTRATE (MERCAPTOPYRUVATE) BINDING.  
 FT ACT\_SITE 247 247  
 FT MUTAGEN 187 187 R->G: LARGE DECREASE IN MST ACTIVITY;  
 FT MUTAGEN 196 196 SOME DECREASE IN RHODANES ACTIVITY.  
 FT MUTAGEN 247 247 R->G: DECREASED MST ACTIVITY; INCREASED  
 FT MUTAGEN 248 248 R->S: LOSS OF BOTH MST AND RHODANES  
 FT MUTAGEN 248 248 ACTIVITIES.  
 FT MUTAGEN 249 249 G->R: DECREASED MST ACTIVITY; INCREASED  
 FT MUTAGEN 249 249 RHODANES ACTIVITY.  
 FT MUTAGEN 249 249 S->K: SLIGHT DECREASE IN MST ACTIVITY;  
 FT MUTAGEN 249 249 INCREASED RHODANES ACTIVITY.  
 FT MUTAGEN 249 249 S->A: SLIGHT DECREASE IN MST ACTIVITY.  
 SO SEQUENCE 296 AA; 32809 MW; 0BC176AC1AC717C CRC64;

Query Match 87.9%; Score 29; DB 1; Length 296;  
 Best Local Similarity 100.0%; Pred. No. 99;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LDASM 5  
 DB 31 LDASM 35  
 RESULT 12  
 THTR\_BOVIN STANDARD; PRT; 296 AA.  
 AC P00586;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 01-AUG-1992 (Rel. 23, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Thiosulfate sulfurtransferase (EC 2.8.1.1) (Rhodanese).  
 GN TST.  
 OS Bos taurus (Bovine).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 CC Bovidae; Bovinae; Bos.  
 CC NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=91161544; PubMed=2002017;  
 RA Miller D.M., Delgado R., Chirgwin J.M., Hardies S.C., Horowitz P.M.;  
 RT "Expression of cloned bovine adrenal rhodanese.";  
 RL J. Biol. Chem. 266:4686-4691(1991).  
 RN [2]  
 RP SEQUENCE OF 1-294.  
 RC TISSUE=Liver;  
 RX MEDLINE=79048424; PubMed=711737;  
 RA Russell J., Weng L., Keim P.S., Heinrichson R.L.;  
 RT "The covalent structure of bovine liver rhodanese. Isolation and  
 RT partial structural analysis of cyanogen bromide fragments and the  
 RT complete sequence of the enzyme.";  
 RL J. Biol. Chem. 253:8102-8108(1978).  
 RN [3]  
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).  
 RX MEDLINE=79007483; PubMed=691057;  
 RA Ploegman J.H., Drent G., Kalk K.H., Hol W.G.J.;  
 RT "Structure of bovine liver rhodanese. I. Structure determination at  
 RT 2.5-A resolution and a comparison of the conformation and sequence of  
 RT its two domains.";  
 RL J. Mol. Biol. 123:557-594(1978).  
 RN [4]  
 RP X-RAY CRYSTALLOGRAPHY (1.36 ANGSTROMS).  
 RX MEDLINE=98437562; PubMed=9761843;  
 RA Gliubich F., Berni R., Colapietro M., Barba L., Zanotti G.;  
 RT "Structure of sulfur-substituted rhodanese at 1.36-A resolution.";  
 RL Acta Crystallogr. D 54:481-486(1998).  
 RN [5]  
 RP ACTIVE SITE.  
 RX MEDLINE=79048425; PubMed=711738;  
 RA Weng L., Heinrichson R.L., Westley J.;  
 RT "Active site cysteinyl and arginyl residues of rhodanese. A novel  
 RT formation of disulfide bonds in the active site promoted by  
 RT phenylglyoxal.";  
 RL J. Biol. Chem. 253:8109-8119(1978).  
 RN [6]  
 RP MUTAGENESIS OF ARG-186 AND LYS-249.  
 RX MEDLINE=9419198; PubMed=8132546;  
 RA Luo G.-X., Horowitz P.M.;  
 RT "The sulfurtransferase activity and structure of rhodanese are  
 RT affected by site-directed replacement of Arg-186 or Lys-249.";  
 RL J. Biol. Chem. 269:8220-8225(1994).  
 CC -1- FUNCTION: FORMATION OF IRON-SULFUR COMPLEXES AND CYANIDE  
 CC DETOXIFICATION. BINDS MOLECULAR OXYGEN AND SULFUR.  
 CC -1- CATALYTIC ACTIVITY: Thiosulfate + cyanide = sulfite + thiocyanate.  
 CC -1- SUBUNIT: MONOMER.  
 CC -1- SUBCELLULAR LOCATION: Mitochondrial matrix.  
 CC -1- TISSUE SPECIFICITY: FOUND IN NUMEROUS TISSUES.

CC -1- DOMAIN: THE STRUCTURE CONSISTS OF 2 DOMAINS OF VERY SIMILAR  
 CC CONFORMATION, SUGGESTING A COMMON EVOLUTIONARY ORIGIN. HOWEVER,  
 CC THE SEQUENCES OF THE 2 DOMAINS ARE VERY DIFFERENT.  
 CC -1- SIMILARITY: BELONGS TO THE RHODANSE FAMILY.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL: M58561; AAA30753.1; -.  
 DR PIR: A00727; ROBO.  
 DR PIR: A23704; A23704.  
 DR PDB: 1RHD; 27-JAN-84.  
 DR PDB: 1RHS; 21-JAN-98.  
 DR PDB: 2ORA; 01-AUG-96.  
 DR PDB: 1ORB; 15-OCT-95.  
 DR PDB: 1BOH; 27-APR-99.  
 DR PDB: 1BOI; 27-APR-99.  
 DR InterPro: IPR001763; Rhodanese-1like.  
 DR InterPro: IPR001307; Rhodanese.  
 DR Pfam: PF00581; Rhodanese; 2.  
 DR SMART: SM00430; RHOD; 2.  
 DR PROSITE: PS00380; RHODANSE\_1; 1.  
 DR PROSITE: PS00683; RHODANSE\_2; 1.  
 DR Transferrase; Mitochondrion; 3D-structure.  
 KW INIT MET 0 0  
 FT DOMAIN 1 142 A DOMAIN.  
 FT 143 158 HINGE.  
 FT 159 236 B DOMAIN.  
 FT DOMAIN 186 186 MAY PLAY A ROLE IN SUBSTRATE BINDING.  
 FT ACT\_SITE 247 247  
 FT ACT\_SITE 248 248  
 FT ACT\_SITE 249 249  
 FT ACT\_SITE 249 249  
 FT VARIANT 1 2  
 FT 186 186  
 FT MUTAGEN 249 249  
 FT CONFLICT 99 99  
 FT CONFLICT 214 214  
 FT CONFLICT 219 219  
 FT STRAND 9 10  
 FT HELIX 12 21  
 FT TURN 22 22  
 FT STRAND 24 24  
 FT TURN 25 27  
 FT STRAND 28 32  
 FT HELIX 40 47  
 FT TURN 48 49  
 FT STRAND 51 51  
 FT TURN 51 51  
 FT STRAND 53 53  
 FT TURN 56 57  
 FT STRAND 60 61  
 FT TURN 66 67  
 FT HELIX 77 82  
 FT TURN 91 92  
 FT STRAND 94 97  
 FT TURN 102 103  
 FT HELIX 108 117  
 FT TURN 118 118  
 FT STRAND 123 126  
 FT TURN 127 128  
 FT HELIX 129 136  
 FT TURN 137 137  
 FT STRAND 141 141  
 FT TURN 158 159  
 FT STRAND 161 162

(BY SIMILARITY).  
 MISSING (IN SOME PREPARATIONS, BUT THESE  
 STILL EXHIBIT COMPLETE ENZYME ACTIVITY).  
 K->A: NO RHODANSE ACTIVITY.  
 R->L: REDUCED RHODANSE ACTIVITY.  
 D -> N (IN REF. 2).  
 N -> D (IN REF. 2).  
 D -> N (IN REF. 2).

SUBSTRATE (THIOSULFATE) BINDING  
 (BY SIMILARITY)  
 SUBSTRATE (THIOSULFATE) BINDING  
 (BY SIMILARITY)

FT TURN 164 165  
 FT HELIX 166 173  
 FT STRAND 177 180  
 FT HELIX 184 188  
 FT TURN 189 189  
 FT STRAND 203 203  
 FT TURN 203 203  
 FT STRAND 205 206  
 FT TURN 208 209  
 FT STRAND 212 215  
 FT TURN 216 216  
 FT STRAND 218 219  
 FT TURN 222 222  
 FT STRAND 225 234  
 FT HELIX 225 236  
 FT TURN 239 240  
 FT STRAND 243 246  
 FT TURN 252 253  
 FT HELIX 254 263  
 FT TURN 264 264  
 FT TURN 266 267  
 FT STRAND 269 271  
 FT TURN 272 274  
 FT HELIX 275 281  
 FT STRAND 284 286  
 FT STRAND 288 288  
 SQ SEQUENCE 296 AA; 33164 MW; C8769696FA6AC111 CRC64;  
 Query Match 87.9%; Score 29; DB 1; Length 296;  
 Best Local Similarity 100.0%; Pred. No. 99;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 1 LDASW 5  
 31 LDASW 35  
 DB  
 RESULT 13  
 THTR\_CRIGR STANDARD; PRT; 296 AA.  
 ID THTR\_CRIGR AC P46635;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Thiosulfate sulfotransferase (EC 2.8.1.1) (Rhodanese).  
 GN 1ST.  
 OS Cricetus griseus (Chinese hamster).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;  
 OC Cricetus.  
 OC NCBI\_Taxid=10029;  
 OX [1]  
 RN RP SEQUENCE FROM N.A.  
 RC TISSUE-Ovary;  
 RX MEDLINE=9610646; PubMed=8535164;  
 RA Trevino R.J., Hunt J., Horowitz P.M., Chirgwin J.M.;  
 RT Chinese hamster rhodanese cDNA: activity of the expressed protein is  
 RT not blocked by a C-terminal extension.";  
 RL Protein Expr. Purif. 6:693-699(1995).  
 CC -1- FUNCTION: FORMATION OF IRON-SULFUR COMPLEXES AND CYANIDE  
 CC DEMONSTRATION. BINDS MOLECULAR OXYGEN AND SULFUR.  
 CC -1- CATALYTIC ACTIVITY: Thiosulfate + cyanide = sulfite + thiocyanate.  
 CC -1- SUBUNIT: MONOMER (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: Mitochondrial matrix.  
 CC -1- DOMAIN: THE STRUCTURE CONSISTS OF 2 DOMAINS OF VERY SIMILAR  
 CC CONFORMATION, SUGGESTING A COMMON EVOLUTIONARY ORIGIN. HOWEVER,  
 CC THE SEQUENCES OF THE 2 DOMAINS ARE VERY DIFFERENT.  
 CC -1- SIMILARITY: BELONGS TO THE RHODANSE FAMILY.  
 CC -----  
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CC -----

DR EMBL: U23943; AAB84305.1; -

DR HSSP: P00586; IRHS.

DR InterPro: IPR001763; Rhodanese-like.

DR InterPro: IPR001307; Rhodanese.

DR Pfam: PF00581; Rhodanese; 2.

DR SMART: SM00450; RHOD; 2.

DR PROSITE: PS00380; RHODANESE\_1; 1.

DR PROSITE: PS00683; RHODANESE\_2; 1.

KW Transferase; Mitochondrion.

FT INIT\_MET 0 0 BY SIMILARITY.

FT DOMAIN 1 142 A DOMAIN.

FT DOMAIN 143 158 HINGE.

FT DOMAIN 159 296 B DOMAIN.

FT ACT\_SITE 186 186 MAY PLAY A ROLE IN SUBSTRATE BINDING (BY SIMILARITY).

FT ACT\_SITE 247 247 BY SIMILARITY.

FT ACT\_SITE 248 248 SUBSTRATE (THIOSULFATE) BINDING (BY SIMILARITY).

FT ACT\_SITE 249 249 SUBSTRATE (THIOSULFATE) BINDING (BY SIMILARITY).

FT ACT\_SITE 249 249 (BY SIMILARITY).

SO SEQUENCE 296 AA; 33205 MW; 8811022BF9BAD666 CRC64;

Query Match 87.9%; Score 29; DB 1; Length 296;  
Best Local Similarity 100.0%; Pred. No. 99;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASW 5  
| | | | |  
Db 31 LDASW 35

RESULT 14

THTR\_HUMAN STANDARD; PRT; 296 AA.

AC Q16762; 15-JUL-1998 (Rel. 36, Created)

DT 15-JUL-1998 (Rel. 36, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Thiosulfate sulfurtransferase (EC 2.8.1.1) (Rhodanese).

GN TST.

OS Homo sapiens (human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

ON NCBI\_TaxID=9606; [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Fetal liver;

RX MEDLINE=97223398; PubMed=9070219;

RA Alta N., Ishii K., Akamatsu Y., Ogasawara Y., Tanabe S.;

RT Cloning and expression of human liver rhodanese cDNA.;

RL Biochem. Biophys. Res. Commun. 231:56-60(1997).

RP SEQUENCE FROM N.A.

RX MEDLINE=20057165; PubMed=10591208;

RA Dunham I., Hunt A.R., Collins J.E., Bruskiewicz R., Beare D.M.,

RA Clamp M., Smink L.J., Alnough R., Almeida J.P., Babbage A.K.,

RA Baguley C., Bailey J., Barlow K.F., Bates K.N., Bessley O.P.,

RA Bird C.P., Blakey S.E., Bridgman A.M., Buck D., Burgess J.,

RA Burdill M.D., Burton J., Carter C., Carter N.P., Chen Y., Clark G.,

RA Clegg S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R.,

RA Conroy D., Corry N.R., Coville G.J., Cox A.V., Davis J., Dawson E.,

RA Dhami P.D., Dockree C., Dodsworth S.J., Durbin R.M., Ellington A.G.,

RA Evans K.L., Fey J.M., Fleming K., French L., Garner A.A.,

RA Gilbert J.G.R., Goward M.E., Graham D.V., Griffiths M.N.D., Hall C.,

RA Hall R.E., Hall-Tamlyn G., Heathcote R.W., Ho S., Holmes S.,

RA Laird S.E., Jones M.C., Kershaw J., Kimberley A.M., King A.,

RA Laird G.K., Langford C.F., Leverisha M.A., Lloyd C., Lloyd D.M.,

RA Martin J.D., Mashreghi-Mohammadi M., Matthews L.H., Mccann O.T.,

RA McClay J., McLaren R., McMurray A.A., Milne S.A., Mortimore B.J.,

RA Ocell C.N., Pavitt R., Pearce A.V., Pearson D., Phillimore B.J.C.T.,

RA Phillips S.H., Plumb R.W., Ramsay H., Ramsey Y., Rogers L., Ross M.T.,

RA Scott C.E., Sehra H.K., Skuce C.D., Smalley S., Smith M.L.,

RA Soderlund C., Spragon L., Steward C.A., Sulston J.E., Swann R.M.,

RA Vaudin M., Wall M., Wallis J.M., Whiteley M.N., Willey D.L.,

RA Williams L., Williams S.A., Williamson H., Wilmer T.E., Wilming L.,

RA Wright C.L., Hubbard T., Bentley D.R., Beck S., Rogers J., Shmizu N.,

RA Minoshima S., Kawasaki K., Sasaki T., Asakawa S., Kudoh J.,

RA Shintani A., Shibuya K., Yoshizaki Y., Aoki N., Mitsuana S.,

RA Roe B.A., Chen F., Chu L., Crabtree J., Deschamps S., Do A., Do T.,

RA Dorman A., Fang F., Fu Y., Hu P., Hua A., Kenton S., Lai H., Lao H.I.,

RA Lewis J., Lewis S., Lin S.-P., Loh P., Malaj E., Nguyen T., Pan H.,

RA Phan S., Qi S., Qian Y., Ray L., Ren Q., Shaull S., Sloan D., Song L.,

RA Wang Q., Wang Y., Wang Z., White J., Williamson D., Wu H., Yao Z.,

RA Zhan M., Zhang G., Chissoe S., Murray J., Miller N., Minx P.,

RA Fulton R., Johnson D., Bemis G., Bentley D., Bradshaw H., Bourne S.,

RA Cordes M., Du Z., Fulton L., Goela D., Graves T., Hawkins J.,

RA Hinds K., Kemp K., Latreille P., Layman D., Oerter P., Roffing T.,

RA Schuet P., Walker C., Wamsley A., Wohlmann P., Pepin K., Nelson J.,

RA Kori I., Bedell J.A., Hillier L., Mardis E., Waterston R., Wilson R.,

RA Emanuel B.S., Shaikh T., Kuraishi H., Salta S., Budarf M.L.,

RA Mcdermid H.E., Johnson A., Wong A.C.C., Morrow B.E., Edelman L.,

RA Kim U.J., Shizuya H., Simon M.I., Dumanski J.P., Peyrard M., Kedra D.,

RA Seroussi E., Franssen I., Tapia I., Bruder C.E., O'Brien K.P.,

RA Malkinson P., Bodentelch A., Hartman K., Hu X., Khan A.S., Lane L.,

RA Tlathun Y., Wright H.;

RT "The DNA sequence of human chromosome 22.;"

RL Nature 402:489-495(1999).

RP SEQUENCE FROM N.A.

RC TISSUE=uterus;

RA Strausberg R.;

RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: FORMATION OF IRON-SULFUR COMPLEXES. CYANIDE

CC DETOXIFICATION OR MODIFICATION OF SULFUR-CONTAINING ENZYMES.

CC OTHER THIOL COMPOUNDS. BESIDES CYANIDE. CAN ACT AS SULFUR ION

CC ACCEPTORS. ALSO HAS WEAK MERCAPTOPROPYLATE SULFURTRANSFERASE (NST)

CC ACTIVITY (BY SIMILARITY).

CC -1- CATALYTIC ACTIVITY: Thiosulfate + cyanide = sulfite + thiocyanate.

CC -1- SUBUNIT: MONOMER.

CC -1- SUBCELLULAR LOCATION: Mitochondrial matrix.

CC -1- DOMAIN: THE STRUCTURE CONSISTS OF 2 DOMAINS OF VERY SIMILAR

CC CONFORMATION, SUGGESTING A COMMON EVOLUTIONARY ORIGIN. HOWEVER,

CC THE SEQUENCES OF THE 2 DOMAINS ARE VERY DIFFERENT.

CC -----

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CC -----

DR EMBL: D87292; BAAL3327.1; -

DR EMBL: Z73420; CAA97762.1; -

DR EMBL: BC010148; AAH10148.1; -

DR HSSP: P00586; IRHS.

DR Genew: HGNC:12388; TST.

DR MIM: 180370; -

DR InterPro: IPR001763; Rhodanese-like.

DR InterPro: IPR001307; Rhodanese.

DR Pfam: PF00581; Rhodanese; 2.

DR SMART: SM00450; RHOD; 2.

DR PROSITE: PS00380; RHODANESE\_1; 1.

DR PROSITE: PS00683; RHODANESE\_2; 1.

KW Transferase; Mitochondrion.

FT INIT\_MET 0 0 BY SIMILARITY.

FT DOMAIN 1 142 A DOMAIN.

FT DOMAIN 143 158 HINGE.

FT DOMAIN 159 296 B DOMAIN.

FT ACT\_SITE 186 186 MAY PLAY A ROLE IN SUBSTRATE BINDING (BY SIMILARITY).

FT ACT\_SITE 247 247 BY SIMILARITY.

FT ACT\_SITE 248 248 SUBSTRATE (THIOSULFATE) BINDING

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FT ACT_SITE 249 249 (BY SIMILARITY).
FT SEQUENCE 296 AA: 33297 MW: 872C52008AE8DC5B CRC64;
SQ SEQUENCE 296 AA: 33297 MW: 872C52008AE8DC5B CRC64;

Query Match
Best Local Similarity 100.0%; Score 29; DB 1; Length 296;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASW 5
DB 31 LDASW 35

RESULT 15
THTR_MOUSE STANDARD; PRT; 296 AA.
AC P52196;
DT 01-OCT-1996 (Rel. 34, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Thiosulfate sulfurtransferase (EC 2.8.1.1) (Rhodanese).
GN TST.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C; TISSUE-Liver;
RX MEDLINE=96074596; PubMed=748186;
RA Dooley T.P., Nair S.K., Garcia R.E., Courtney B.C.;
RT "Mouse rhodanese gene (Tst): cDNA cloning, sequencing, and
RT recombinant protein expression."
RT Biochem. Biophys. Res. Commun. 216:1101-1109(1995).
CC -1- FUNCTION: FORMATION OF IRON-SULFUR COMPLEXES AND CYANIDE
CC DETOXIFICATION.
CC -1- CATALYTIC ACTIVITY: Thiosulfate + cyanide = sulfite + thiocyanate.
CC -1- SUBUNIT: MONOMER.
CC -1- SUBCELLULAR LOCATION: Mitochondrial matrix.
CC -1- TISSUE SPECIFICITY: FOUND IN NUMEROUS TISSUES.
CC -1- DOMAIN: THE STRUCTURE CONSISTS OF 2 DOMAINS OF VERY SIMILAR
CC CONFORMATION, SUGGESTING A COMMON EVOLUTIONARY ORIGIN. HOWEVER,
CC THE SEQUENCES OF THE 2 DOMAINS ARE VERY DIFFERENT.
CC -1- SIMILARITY: BELONGS TO THE RHODANESE FAMILY.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL: U35741; AAC52342.1; -.
CC DR HSSP: P00586; IRHS.
DR SWISS-2DPAGE: P52196; MOUSE.
DR MGD: MGI:96832; Tst.
DR InterPro: IPR001763; Rhodanese-1like.
DR InterPro: IPR001307; Rhodanese.
DR Pfam: PF00581; Rhodanese; 2.
DR SMART: SM00450; RHOD; 2.
DR PROSITE: PS00380; RHODANESE_1; 1.
DR PROSITE: PS00683; RHODANESE_2; 1.
DR Transferrase; Mitochondrion.
KW INIT_MET
FT DOMAIN 1 142 A DOMAIN.
FT DOMAIN 143 158 HINGE.
FT DOMAIN 159 296 B DOMAIN.
FT ACT_SITE 186 186 MAY PLAY A ROLE IN SUBSTRATE BINDING (BY
FT ACT_SITE 247 247 SIMILARITY).
FT ACT_SITE 248 248 SUBSTRATE (THIOSULFATE) BINDING

```

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FT ACT_SITE 249 249 (BY SIMILARITY).
FT SEQUENCE 296 AA: 33334 MW: 82089D880F9AE55A CRC64;
SQ SEQUENCE 296 AA: 33334 MW: 82089D880F9AE55A CRC64;

Query Match
Best Local Similarity 100.0%; Score 29; DB 1; Length 296;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASW 5
DB 31 LDASW 35

```

Search completed: May 30, 2003, 15:48:55  
 Job time : 4.11842 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 30, 2003, 14:32:12 ; Search time 6.03947 Seconds  
(without alignments)  
29.231 Million cell updates/sec

Title: US-09-643-260-10  
Perfect score: 33  
Sequence: 1 LDASWL 6

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA:\*  
1: /cgn2\_6/ptodata/1/1aa/5a\_COMB.pep:\*  
2: /cgn2\_6/ptodata/1/1aa/5b\_COMB.pep:\*  
3: /cgn2\_6/ptodata/1/1aa/6a\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/1aa/6b\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/PCUTUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/Backfilest1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30	90.9	919	4	US-08-985-916-16
2	30	90.9	935	4	US-09-271-438A-3
3	30	90.9	935	4	US-09-271-438A-8
4	29	87.9	136	4	US-09-370-838-123
5	28	84.8	210	4	US-08-611-587-4
6	28	84.8	219	4	US-09-247-373B-52
7	28	84.8	323	4	US-09-029-213B-25
8	28	84.8	523	4	US-09-323-195A-17
9	27	81.8	36	1	US-08-118-270-244
10	27	81.8	36	5	PCr-US93-08528-244
11	27	81.8	263	2	US-08-790-137-4
12	27	81.8	263	2	US-08-824-874-5
13	27	81.8	263	3	US-08-807-151-5
14	27	81.8	263	4	US-09-210-084-5
15	27	81.8	263	4	US-09-478-957-5
16	27	81.8	385	4	US-08-694-915-2
17	27	81.8	413	2	US-08-960-756-2
18	27	81.8	416	2	US-08-694-915-4
19	27	81.8	423	1	US-08-844-064-7
20	27	81.8	423	3	US-09-009-433-7
21	27	81.8	561	2	US-08-532-795-2
22	27	81.8	569	2	US-08-532-795-23
23	27	81.8	569	2	US-08-532-795-29
24	27	81.8	570	2	US-08-532-795-25
25	27	81.8	571	2	US-08-532-795-19
26	27	81.8	571	2	US-08-532-795-21
27	27	81.8	574	2	US-08-532-795-27

28	27	81.8	614	1	US-08-262-338A-4	Sequence 4, Appl1
29	27	81.8	614	1	US-08-460-114A-4	Sequence 4, Appl1
30	27	81.8	614	1	US-09-347-878-38	Sequence 38, Appl1
31	27	81.8	614	4	US-09-133-966A-4	GENERAL INFORMA
32	27	81.8	883	2	US-08-953-492-2	Sequence 2, Appl1
33	27	81.8	1015	2	US-08-374-483-4	Sequence 4, Appl1
34	27	81.8	1015	2	US-08-374-483-7	Sequence 7, Appl1
35	27	81.8	2089	1	US-08-418-893D-23	Sequence 23, Appl1
36	27	81.8	2089	1	US-08-418-893D-24	Sequence 24, Appl1
37	26	78.8	19	3	US-08-851-843A-185	Sequence 185, App
38	26	78.8	19	4	US-08-974-849A-304	Sequence 304, App
39	26	78.8	19	4	US-08-854-050-185	Sequence 185, App
40	26	78.8	19	4	US-09-430-323-185	Sequence 185, App
41	26	78.8	29	1	US-08-190-802A-256	Sequence 256, App
42	26	78.8	29	4	US-08-477-346-256	Sequence 256, App
43	26	78.8	29	4	US-08-473-089-256	Sequence 256, App
44	26	78.8	29	4	US-08-487-072A-256	Sequence 256, App
45	26	78.8	30	1	US-08-190-802A-217	Sequence 217, App

## ALIGNMENTS

```

RESULT 1
US-08-985-916-16
; Sequence 16, Application US/08985916
; Patent No. 6221636
GENERAL INFORMATION:
APPLICANT: ATSUSHI HAYAKAWA, MASAKAZU SUGIMOTO, YASUHIKO YOSHIHARA, AND TSUYOSH
TITLE OF INVENTION: METHOD FOR PRODUCING L-LYSINE
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESSES:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
CITY: ARLINGTON
COUNTRY: VA
ZIP: 22152
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,916
FILING DATE: 05-DEC-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 8-325658
FILING DATE: 05-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: NORMAN F. OBLON
REGISTRATION NUMBER: 24,618
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 919 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-985-916-16
Query Match 90.9%; Score 30; DB 4; Length 919;
Best Local Similarity 83.3%; Pred. No. 9.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 1 LDASWL 6
Db 105 LDATWL 110
RESULT 2

```

US-09-271-438A-3  
; Sequence 3, Application US/09271438A

; Patent No. 6331419

; GENERAL INFORMATION:

; APPLICANT: IZUI, Hiroshi

; APPLICANT: ONO, Eiji

; APPLICANT: MATSUI, Kazuhiko

; APPLICANT: MORIYA, Mika

; APPLICANT: ITO, Hisao

; APPLICANT: HARA, Yoshihiko

; TITLE OF INVENTION: L-GLUTAMIC ACID-PRODUCING BACTERIUM AND METHOD FOR PRODUCING L-GI

; FILE REFERENCE: 0010-0989-0

; CURRENT APPLICATION NUMBER: US/09/271,438A

; CURRENT FILING DATE: 1999-03-18

; PRIOR APPLICATION NUMBER: JP10-69068

; PRIOR FILING DATE: 1998-03-18

; PRIOR APPLICATION NUMBER: JP10-297129

; PRIOR FILING DATE: 1998-10-19

; NUMBER OF SEQ ID NOS: 15

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 3

; LENGTH: 935

; TYPE: PR

; ORGANISM: Enterobacter agglomerans

US-09-271-438A-3

Query Match 90.9%; Score 30; DB 4; Length 935;

Best Local Similarity 83.3%; Pred. No. 9.9e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6

DB 10 LDSSWL 15

RESULT 3  
US-09-271-438A-8

; Sequence 8, Application US/09271438A

; Patent No. 6331419

; GENERAL INFORMATION:

; APPLICANT: IZUI, Hiroshi

; APPLICANT: ONO, Eiji

; APPLICANT: MATSUI, Kazuhiko

; APPLICANT: MORIYA, Mika

; APPLICANT: ITO, Hisao

; APPLICANT: HARA, Yoshihiko

; TITLE OF INVENTION: L-GLUTAMIC ACID-PRODUCING BACTERIUM AND METHOD FOR PRODUCING L-GI

; FILE REFERENCE: 0010-0989-0

; CURRENT APPLICATION NUMBER: US/09/271,438A

; CURRENT FILING DATE: 1999-03-18

; PRIOR APPLICATION NUMBER: JP10-69068

; PRIOR FILING DATE: 1998-03-18

; PRIOR APPLICATION NUMBER: JP10-297129

; PRIOR FILING DATE: 1998-10-19

; NUMBER OF SEQ ID NOS: 15

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 8

; LENGTH: 935

; TYPE: PR

; ORGANISM: Enterobacter agglomerans

US-09-271-438A-8

Query Match 90.9%; Score 30; DB 4; Length 935;

Best Local Similarity 83.3%; Pred. No. 9.9e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6

DB 10 LDSSWL 15

RESULT 4  
US-09-370-838-123

; Sequence 123, Application US/09370838

; Patent No. 6444425

; GENERAL INFORMATION:

; APPLICANT: Reed, Steven G.

; APPLICANT: Lodes, Michael J.

; APPLICANT: Nohamath, Roadch

; APPLICANT: Secrist, Heather

; TITLE OF INVENTION: COMPOUNDS FOR THERAPY AND DIAGNOSIS OF

; FILE REFERENCE: 210121.475C1

; CURRENT APPLICATION NUMBER: US/09/370,838

; CURRENT FILING DATE: 1999-08-09

; EARLIER APPLICATION NUMBER: US 09/285,323

; EARLIER FILING DATE: 1999-04-02

; NUMBER OF SEQ ID NOS: 289

; SOFTWARE: FastSeq for Windows version 3.0

; SEQ ID NO 123

; LENGTH: 136

; TYPE: PR

; ORGANISM: Homo sapien

US-09-370-838-123

Query Match 87.9%; Score 29; DB 4; Length 136;

Best Local Similarity 100.0%; Pred. No. 2.2e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASW 5

DB 32 LDASW 36

RESULT 5  
US-08-611-587-4

; Sequence 4, Application US/08611587

; Patent No. 6150091

; GENERAL INFORMATION:

; APPLICANT: PANDOLFO, MASSIMO

; APPLICANT: MONTERMINI, LAURA

; APPLICANT: MOLTO, MARIA D.

; APPLICANT: Koenig, Michael

; APPLICANT: Campuzano, Victoria

; TITLE OF INVENTION: Direct Diagnosis of Friedreich Ataxia

; NUMBER OF SEQUENCES: 33

; CORRESPONDENCE ADDRESS:

; ADDRESS: Fulbright & Jaworski L.L.P. Patent Dept.

; STREET: 1301 McKinney, Suite 5100

; CITY: Houston

; STATE: Texas

; COUNTRY: U.S.

; ZIP: 77010

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/611,587

; FILING DATE: 03-MAR-1996

; CLASSIFICATION: 436

; ATTORNEY/AGENT INFORMATION:

; NAME: Brashers-Macatee, Sarah J.

; REGISTRATION NUMBER: 38,087

; REFERENCE/DOCKET NUMBER: D-5901

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 713-651-5246

; TELEFAX: 713-651-5246

; TELEFAX: 76-2829

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 210 amino acids

TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHEICAL: NO  
ANTI-SENSE: NO  
POSITION IN GENOME:  
UNITS: bp  
US-08-611-587-4

Query Match 84.8%; Score 28; DB 4; Length 210;  
Best Local Similarity 83.3%; Pred. No. 5.1e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LDASWL 6  
11111  
Db 198 LDLSWL 203

RESULT 6  
US-09-247-373B-52  
; Sequence 52, Application US/09247373B  
; Patent No. 6168954  
; GENERAL INFORMATION:  
; APPLICANT: MCGONIGLE, BRIAN  
; APPLICANT: O'KEEFE, DANIEL  
; TITLE OF INVENTION: SOYBEAN GLUTATHIONE-S-TRANSFERASE ENZYMES  
; FILE REFERENCE: CL-1108-A  
; CURRENT APPLICATION NUMBER: US/09/247,373B  
; CURRENT FILING DATE: 1999-02-10  
; PRIOR APPLICATION NUMBER: 08/924,747  
; PRIOR FILING DATE: 1997-09-05  
; NUMBER OF SEQ ID NOS: 56  
; SOFTWARE: Microsoft Office 97  
; SEQ ID NO 52  
; LENGTH: 219  
; TYPE: PRT  
; ORGANISM: SOYBEAN  
US-09-247-373B-52

Query Match 84.8%; Score 28; DB 4; Length 219;  
Best Local Similarity 66.7%; Pred. No. 5.3e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6  
11111  
Db 102 LDASWL 107

RESULT 7  
US-09-029-213B-25  
; Sequence 25, Application US/09029213B  
; Patent No. 6180098  
; GENERAL INFORMATION:  
; APPLICANT: CHRISTIAN, Peter D.  
; TITLE OF INVENTION: RECOMBINANT HELICOVERA BACULOVIRUSES  
; NUMBER OF SEQUENCES: 27  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: McDermott, Will & Emery  
; STREET: 600 13th Street, NW  
; CITY: Washington  
; STATE: District of Columbia  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/029,213B  
; FILING DATE: 31-AUG-1998

CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
; NAME: Joseph Hyosuk Kim  
; REGISTRATION NUMBER: 41,425  
; REFERENCE/DOCKET NUMBER: 50179-048  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-756-8000  
; TELEFAX: 202-756-8087  
; INFORMATION FOR SEQ ID NO: 25:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 323 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-029-213B-25

Query Match 84.8%; Score 28; DB 4; Length 323;  
Best Local Similarity 66.7%; Pred. No. 7.7e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6  
11111  
Db 191 LDSSWI 196

RESULT 8  
US-09-323-195A-17  
; Sequence 17, Application US/09323195A  
; Patent No. 6462257  
; GENERAL INFORMATION:  
; APPLICANT: Pullman, Gerald  
; APPLICANT: Cairney, John  
; APPLICANT: Pereira, Ranjan  
; TITLE OF INVENTION: VICILIN-LIKE SEED STORAGE PROTEIN GENE PROMOTER AND  
; TITLE OF INVENTION: METHODS OF USING THE SAME  
; FILE REFERENCE: IPST0009  
; CURRENT APPLICATION NUMBER: US/09/323,195A  
; CURRENT FILING DATE: 1999-06-01  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 17  
; LENGTH: 523  
; TYPE: PRT  
; ORGANISM: Pinus taeda  
US-09-323-195A-17

Query Match 84.8%; Score 28; DB 4; Length 523;  
Best Local Similarity 66.7%; Pred. No. 1.2e+03;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6  
11111  
Db 111 LDATWI 116

RESULT 9  
US-08-118-270-244  
; Sequence 244, Application US/08118270  
; Patent No. 5508384  
; GENERAL INFORMATION:  
; APPLICANT: Murphy, Randall B.  
; APPLICANT: Schuster, David I.  
; TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN  
; TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF  
; NUMBER OF SEQUENCES: 348  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEWMARK  
; STREET: 419 Seventh Street, N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/118,270  
FILING DATE: 09-SEP-1993  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 07/943,236  
FILING DATE: 10-SEP-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Townsend, Kevin G.  
REGISTRATION NUMBER: 34,033  
REFERENCE/DOCKET NUMBER: MURPHY-2A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
TELEX: 248633  
INFORMATION FOR SEQ ID NO: 244:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-118-270-244

Query Match 81.8%; Score 27; DB 1; Length 36;  
Best Local Similarity 66.7%; Pred. No. 1.3e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6  
111111  
DB 18 LDASWL 23

RESULT 10  
PCT-US93-08528-244  
Sequence 244, Application PC/RUS9308528  
GENERAL INFORMATION:  
APPLICANT: New York University  
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN  
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF  
NUMBER OF SEQUENCES: 348  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROWDY AND NEIMARK  
STREET: 419 Seventh Street, N.W., Suite 300  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/08528  
FILING DATE: 09-SEP-1993  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 07/943,236  
FILING DATE: 10-SEP-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Townsend, Kevin G.  
REGISTRATION NUMBER: 34,033  
REFERENCE/DOCKET NUMBER: MURPHY-2 PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
TELEX: 248633  
INFORMATION FOR SEQ ID NO: 244:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids

TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
PCT-US93-08528-244

Query Match 81.8%; Score 27; DB 5; Length 36;  
Best Local Similarity 66.7%; Pred. No. 1.3e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6  
111111  
DB 18 LDASWL 23

RESULT 11  
US-08-790-137-4  
Sequence 4, Application US/08790137  
Patent No. 5840871  
GENERAL INFORMATION:  
APPLICANT: Hillman, Jennifer L.  
TITLE OF INVENTION: A NOVEL PROSTATE-ASSOCIATED  
TITLE OF INVENTION: KALIKREIN  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/790,137  
FILING DATE: Filed Herewith  
CLASSIFICATION: 424  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J.  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0195 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-845-4166  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 263 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: GenBank  
CLONE: 55527  
US-08-790-137-4

Query Match 81.8%; Score 27; DB 2; Length 263;  
Best Local Similarity 66.7%; Pred. No. 9.3e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6  
111111  
DB 55 LDASWL 60

RESULT 12  
US-08-824-874-5

```

; Sequence 5, Application US/08824874
; Patent No. 5962300
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; TITLE OF INVENTION: NOVEL KALLIKREIN
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/824,874
; FILING DATE: Filed Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0252 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 263 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 55527
; US-08-824-874-5

Query Match      81.8%; Score 27; DB 2; Length 263;
Best Local Similarity 66.7%; Pred. No. 9.3e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 LDASWL 6
DB      55 LDANWV 60

RESULT 13
US-08-807-151-5
; Sequence 5, Application US/08807151
; Patent No. 6043033
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Lal, Preeti
; TITLE OF INVENTION: NOVEL HUMAN PROSTATE-ASSOCIATED
; TITLE OF INVENTION: PROTEASE
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: US
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/824,874
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0252 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 263 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 55527
; US-08-807-151-5

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; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/807,151
; FILING DATE: Filed Herewith
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0227 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 263 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 55527
; US-08-807-151-5

Query Match      81.8%; Score 27; DB 3; Length 263;
Best Local Similarity 66.7%; Pred. No. 9.3e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 LDASWL 6
DB      55 LDANWV 60

RESULT 14
US-09-210-084-5
; Sequence 5, Application US/09210084
; Patent No. 6197511
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; TITLE OF INVENTION: NOVEL KALLIKREIN
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/210,084
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/824,874
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0252 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 263 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 55527
; US-08-807-151-5

```

LENGTH: 263 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 IMMEDIATE SOURCE:  
 LIBRARY: GenBank  
 CLONE: 55527  
 US-09-210-084-5

Query Match 81.8%; Score 27; DB 4; Length 263;  
 Best Local Similarity 66.7%; Pred. No. 9.3e+02;  
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDASWL 6  
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 Db 55 LDANV 60

RESULT 15  
 US-09-478-957-5  
 ; Sequence 5, Application US/09478957  
 ; Patent No. 6350448  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bandman, Olga  
 ; TITLE OF INVENTION: NOVEL HUMAN PROSTATE-ASSOCIATED  
 ; TITLE OF INVENTION: PROTEASE  
 ; NUMBER OF SEQUENCES: 5  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
 ; STREET: 3174 Porter Drive  
 ; CITY: Palo Alto  
 ; STATE: CA  
 ; COUNTRY: US  
 ; ZIP: 94304  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: DOS  
 ; SOFTWARE: FASTSEQ Version 2.0  
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 ; APPLICATION NUMBER: US/09/478,957  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/807,151  
 ; FILING DATE:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Billings, Lucy J.  
 ; REGISTRATION NUMBER: 36,749  
 ; REFERENCE/DOCKET NUMBER: PF-0227 US  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 415-855-0555  
 ; TELEFAX: 415-845-4166  
 ; INFORMATION FOR SEQ ID NO: 5:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 263 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; IMMEDIATE SOURCE:  
 ; LIBRARY: GenBank  
 ; CLONE: 55527  
 ; US-09-478-957-5

Query Match 81.8%; Score 27; DB 4; Length 263;  
 Best Local Similarity 66.7%; Pred. No. 9.3e+02;  
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDASWL 6  
 |||:  
 Db 55 LDANV 60

Search completed: May 30, 2003, 14:41:27  
 Job time: 7.03947 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 30, 2003, 14:32:12 ; Search time 19.6974 Seconds  
(without alignments)  
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Title: US-09-643-260-10  
Perfect score: 33  
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Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues  
Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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22: /SID22/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:\*  
23: /SID22/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	33	100.0	6	23	ABB08732
2	33	100.0	6	23	AA048515
3	33	100.0	105	22	AA092524
4	33	100.0	756	23	ABB77295
5	31	93.9	618	21	AA032182
6	31	93.9	676	21	AA032181
7	31	93.9	763	21	AA032180
8	30	90.9	117	22	AB020551
9	30	90.9	119	21	AA042606
10	30	90.9	156	22	AA039336

11	30	90.9	189	22	AA039378	Human gene 39 enco
12	30	90.9	191	22	AA014439	Human novel prote
13	30	90.9	221	22	AA003119	Streptococcus pyog
14	30	90.9	221	23	AB027441	Streptococcus poly
15	30	90.9	261	21	AA053628	A bone marrow secr
16	30	90.9	261	21	AA052388	Human transmembran
17	30	90.9	277	22	AA014203	Human novel protei
18	30	90.9	431	22	AB020554	Human novel protei
19	30	90.9	919	11	AA005512	Phosphoenolpyruvat
20	30	90.9	919	17	AA055580	Bacterial phosphoe
21	30	90.9	919	19	AA068151	Phosphoenolpyruvat
22	30	90.9	919	20	AA029634	C glutamylum prote
23	30	90.9	919	22	AA03216	Corynebacterium g1
24	30	90.9	924	22	AA079297	Alpha-ketoglutarat
25	30	90.9	935	20	AA031987	Succinate dehydrog
26	30	90.9	935	22	AA000224	Human KRPI tryptic
27	29	87.9	12	23	AB061529	Human KRPI tryptic
28	29	87.9	90	22	AB002926	Human secreted pro
29	29	87.9	121	21	AA002267	Human immune/haema
30	29	87.9	122	22	AA089910	Human lung tumour
31	29	87.9	136	20	AA029543	Human lung tumour
32	29	87.9	136	21	AA044455	Human lung tumour
33	29	87.9	136	22	AA013796	Human lung tumour
34	29	87.9	146	22	AB025119	Novel human diagno
35	29	87.9	168	22	AB003169	Novel human diagno
36	29	87.9	183	23	AA022840	Human phospholipas
37	29	87.9	220	21	AA014119	Bordetella pertuss
38	29	87.9	256	23	AB091837	Hericicidally activ
39	29	87.9	297	22	AA078633	Human protein seq
40	29	87.9	305	22	AA036889	Staphylococcus aur
41	29	87.9	306	22	AA079617	Thiosulphate sulph
42	29	87.9	307	21	AA082729	Novel human diagno
43	29	87.9	314	22	AB029631	Novel human diagno
44	29	87.9	317	22	AA092257	C glutamylum prote
45	29	87.9	317	22	AB030210	Novel human diagno

## ALIGNMENTS

RESULT 1	ABB08732	standard; peptide: 6 AA.
ID	ABB08732	
XX	ABB08732:	
AC	14-JUN-2002	(first entry)
XX		
DT		
XX		
DE	Mutated IKKbeta NEMO binding domain peptide SEQ ID NO 10.	
XX		
XX	IKKbeat: IKKalpha; NEMO; NEMO binding domain; NBD; NF-kappaB; NF-kB;	
KW	kinase activation; leukocyte; inflammation; E-selectin; osteoclast;	
KW	autoimmune disease; transplant rejection; osteoporosis; cancer;	
KW	Alzheimer's disease; viral; infection; asthma; anaphylaxis; psoriasis;	
KW	rheumatoid arthritis; Crohn's disease; multiple sclerosis; HIV;	
KW	corticosteroid; immunosuppression; antiinflammatory; immunosuppressive;	
KW	osteopathic; cytoskeletal; nootropic; neuroprotective; anti-HIV; human;	
KW	antiarteriosclerotic; virucide; antiaesthetic; antiallergic;	
KW	dermatological; antibacterial; antiparasitic; antineoplastic;	
KW	antiarthritic; osteopathic; antiuicer; mutant; muten.	
XX		
OS	Homo sapiens.	
XX	Synthetic.	
XX		
FT	Key	Location/Qualifiers
FT	Misc-difference 3	/note="Wildtype Trp substituted by Ala"
XX		
XX	WC00183547-A2.	
XX		
XX	08-NOV-2001.	
PD		
XX		
XX		
PF	02-MAY-2001; 2001MO-US40654.	

XX 02-MAY-2000; 2000US-201261P.  
PR 22-AUG-2000; 2000US-0643260.  
XX (UYVA ) UNIV YALE.  
XX May MJ, Ghosh S;  
PI WPI; 2002-179350/23.  
DR  
XX Modulating NF-kappaB induction in a cell, useful for treating e.g.  
PT inflammatory disorders, osteoporosis and cancer, comprises contacting a  
PT cell with an anti-inflammatory compound comprising at least one NEMO  
PT binding domain -  
XX  
XX Claim 23; Page 44; 82pp; English.  
PS  
XX  
XX The invention relates to modulating NF-kappaB (NF-KB) induction in a cell  
CC comprises contacting a cell with an anti-inflammatory compound  
CC (ABB08725-ABB08742) comprising at least one NEMO binding domain  
CC (ABB7713). The compound has acts through selective inhibition of  
CC cytokine-mediated NF-kB activation by blocking the interaction of NEMO  
CC with IKBeta at the NEMO binding domain. Blockage of IKBeta-NEMO  
CC interaction results in inhibition of IKBeta kinase activation and  
CC subsequent decreased phosphorylation of Ikbppa. The compound may also  
CC act (directly or indirectly) by blocking the recruitment of leukocytes  
CC into sites of acute and chronic inflammation, by down-regulating the  
CC expression of E-selectin on leukocytes or by blocking osteoclast  
CC differentiation. The compound is useful in treating NF-kB mediated  
CC conditions, where the condition is an inflammatory disorder, an  
CC autoimmune disease, transplant rejection, osteoporosis, cancer,  
CC Alzheimer's disease, atherosclerosis, a viral infection or ataxia  
CC telangiectasia. The inflammatory disorder is asthma, allergies,  
CC urticaria, anaphylaxis, cutaneous inflammation, sepsis, psoriasis,  
CC rheumatoid arthritis, osteoarthritis, psoriatic arthritis, inflammatory  
CC bowel disease, chronic obstructive pulmonary disease, vasculitis and  
CC bursitis. The inflammatory disorder may also be dermatitis, eczema,  
CC psoriasis, osteoarthritis, psoriatic arthritis, lupus and  
CC sporidylarthritis. Also for Crohn's disease, ulcerative colitis,  
CC polymyalgia, scleroderma, Wegner's granulomatosis, temporal arteritis,  
CC cryoglobulinemia or multiple sclerosis. For chronic viral infections  
CC caused by Epstein-Barr, cytomegalovirus or herpes simplex. Other viral  
CC diseases include HIV and influenza. The compound may also be useful for  
CC treating anaphylaxis, drug and food sensitivity, contact dermatitis,  
CC sunburn or aging. The compound may be used to replace corticosteroids in  
CC any application in which corticosteroids are used, including  
CC immunosuppression in transplants and cancer therapy. Also for identifying  
CC anti-inflammatory compounds and for diagnosis of an inflammatory disorder.  
CC The compound may be administered alone or in combination with other known  
CC anti-inflammatory agents. The present sequence is that of a mutated NEMO  
CC binding domain of IKBeta.  
XX  
SQ Sequence 6 AA;  
Query Match 100.0%; Score 33; DB 23; Length 6;  
Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 2  
AAM48515  
ID AAM48515 standard; Peptide: 6 AA.  
XX  
AC AAM48515;  
XX  
DT 20-MAR-2002 (first entry)  
XX  
DE NBD mutant peptide SEQ ID NO 10.  
XX

KW Anti-inflammatory; antiasthmatic; cytostatic; antipsoriatic; neutrophic;  
KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;  
KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;  
KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;  
KW cytokine; NFkappaB; Ikbppa kinase beta; IKBeta; cancer; psoriasis;  
KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
KW autoimmune disorder; multiple sclerosis; transplant rejection;  
KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.  
XX  
OS Synthetic.  
XX  
PN WO200183554-A2.  
XX  
PD 08-NOV-2001.  
XX  
PF 02-MAY-2001; 2001MO-US14346.  
XX  
PR 02-MAY-2000; 2000US-201261P.  
XX 22-AUG-2000; 2000US-0643260.  
XX (PRAE-) PRAECIS PHARM INC.  
XX (UYVA ) UNIV YALE.  
XX  
PI May MJ, Ghosh S, Findeis MA, Phillips K;  
XX WPI; 2002-121889/16.  
DR  
XX Novel anti-inflammatory compound comprising membrane translocation  
PT domain fused to NEMO binding sequence, useful for blocking nuclear  
PT factor kappaB activation, and for treating asthma, lung inflammation,  
PT psoriasis -  
XX  
XX Example 6; Page 47; 88pp; English.  
PS  
XX The invention relates to an anti-inflammatory compound (especially  
CC AAM48628-AAM48645), comprising a membrane translocation domain  
CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15  
CC amino acid residues, fused to a NEMO binding sequence  
CC (AAM48525-AAM48619). The anti-inflammatory compounds have antiasthmatic,  
CC cytostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,  
CC antibacterial, immunosuppressive, dermatological, neuroprotective,  
CC neutrophic, antiatherosclerotic, virucide and antiallergic activity. The  
CC compounds act as selective inhibitors of cytokine-mediated NFkappaB  
CC activation by blocking interaction of Ikbppa kinase beta (IKBbeta) at  
CC the NEMO binding domain that results in inhibition of IKBeta kinase  
CC activation and subsequent decreased phosphorylation of Ikbppa. The  
CC compounds are useful for treating inflammatory disorders, e.g. asthma,  
CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,  
CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,  
CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,  
CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;  
CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia  
CC telangiectasia. The compounds are also useful for treating  
CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,  
CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and  
CC arthritis.  
XX  
SQ Sequence 6 AA;  
Query Match 100.0%; Score 33; DB 23; Length 6;  
Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 3  
AAG92524  
ID AAG92524 standard; Protein: 105 AA.  
XX

AC AAG2524;  
 XX 26-SEP-2001 (first entry)  
 XX C glutamicum protein fragment SEQ ID NO: 6278.  
 DE Coryneform bacterium; amino acid synthesis; vitamin; saccharide;  
 XX organic synthesis.  
 XX Corynebacterium glutamicum.  
 XX EP1108790-A2.  
 XX 20-JUN-2001.  
 XX 18-DEC-2000; 2000EP-0127688.  
 XX 16-DEC-1999; 99JP-0377484.  
 XX 07-APR-2000; 2000JP-0159162.  
 XX 03-AUG-2000; 2000JP-0280988.  
 XX (KYOWA) KYOWA HAKKO KOGYO KK.  
 XX Nakagawa S, Mizoguchi H, Ando S, Hayashi M, Ochiai K, Yokoi H;  
 PI Tateishi N, Senoh A, Ikeda M, Ozaki A;  
 XX WPI; 2001-376931/40.  
 DR N-PSDB; AAH67743.  
 XX Novel polynucleotides derived from Coryneform bacteria, for identifying  
 PT mutation point of a gene, measuring expression of a gene, analysing  
 PT expression profile or pattern of a gene and identifying homologous gene  
 XX  
 PS Claim 17; SEQ ID NO: 6278; 246bp + Sequence Listing; English.  
 CC The present invention provides a number of nucleotide and protein  
 CC sequences from the Coryneform bacterium Corynebacterium glutamicum. These  
 CC are useful for identifying the mutation point of a gene derived from a  
 CC mutant of coryneform bacterium, measuring expression amount and  
 CC analysing the expression profile or expression pattern of a gene derived  
 CC from Coryneform bacterium, and identifying a homologue of a gene derived  
 CC from coryneform bacterium. Coryneform bacteria are useful for producing  
 CC amino acids, nucleic acids, vitamins, saccharides and organic acids,  
 CC particularly L-lysine. The present sequence is a protein described  
 CC in the exemplification of the invention.  
 CC Note: The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from the  
 CC European Patent Office.  
 CC  
 SQ Sequence 105 AA;  
 Query Match 100.0%; Score 33; DB 22; Length 105;  
 Best Local Similarity 100.0%; Pred. No. 81;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LDASWL 6  
 Db 48 LDASWL 53  
 RESULT 4  
 ABB77295  
 ID ABB77295 standard; protein; 756 AA.  
 AC ABB77295;  
 XX 14-JUN-2002 (first entry)  
 XX Human IKKbeta mutant W739A.  
 DE Human IKKbeta mutant W739A.  
 XX IKKbeta; IKKalpha; NEMO; NEMO binding domain; NBD; NF-kappaB; NF-kB;  
 KM kinase activation; leukocyte; inflammation; E-selectin; osteoclast;

KW autoimmune disease; transplant rejection; osteoporosis; cancer;  
 KW Alzheimer's disease; viral infection; asthma; anaphylaxis; psoriasis;  
 KW rheumatoid arthritis; Crohn's disease; multiple sclerosis; HIV;  
 KW corticosteroid; immunosuppression; antiinflammatory; immunosuppressive;  
 KW osteopathic; cytostatic; nootropic; neuroprotective; anti-HIV; human;  
 KW antiarteriosclerotic; virucide; antiparasitic; antiallergic;  
 KW dermatological; antibacterial; antipsoriatic; antineoplastic;  
 KW antiarthritic; osteopathic; antitumor; mutant; mutein.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 XX Key Location/Qualifiers  
 FH MISC-difference 739 /note="Wildtype Trp substituted by Ala"  
 FT  
 FT  
 XX WO200183547-A2.  
 XX 08-NOV-2001.  
 XX 02-MAY-2001; 2001WO-US40654.  
 XX 02-MAY-2000; 2000US-201261P.  
 XX 22-AUG-2000; 2000US-0643260.  
 XX (UYVA) UNIV YALE.  
 XX May MJ, Ghosh S;  
 XX WPI; 2002-179350/23.  
 DR Modulating NF-kappaB induction in a cell, useful for treating e.g.  
 XX inflammatory disorders, osteoporosis and cancer, comprises contacting a  
 PT cell with an anti-inflammatory compound comprising at least one NEMO  
 PT binding domain  
 PT  
 PS  
 XX  
 PS Example 11; Page -; 82pp; English.  
 CC The invention relates to modulating NF-kappaB (NF-kB) induction in a cell  
 CC comprises contacting a cell with an anti-inflammatory compound  
 CC (ABB08725-ABB08742) comprising at least one NEMO binding domain  
 CC (ABB77313). The compound has acts through selective inhibition of  
 CC cytokine-mediated NF-kB activation by blocking the interaction of NEMO  
 CC with IKKbeta at the NEMO binding domain. Blockage of IKKbeta-NEMO  
 CC interaction results in inhibition of IKKbeta kinase activation and  
 CC subsequent decreased phosphorylation of Ikbapab. The compound may also  
 CC act (directly or indirectly) by blocking the recruitment of leukocytes  
 CC into sites of acute and chronic inflammation, by down-regulating the  
 CC expression of E-selectin on leukocytes or by blocking osteoclast  
 CC differentiation. The compound is useful in treating NF-kB mediated  
 CC conditions, where the condition is an inflammatory disorder, an  
 CC autoimmune disease, transplant rejection, osteoporosis, cancer,  
 CC Alzheimer's disease, atherosclerosis, a viral infection or ataxia  
 CC telangiectasia. The inflammatory disorder is asthma, allergies,  
 CC urticaria, anaphylaxis, cutaneous inflammation, sepsis, psoriasis,  
 CC rheumatoid arthritis, osteoarthritis, psoriatic arthritis, inflammatory  
 CC bowel disease, chronic obstructive pulmonary disease, vasculitis and  
 CC bursitis. The inflammatory disorder may also be dermatitis, eczema,  
 CC psoriasis, osteoarthritis, psoriatic arthritis, lupus and  
 CC spondylarthritis. Also for Crohn's disease, ulcerative colitis,  
 CC polymyalgia, scleroderma, Wegner's granulomatosis, temporal arteritis,  
 CC cryoglobulinaemia or multiple sclerosis. For chronic viral infections  
 CC caused by Epstein-Barr, cytomegalovirus or herpes simplex. Other viral  
 CC diseases include HIV and influenza. The compound may also be useful for  
 CC treating anaphylaxis, drug and food sensitivity, contact dermatitis,  
 CC sunburn or aging. The compound may be used to replace corticosteroids in  
 CC immunosuppression in transplants and cancer therapy. Also for identifying  
 CC antiinflammatory compounds and for diagnosis of an inflammatory disorder.  
 CC The compound may be administered alone or in combination with other known  
 CC anti-inflammatory agents. The present sequence is that of an IKKbeta  
 CC mutant, useful in examples of the invention.  
 CC Note: The present sequence is not given in the specification but is

CC derived from GenBank Accession No. 014920 (AB077294).  
XX Sequence 756 AA;  
Query Match 100.0%; Score 33; DB 23; Length 756;  
Best Local Similarity 100.0%; Pred. No. 6.6e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LDASWL 6  
DB 737 LDASWL 742  
RESULT 5  
AAG32182  
ID AAG32182 standard; Protein; 618 AA.  
XX AAG32182;  
AC  
XX 17-OCT-2000 (first entry)  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 38774.  
XX  
XX Protein identification; signal transduction pathway; metabolic pathway;  
KM hydridisation assay; genetic mapping; gene expression control; promoter;  
KM termination sequence.  
XX Arabidopsis thaliana.  
OS  
XX  
XX EPI033405-A2.  
PN  
XX  
XX 06-SEP-2000.  
PD  
XX  
XX 25-FEB-2000; 2000EP-0301439.  
PF  
XX  
XX 25-FEB-1999; 99US-0121825.  
PR 05-MAR-1999; 99US-0123180.  
PR 09-MAR-1999; 99US-0123548.  
PR 23-MAR-1999; 99US-0125788.  
PR 25-MAR-1999; 99US-0126264.  
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Query Match 93.3%; Score 31; DB 21; Length 618;  
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Query Match      93.9%; Score 31; DB 21; Length 763;
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XX ABG20551;
XX 18-FEB-2002 (first entry)
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KM food supplement; medical imaging; diagnostic; genetic disorder.
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XX Homo sapiens.
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XX WO200175067-A2.
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XX 23-AUG-2000; 2000US-0649167.
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XX (HYSE-) HYSEQ INC.
XX
XX Drmanac RT, Liu C, Tang YT;
XX
XX WPI; 2001-639362/73.
XX
XX N-PSDB; AAS84738.
XX
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity
XX
XX Claim 20; SEQ ID NO 50910; 103pp; English.
XX
XX The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human
CC diagnostic amino acid sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 117 AA:

```

```

Query Match      90.9%; Score 30; DB 22; Length 117;
Best Local Similarity 83.3%; Pred. No. 3.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

OY 1 LDASWL 6
DB 38 LDASWL 43

```

```

RESULT 9
AAB42606
ID AAB42606 standard; Protein; 119 AA.

```

```

XX AAB42606;
XX 08-FEB-2001 (first entry)
XX
XX Human ORFX ORF2370 polypeptide sequence SEQ ID NO:4740.
XX

```

KW Human: open reading frame: ORFX; detection: cytostatic; hepatotropic;  
 KW vulnery; antipsoriatic; antiparkinsonian; neurotropic; neuroprotective;  
 KW anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant;  
 KW immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;  
 KW hypotensive; dermatological; immunosuppressive; antiinflammatory;  
 KW antiviral; antibacterial; antifungal; antirheumatic; antithyroid;  
 KW antianaemic; gene therapy; cancer; proliferative disorder; hypertension;  
 KW neurodegenerative disorder; osteoarthritis; graft vs host disease;  
 KW cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;  
 KW cholesterol ester storage; systemic lupus erythematosus; infection;  
 KW severe combined immunodeficiency; malaria; autoimmune disorder; asthma;  
 KW allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;  
 KW bone damage; cartilage damage; antiinflammatory disease; coagulation;  
 KW thrombosis; contraceptive.  
 OS Homo sapiens.  
 XX W0200058473-A2.  
 XX 05-OCT-2000.  
 XX 31-MAR-2000; 2000WO-US08621.  
 XX 31-MAR-1999; 99US-0127607.  
 XX 02-APR-1999; 99US-0127636.  
 XX 05-APR-1999; 99US-0127728.  
 XX 30-MAR-2000; 2000US-0540763.  
 XX (CURA-) CURAGEN CORP.  
 XX Shinkets RA, Leach M;  
 XX WPI; 2000-602362/57.  
 XX N-PSDB; AAC76815.  
 XX Novel nucleic acids and peptides derived from open reading frame X,  
 XX useful for treating e.g. cancers, proliferative disorders,  
 XX neurodegenerative disorders and cardiovascular disease -  
 XX Claim 11: Page 3920; 5507pp; English.  
 XX AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,  
 XX which represent the human ORFX open reading frames 1 to 3161. The ORFX  
 XX sequences have activities such as: cytostatic; hepatotropic; vulnery;  
 XX antipsoriatic; antiparkinsonian; neurotropic; neuroprotective;  
 XX osteopathic; anticonvulsant; antiarthritic; immunosuppressant;  
 XX immunostimulant; cardiant; thrombolytic; coagulant; vasotropic;  
 XX antidiabetic; hypotensive; dermatological; immunosuppressive;  
 XX antiinflammatory; antibacterial; antiviral; antifungal; antirheumatic;  
 XX antithyroid; and antianaemic. The sequences can be used for determining  
 XX the presence of or predisposition to, or preventing or treating  
 XX pathological conditions associated with an ORFX-associated disorder. The  
 XX nucleic acids can be used to express ORFX proteins in gene therapy. The  
 XX vectors. The proteins and nucleic acids may be used to treat cancers,  
 XX proliferative disorders, neurodegenerative disorders, osteoarthritis,  
 XX graft vs host disease, cardiovascular disease, diabetes mellitus,  
 XX hypertension, hypothyroidism, cholesterol ester storage, systemic lupus  
 XX erythematosus, severe combined immunodeficiency (SCID), AIDS, viral,  
 XX bacterial or fungal infection, malaria, autoimmune disorders, asthma,  
 XX allergies, aplastic anaemia, burns, wounds, bone and cartilage damage,  
 XX nocturnal haemoglobinuria, antiinflammatory disease; to enhance  
 XX coagulation; to inhibit thrombosis; and as a contraceptive.  
 XX Sequence 119 AA;  
 QY Query Match 90.9%; Score 30; DB 21; Length 119;  
 Db Best Local Similarity 83.3%; Pred. NO. 3.3e+00; Indels 0; Gaps 0;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RESULT 10  
 AAE03936  
 ID AAE03936 standard; Protein: 156 AA.  
 XX  
 AC AAE03936;  
 XX  
 DT 09-AUG-2001 (first entry)  
 XX  
 DE Human gene 39 encoded secreted protein HBMD08, SPQ ID NO:99.  
 XX  
 KW Human: secreted protein; proliferative disorder; cancer; tumour;  
 KW foetal abnormality; developmental abnormality; haematopoietic disorder;  
 KW immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis;  
 KW inflammation; allergy; neurological disorder; Alzheimer's disease;  
 KW Parkinson's disease; cognitive disorder; schizophrenia; asthma;  
 KW skin disorder; psoriasis; sepsis; diabetes; atherosclerosis;  
 KW cardiovascular disorder; angiotensin disorder; kidney disorder;  
 KW gastrointestinal disorder; pregnancy-related disorder;  
 KW endocrine disorder; infection; wound healing; vulnery;  
 KW cell culture; chemotaxis; food additive; gene therapy;  
 KW binding partner identification.  
 XX  
 OS Homo sapiens.  
 XX  
 XX Key Location/Qualifiers  
 XX Peptide 1..28  
 XX Protein 29..156  
 XX /note="Mature secreted protein"  
 XX W0200077022-A1.  
 XX 21-DEC-2000.  
 XX 01-JUN-2000; 2000WO-US15136.  
 XX 11-JUN-1999; 99US-0138629.  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 XX Rosen CA, Ruben SM, Komatsoulis GA;  
 XX WPI; 2001-367020/38.  
 XX N-PSDB; AAD08383.  
 XX  
 XX Nucleic acids encoding 50 human secreted polypeptides, useful for  
 XX preventing, diagnosing and/or treating diseases, e.g. Parkinson's  
 XX disease, botulism, cancers and Sclerular syndrome -  
 XX Claim 11: Page 547; 614pp; English.  
 XX AAD08345-AAD08394 represent cDNAs corresponding to 50 human secreted  
 XX protein genes and AAE03898-AAE03947 represent the proteins they encode.  
 XX AAE03948-AAE03996 represent human secreted protein fragments or variants.  
 XX The genes and their secreted proteins are useful for preventing,  
 XX treating or ameliorating medical conditions, e.g., by protein or gene  
 XX therapy. Pathological conditions can be diagnosed by determining the  
 XX amount of the new protein in a sample or by determining the presence of  
 XX mutations in the new genes. Specific uses are described for each of the  
 XX 50 genes, based on the tissues in which they are most highly expressed,  
 XX and include developing products for the diagnosis or treatment of  
 XX proliferative disorders, cancer, tumours, foetal and developmental  
 XX abnormalities, haematopoietic disorders, diseases of the immune system,  
 XX AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation,  
 XX allergies, neurological disorders (e.g., Alzheimer's disease,  
 XX Parkinson's disease), cognitive disorders, schizophrenia, asthma,  
 XX skin disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis,  
 XX cardiovascular disorders, angiotensin disorders, kidney disorders,  
 XX gastrointestinal disorders, pregnancy-related disorders, endocrine  
 XX disorders, and infections. The proteins can also be used to aid wound  
 XX healing and epithelial cell proliferation, to prevent skin aging due to  
 XX sunburn, to maintain organs before transplantation, for supporting cell

CC culture of primary tissues, to regenerate tissues, to identify their  
CC cognate ligands or binding partners, and in chemotaxis, and can be used  
CC as a food additive or preservative to modify storage properties.  
CC Antibodies specific for a protein of the invention can be used in  
CC alleviating symptoms associated with the disorders mentioned above, and  
CC in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked  
CC immunosorbent assay (ELISA). The present sequence represents a human  
CC secreted protein of the invention.  
XX  
SQ Sequence 156 AA:  
Query Match 90.9%; Score 30; DB 22; Length 156;  
Best Local Similarity 83.3%; Pred. No. 4.3e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
OY 1 LDASWL 6  
Db 56 LDASWV 61  
RESULT 11  
AAE03978  
ID AAE03978 standard; Protein; 189 AA.  
XX  
AC AAE03978;  
XX  
DT 09-AUG-2001 (first entry)  
XX  
DE Human gene 39 encoded secreted protein fragment, SEQ ID NO:172.  
XX  
KW Human: secreted protein; proliferative disorder; cancer; tumour;  
KW foetal abnormality; developmental abnormality; haematopoietic disorder;  
KW immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis;  
KW inflammation; allergy; neurological disorder; Alzheimer's disease;  
KW Parkinson's disease; cognitive disorder; schizophrenia; asthma;  
KW skin disorder; psoriasis; sepsis; diabetes; atherosclerosis;  
KW cardiovascular disorder; angiotensin disorder; kidney disorder;  
KW gastrointestinal disorder; pregnancy-related disorder;  
KW endocrine disorder; infection; wound healing; vulnery;  
KW cell culture; chemotaxis; food additive; gene therapy;  
KW binding partner identification.  
XX  
OS Homo sapiens.  
XX  
PN WO200077022-A1.  
XX  
PD 21-DEC-2000.  
XX  
PF 01-JUN-2000; 2000WO-US15136.  
XX  
PR 11-JUN-1999; 99US-0138629.  
XX  
PA (HDMA-) HDMA GENOME SCI INC.  
XX  
PI Rosen CA, Ruben SM, Komatsoulis GA;  
XX  
DR WPI; 2001-367020/38.  
XX  
PT Nucleic acids encoding 50 human secreted polypeptides, useful for  
XX preventing, diagnosing and/or treating diseases, e.g. Parkinson's  
XX disease, botulism, cancers and Schmitler syndrome -  
XX  
PS Disclosure; Page 593; 614pp; English.  
XX  
CC AAD08345-AAD08394 represent cDNAs corresponding to 50 human secreted  
CC protein genes and AAE03978-AAE03947 represent the proteins they encode.  
CC AAE03948-AAE03996 represent human secreted protein fragments or variants.  
CC The genes and their secreted proteins are useful for preventing,  
CC treating or ameliorating medical conditions, e.g., by protein or gene  
CC therapy. Pathological conditions can be diagnosed by determining the  
CC amount of the new protein in a sample or by determining the presence of  
CC mutations in the new genes. Specific uses are described for each of the  
CC 50 genes, based on the tissues in which they are most highly expressed,

CC and include developing products for the diagnosis or treatment of  
CC proliferative disorders, cancer, tumours, foetal and developmental  
CC abnormalities, haematopoietic disorders, diseases of the immune system,  
CC AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation,  
CC allergies, neurological disorders (e.g., Alzheimer's disease,  
CC Parkinson's disease), cognitive disorders, schizophrenia, asthma,  
CC skin disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis,  
CC cardiovascular disorders, angiogenic disorders, kidney disorders,  
CC gastrointestinal disorders, pregnancy-related disorders, endocrine  
CC disorders, and infections. The proteins can also be used to aid wound  
CC healing and epithelial cell proliferation, to prevent skin aging due to  
CC sunburn, to maintain organs before transplantation, for supporting cell  
CC culture of primary tissues, to regenerate tissues, to identify their  
CC cognate ligands or binding partners, and in chemotaxis, and can be used  
CC as a food additive or preservative to modify storage properties.  
CC Antibodies specific for a protein of the invention can be used in  
CC alleviating symptoms associated with the disorders mentioned above, and  
CC in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked  
CC immunosorbent assay (ELISA). The present sequence represents a human  
CC secreted protein fragment referred to in the disclosure of the invention.  
XX  
SQ Sequence 189 AA:  
Query Match 90.9%; Score 30; DB 22; Length 189;  
Best Local Similarity 83.3%; Pred. No. 5.3e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
OY 1 LDASWL 6  
Db 164 LDASWV 169  
RESULT 12  
AAU14439  
ID AAU14439 standard; Protein; 191 AA.  
XX  
AC AAU14439;  
XX  
DT 24-OCT-2001 (first entry)  
XX  
DE Human novel protein #310.  
XX  
KW Human: novel protein; antianaemic; osteopathic; antiinflammatory;  
KW immunomodulatory; cytostatic; neuroprotective; vulnery; nootropic;  
KW anticonvulsant; antiarthritic; cerebroprotective; antiviral;  
KW antibacterial; antiallergic; dermatological; haemostatic; antiasthmatic;  
KW thrombolytic; immunogen; antibody; gene therapy; neurological disorder;  
KW Parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis;  
KW tissue regeneration; immune disorder.  
XX  
OS Homo sapiens.  
XX  
PN WO200155437-A2.  
XX  
PD 02-AUG-2001.  
XX  
PF 25-JAN-2001; 2001WO-US02623.  
XX  
PR 25-JAN-2000; 2000US-0491404.  
XX  
PA (HYSE-) HYSE INC.  
XX  
PI Tang YT, Liu C, Drmanac RT;  
XX  
DR WPI; 2001-451939/48.  
XX  
DR N-PsDB; AAS22744.  
XX  
PT Isolated polypeptides useful for treating anti-inflammatory diseases,  
XX nervous system disorders, and for regenerating bone and cartilage -  
XX  
PS Example 4; Page 816; 894pp; English.  
XX  
CC The invention relates to polynucleotides encoding novel human

CC proteins or their active domains. The polypeptides, polynucleotides and  
 CC antibodies raised against the polypeptides are used in a method of  
 CC treatment of a mammal and prevention of disorders caused by the aberrant  
 CC protein expression or activity. The polypeptides can be used as  
 CC molecular weight markers, food supplements, and in antibody production.  
 CC The polypeptides are used to identify compounds which bind to the  
 CC polypeptides. Polynucleotides of the invention are used as probes and  
 CC primers, for sequencing, for chromosome or gene mapping, in the  
 CC production of recombinant proteins, and in generating anti-sense DNA or  
 CC RNA and in gene therapy. Polypeptides of the invention can be used to  
 CC target drugs to a tumour. In assays to determine biological activity, to  
 CC raise antibodies/elicit an immune response, to determine quantitative  
 CC protein levels, as tissue markers, and to isolate receptors or ligands.  
 CC Polypeptides of the invention may also be useful in treating platelet  
 CC disorders, stem cell disorders, regenerating bone, cartilage, tendon,  
 CC ligament and/or nerve tissue, wound healing, treating burns, promoting  
 CC the proliferation, differentiation and survival of stem cells, as a  
 CC contraceptive, treating osteoporosis and osteoarthritis, anaemia,  
 CC Alzheimer's, Parkinson's and Huntington's diseases, amyotrophic lateral  
 CC sclerosis, stroke, immune deficiencies resulting from bacterial, viral or  
 CC fungal infection or from autoimmunity, cancer, allergy, asthma,  
 CC graft-versus-host disease, eczema, haemophilia, thrombosis,  
 CC anti-inflammatory diseases, nervous system disorders, and infection.  
 CC The present sequence represents a protein of the invention.

CC  
 XX Sequence 191 AA;

Query Match  
 Best Local Similarity 83.3%; Score 30; DB 22; Length 191;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6  
 DB 161 LDASWL 166

RESULT 13

AAU03119 standard; Protein; 221 AA.

AC AAU03119;

DT 23-OCT-2001 (first entry)

DE Streptococcus pyogenes virulence protein #1.

XX Virulence; attenuated microorganism; Streptococcal infection;

KW Gram-positive bacteria; antimicrobial; impetigo; pneumonia.

OS Streptococcus pyogenes.

XX WO200148208-A2.

PD 05-JUL-2001.

PF 22-DEC-2000; 2000WO-GB04997.

XX 23-DEC-1999; 99GB-0030462.

PR 23-DEC-1999; 99GB-0030463.

PR 23-DEC-1999; 99GB-0030464.

PR 23-DEC-1999; 99GB-0030466.

PR 23-DEC-1999; 99GB-0030467.

PR 23-DEC-1999; 99GB-0030469.

PR 23-DEC-1999; 99GB-0030471.

PR 23-DEC-1999; 99GB-0030472.

PR 23-DEC-1999; 99GB-0030473.

PR 17-FEB-2000; 2000GB-0003725.

PR 17-FEB-2000; 2000GB-0003726.

PR 17-FEB-2000; 2000GB-0003727.

PR 17-FEB-2000; 2000GB-0003728.

PR 17-FEB-2000; 2000GB-0003729.

PR 17-FEB-2000; 2000GB-0003730.

PR 17-FEB-2000; 2000GB-0003731.

PR 17-FEB-2000; 2000GB-0003732.

PR 17-FEB-2000; 2000GB-0003733.

PR 02-MAY-2000; 2000GB-0010585.

PR 02-MAY-2000; 2000GB-0010587.

XX (MCCR-) MICROSCIENCE LTD.

XX Clarke EE, Zhou L, Shea JE, Feldman RG, Holden DW;

XX WPI: 2001-418285/44.

XX N-PSDB; AAS06351.

XX Novel peptide obtained from Streptococcus pyogenes useful for treating

XX or preventing a condition associated with infection by Streptococcal or

XX Gram-positive bacteria, preferably pneumonia

XX Claim 4; Page 26-27; 91pp; English.

XX AAU03119-AAU03149 represent novel Streptococcus pyogenes virulence

XX proteins #1-31. The S. pyogenes virulence genes can be used to

XX produce attenuated microorganisms comprising a mutation that disrupt

XX the expression of the virulence protein. The virulence genes, proteins

XX or an attenuated microorganism are useful for therapeutic or diagnostic

XX purposes. DNA encoding the virulence proteins, the proteins themselves,

XX an attenuated microorganism or a vaccine comprising the virulence

XX protein are useful for the manufacture of a medicament for use in

XX the treatment or prevention of a condition associated with infection,

XX by Streptococcal or Gram-positive bacteria, for veterinary treatment,

XX and in a screening assay for the identification of an antimicrobial

XX drug. Disorders which can be treated using S. pyogenes virulence

XX polynucleotide and polypeptide sequences include non-invasive infections

XX and invasive infections e.g. impetigo, pharyngitis, necrotising

XX fasciitis, bacteraemia, streptococcal toxic shock syndrome (STSS),

XX pneumonia and rheumatic fever. The virulence proteins are also useful

XX in the preparation of antibodies.

QY 1 LDASWL 6

DB 36 LDASWL 41

Query Match

Best Local Similarity 83.3%; Score 30; DB 22; Length 221;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6

DB 36 LDASWL 41

Query Match

Best Local Similarity 83.3%; Score 30; DB 22; Length 221;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6

DB 36 LDASWL 41

Query Match

Best Local Similarity 83.3%; Score 30; DB 22; Length 221;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6

DB 36 LDASWL 41

Query Match

Best Local Similarity 83.3%; Score 30; DB 22; Length 221;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6

DB 36 LDASWL 41

Query Match

Best Local Similarity 83.3%; Score 30; DB 22; Length 221;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6

DB 36 LDASWL 41

Query Match

Best Local Similarity 83.3%; Score 30; DB 22; Length 221;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6

DB 36 LDASWL 41

Query Match

Best Local Similarity 83.3%; Score 30; DB 22; Length 221;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6

DB 36 LDASWL 41

Query Match

Best Local Similarity 83.3%; Score 30; DB 22; Length 221;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6

DB 36 LDASWL 41

Query Match

Best Local Similarity 83.3%; Score 30; DB 22; Length 221;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6

DB 36 LDASWL 41

Query Match

Best Local Similarity 83.3%; Score 30; DB 22; Length 221;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6

DB 36 LDASWL 41

Query Match

Best Local Similarity 83.3%; Score 30; DB 22; Length 221;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6

DB 36 LDASWL 41

Query Match

Best Local Similarity 83.3%; Score 30; DB 22; Length 221;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6

DB 36 LDASWL 41

Query Match

Best Local Similarity 83.3%; Score 30; DB 22; Length 221;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6

DB 36 LDASWL 41

Query Match

Best Local Similarity 83.3%; Score 30; DB 22; Length 221;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6

DB 36 LDASWL 41

Query Match

Best Local Similarity 83.3%; Score 30; DB 22; Length 221;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6

DB 36 LDASWL 41

Query Match

Best Local Similarity 83.3%; Score 30; DB 22; Length 221;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6

DB 36 LDASWL 41

Query Match

Best Local Similarity 83.3%; Score 30; DB 22; Length 221;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6

DB 36 LDASWL 41

Query Match

Best Local Similarity 83.3%; Score 30; DB 22; Length 221;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6

DB 36 LDASWL 41

Query Match

Best Local Similarity 83.3%; Score 30; DB 22; Length 221;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6

DB 36 LDASWL 41

Query Match

Best Local Similarity 83.3%; Score 30; DB 22; Length 221;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6

DB 36 LDASWL 41

Query Match

Best Local Similarity 83.3%; Score 30; DB 22; Length 221;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6

DB 36 LDASWL 41

Query Match

Best Local Similarity 83.3%; Score 30; DB 22; Length 221;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6

DB 36 LDASWL 41

Query Match

Best Local Similarity 83.3%; Score 30; DB 22; Length 221;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6

DB 36 LDASWL 41

Query Match

Best Local Similarity 83.3%; Score 30; DB 22; Length 221;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6

DB 36 LDASWL 41

Query Match

Best Local Similarity 83.3%; Score 30; DB 22; Length 221;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6

DB 36 LDASWL 41

Query Match

Best Local Similarity 83.3%; Score 30; DB 22; Length 221;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6

DB 36 LDASWL 41

Query Match

Best Local Similarity 83.3%; Score 30; DB 22; Length 221;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6

DB 36 LDASWL 41

Query Match

Best Local Similarity 83.3%; Score 30; DB 22; Length 221;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6

DB 36 LDASWL 41

Query Match

Best Local Similarity 83.3%; Score 30; DB 22; Length 221;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6

DB 36 LDASWL 41

Query Match

Best Local Similarity 83.3%; Score 30; DB 22; Length 221;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6

DB 36 LDASWL 41

Query Match

Best Local Similarity 83.3%; Score 30; DB 22; Length 221;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6

DB 36 LDASWL 41

Query Match

Best Local Similarity 83.3%; Score 30; DB 22; Length 221;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6

DB 36 LDASWL 41

Query Match

Best Local Similarity 83.3%; Score 30; DB 22; Length 221;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6

DB 36 LDASWL 41

Query Match

Best Local Similarity 83.3%; Score 30; DB 22; Length 221;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6

DB 36 LDASWL 41

Query Match

Best Local Similarity 83.3%; Score 30; DB 22; Length 221;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDASWL 6

DB 36 LDASWL 41

XX (CHIR-) CHIRON SPA.  
 PA (GENO-) INST GENOMIC RES.  
 XX Telford J, Maignani V, Margalit Ros YI, Grandi G, Fraser C;  
 PI Tettelin H;  
 XX WPI: 2002-352536/38.  
 DR N-PSDB: ABN68072.  
 XX  
 PT New streptococcus protein for the treatment or prevention of infection  
 PT or disease caused by Streptococcus bacteria, such as meningitis, and  
 PT for detecting a compound that binds to the protein -  
 XX  
 PS Claim 1; Page 3561; 4525pp; English.  
 XX  
 CC The invention relates to a protein (ABP25413-ABP30895) from group B  
 CC streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS  
 CC (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in  
 CC the specification. The proteins have antibacterial and antiinflammatory  
 CC activity. (I), nucleic acids encoding (I), ABN6044-ABN71526 and  
 CC antibodies that bind (I) are used in the manufacture of medicaments for  
 CC the treatment or prevention of infection or disease caused by  
 CC Streptococcus bacteria, particularly S. agalactiae and S. pyogenes.  
 CC Nucleic acids encoding (I) are used to detect Streptococcus in a  
 CC biological sample. (I) is used to determine whether a compound binds to  
 CC (I). A composition comprising (I) or a nucleic acid encoding (I), may be  
 CC used as a vaccine or diagnostic composition. The disease caused by  
 CC Streptococcus that is prevented or treated may be meningitis. Nucleic  
 CC acid encoding (I) may be used to recombinantly produce (I) and may be  
 CC used in gene therapy. Antibodies to (I) are used for affinity  
 CC chromatography, immunoassays, and distinguishing/identifying  
 CC Streptococcus proteins.  
 CC  
 SQ Sequence 221 AA:  
 OY 1 LDASWL 6 90.9%; Score 30; DB 23; Length 221;  
 DB 36 LDASWL 41 Best Local Similarity 83.3%; Pred. No. 6.3e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 RESULT 15  
 ID AAY53628  
 AC AAY53628; Protein: 261 AA.  
 DT 22-FEB-2000 (first entry)  
 DE A bone marrow secreted protein designated BMS227.  
 XX  
 KW Bone marrow secreted protein; bone marrow stromal cell; cytokine;  
 KW cell proliferation; cell differentiation; hematopoiesis; anaemia;  
 KW myeloid cell deficiency; lymphoid cell deficiency; myeloid cell;  
 KW erythroid progenitor cell; colony stimulating factor; granulocyte;  
 KW monocyte; macrophage; myelo-suppression; megakaryocyte; platelet;  
 KW platelet disorder; thrombocytopenia; hematopoietic stem cell;  
 KW stem cell disorder; aplastic anaemia; bone differentiation;  
 KW paroxysmal nocturnal hemoglobinuria; bone growth; cartilage; tendon;  
 KW ligament; nerve; wound healing; tissue repair; burn; incision; ulcer;  
 KW bone fracture; cartilage damage; artificial joint.  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..32  
 FT /note="signal peptide"  
 XX  
 PN W09933979-A2.

XX 08-JUL-1999.  
 PD 18-DEC-1998; 96MO-US27008.  
 XX  
 PF  
 XX 30-DEC-1997; 97US-0068958.  
 PR 24-SEP-1998; 98US-0101603.  
 PR 30-SEP-1998; 98US-0102540.  
 XX  
 PA (CHIR) CHIRON CORP.  
 PI Lin H, Cao L;  
 XX  
 DR WPI: 2000-038344/03.  
 DR N-PSDB: AAY36234.  
 XX  
 PT New isolated human polynucleotide and secreted proteins can induce  
 PT production of other cytokines in certain cell populations -  
 XX  
 PS Claim 2; Page 83-84; 120pp; English.  
 XX  
 CC AAY3622-43 represent bone marrow secreted proteins of human bone marrow  
 CC stromal cells. The proteins can exhibit cytokine, cell proliferation, or  
 CC cell differentiation activity (either inducing or inhibiting). They can  
 CC be used to support colony forming cells or factor-dependent cell lines,  
 CC to regulate hematopoiesis, and to treat myeloid or lymphoid cell  
 CC deficiencies. In addition, they may be used to support the growth and  
 CC proliferation of erythroid progenitor cells, and to treat various  
 CC anaemias. They can have colony stimulating factor (CSF) activity and can  
 CC be used to support the growth and proliferation of myeloid cells such as  
 CC granulocytes, monocytes or macrophages, to prevent or treat  
 CC myelo-suppression, to support the growth and proliferation of  
 CC megakaryocytes and platelets, thereby allowing prevention or treatment  
 CC of platelet disorders such as thrombocytopenia, to support the growth  
 CC and proliferation of hematopoietic stem cells, either in place of or in  
 CC conjunction with platelet transfusions, to treat stem cell disorders,  
 CC such as aplastic anaemia and paroxysmal nocturnal hemoglobinuria, or to  
 CC repopulate the stem cell compartment after irradiation or chemotherapy.  
 CC They can be used for growth or differentiation of bone, cartilage,  
 CC tendon, ligament, or nerve tissue, as well as for wound healing and  
 CC tissue repair and replacement, and in the treatment of burns, incisions  
 CC and ulcers, to induce cartilage and/or bone growth in circumstances  
 CC where bone is not normally formed and thus have an application in healing  
 CC bone fractures and cartilage damage or defects, prophylactic use in  
 CC fracture reduction and also in the improved fixation of artificial  
 CC joints.  
 CC  
 SQ Sequence 261 AA:  
 OY 1 LDASWL 6 90.9%; Score 30; DB 21; Length 261;  
 DB 161 LDASWL 166 Best Local Similarity 83.3%; Pred. No. 7.5e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Search completed: May 30, 2003, 14:49:56  
 Job time : 21.7529 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 30, 2003, 14:50:13 ; Search time 10.4605 Seconds

(without alignments)  
58,060 Million cell updates/sec

Title: US-09-643-260-9

Perfect score: 40

Sequence: 1 LNMSWL 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 383519 seqs, 101223694 residues

383519

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08

Maximum Match 1008

Listing first 45 summaries

Database : Published Applications AA.\*

- 1: /cgn2\_6/ptodata/1/pubppa/US08\_NEW\_PUB.pep.\*
- 2: /cgn2\_6/ptodata/1/pubppa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/1/pubppa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/1/pubppa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/1/pubppa/US07\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/ptodata/1/pubppa/US07\_PUBCOMB.pep.\*
- 7: /cgn2\_6/ptodata/1/pubppa/PCTUS\_PUBCOMB.pep.\*
- 8: /cgn2\_6/ptodata/1/pubppa/US08\_PUBCOMB.pep.\*
- 9: /cgn2\_6/ptodata/1/pubppa/US09\_NEW\_PUB.pep.\*
- 10: /cgn2\_6/ptodata/1/pubppa/US09\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/1/pubppa/US10\_NEW\_PUB.pep.\*
- 12: /cgn2\_6/ptodata/1/pubppa/US10\_PUBCOMB.pep.\*
- 13: /cgn2\_6/ptodata/1/pubppa/US60\_NEW\_PUB.pep.\*
- 14: /cgn2\_6/ptodata/1/pubppa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40	100.0	6	US-09-847-940B-9	Sequence 9, Appl1
2	40	100.0	6	US-09-847-946A-9	Sequence 9, Appl1
3	36	90.0	117	US-09-809-391-360	Sequence 360, App
4	36	90.0	464	US-09-815-242-10647	Sequence 10647, A
5	36	90.0	467	US-09-815-242-4997	Sequence 4997, AP
6	35	87.5	6	US-09-847-940B-2	Sequence 2, Appl1
7	35	87.5	6	US-09-847-946A-2	Sequence 2, Appl1
8	35	87.5	6	US-09-847-946A-33	Sequence 33, Appl1
9	35	87.5	7	US-09-847-946A-37	Sequence 37, Appl1
10	35	87.5	8	US-09-847-946A-30	Sequence 30, Appl1
11	35	87.5	8	US-09-847-946A-38	Sequence 38, Appl1
12	35	87.5	9	US-09-847-946A-29	Sequence 29, Appl1
13	35	87.5	9	US-09-847-946A-32	Sequence 32, Appl1
14	35	87.5	9	US-09-847-946A-35	Sequence 35, Appl1
15	35	87.5	9	US-09-847-946A-36	Sequence 36, Appl1
16	35	87.5	10	US-09-847-946A-31	Sequence 31, Appl1
17	35	87.5	10	US-09-847-946A-34	Sequence 34, Appl1
18	35	87.5	11	US-09-847-946A-28	Sequence 28, Appl1
19	35	87.5	11	US-09-847-946A-132	Sequence 132, Appl1

20	35	87.5	11	9	US-09-847-946A-140	Sequence 140, App
21	35	87.5	13	9	US-09-847-946A-143	Sequence 143, App
22	35	87.5	13	9	US-09-847-946A-144	Sequence 144, App
23	35	87.5	13	9	US-09-847-946A-145	Sequence 145, App
24	35	87.5	13	9	US-09-847-946A-148	Sequence 148, App
25	35	87.5	17	9	US-09-847-946A-141	Sequence 141, App
26	35	87.5	17	9	US-09-847-946A-142	Sequence 142, App
27	35	87.5	17	9	US-09-847-946A-146	Sequence 146, App
28	35	87.5	17	9	US-09-847-946A-147	Sequence 147, App
29	35	87.5	18	9	US-09-847-946A-131	Sequence 131, App
30	35	87.5	18	9	US-09-847-946A-135	Sequence 135, App
31	35	87.5	18	9	US-09-847-946A-136	Sequence 136, App
32	35	87.5	22	9	US-09-847-946A-133	Sequence 133, App
33	35	87.5	22	9	US-09-847-946A-134	Sequence 134, App
34	35	87.5	22	9	US-09-847-946A-137	Sequence 137, App
35	35	87.5	22	9	US-09-847-946A-138	Sequence 138, App
36	35	87.5	22	9	US-09-847-946A-139	Sequence 139, App
37	35	87.5	28	9	US-09-847-940B-18	Sequence 18, App
38	35	87.5	28	9	US-09-847-946A-18	Sequence 18, Appl
39	35	87.5	22	10	US-09-771-161A-141	Sequence 141, App
40	35	87.5	745	9	US-09-844-988-10	Sequence 10, Appl
41	35	87.5	745	9	US-10-243-408-4	Sequence 4, Appl1
42	35	87.5	745	9	US-10-059-585-35	Sequence 35, Appl
43	35	87.5	745	10	US-09-796-872-2	Sequence 2, Appl1
44	35	87.5	745	10	US-09-844-908-10	Sequence 10, Appl1
45	35	87.5	756	9	US-09-844-988-9	Sequence 9, Appl1

#### ALIGNMENTS

RESULT 1  
US-09-847-940B-9  
; Sequence 9, Application US/09847940B  
; Patent No. US20020156000A1  
; GENERAL INFORMATION:  
; APPLICANT: May, Michael J.  
; APPLICANT: Ghosh, Sankar  
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
; FILE REFERENCE: PPI-117CP  
; CURRENT APPLICATION NUMBER: US/09/847,940B  
; CURRENT FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: 09/643,260  
; PRIOR FILING DATE: 2000-08-22  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 9  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: NBD mutants  
US-09-847-940B-9

Query Match 100.0%; Score 40; DB 9; Length 6;  
Best Local Similarity 100.0%; Pred. No. 3.4e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LNMSWL 6  
Db 1 LNMSWL 6

RESULT 2  
US-09-847-946A-9  
; Sequence 9, Application US/09847946A  
; Publication No. US20030054999A1  
; GENERAL INFORMATION:  
; APPLICANT: May, Michael J  
; APPLICANT: Ghosh, Sankar  
; APPLICANT: Phillips, Mark A  
; APPLICANT: Hannig, Gerhard

;; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
;; FILE REFERENCE: PPI-119  
;; CURRENT APPLICATION NUMBER: US/09/847,946A  
;; CURRENT FILING DATE: 2001-05-02  
;; PRIOR APPLICATION NUMBER: 60/201,261  
;; PRIOR FILING DATE: 2000-05-02  
;; PRIOR APPLICATION NUMBER: 09/643,260  
;; PRIOR FILING DATE: 2000-08-22  
;; NUMBER OF SEQ ID NOS: 160  
;; SOFTWARE: PatentIn Ver. 2.0  
;; SEQ ID NO 9  
;; LENGTH: 6  
;; TYPE: prt  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Description of Artificial Sequence:NBD peptide  
US-09-847-946A-9

Query Match  
Best Local Similarity 100.0%; Score 40; DB 9; Length 6;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNMSWL 6  
|||||  
Db 1 LNMSWL 6

RESULT 3  
US-09-809-391-360  
;; Sequence 360, Application US/09809391  
;; Publication No. US20030049618A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Ruben et al.  
;; TITLE OF INVENTION: 186 Human Secreted proteins  
;; FILE REFERENCE: P2002P2  
;; CURRENT APPLICATION NUMBER: US/09/809,391  
;; CURRENT FILING DATE: 2001-03-16  
;; Prior application data removed - consult PALM or file wrapper  
;; NUMBER OF SEQ ID NOS: 761  
;; SOFTWARE: PatentIn Ver. 2.0  
;; SEQ ID NO 360  
;; LENGTH: 117  
;; TYPE: prt  
;; ORGANISM: Homo sapiens  
US-09-809-391-360

Query Match  
Best Local Similarity 100.0%; Score 36; DB 9; Length 117;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNMSW 5  
|||||  
Db 30 LNMSW 34

RESULT 4  
US-09-815-242-10647  
;; Sequence 10647, Application US/09815242  
;; Patent No. US20020061569A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Haselbeck, Robert  
;; APPLICANT: Ohlsen, Karl L.  
;; APPLICANT: Zyskind, Judith W.  
;; APPLICANT: Wall, Daniel  
;; APPLICANT: Trawick, John D.  
;; APPLICANT: Carr, Grant J.  
;; APPLICANT: Yamamoto, Robert T.  
;; APPLICANT: Xu, H. Howard  
;; TITLE OF INVENTION: Identification of Essential Genes in  
;; TITLE OF INVENTION: Prokaryotes  
;; FILE REFERENCE: ELITRA.011A  
;; CURRENT APPLICATION NUMBER: US/09/815,242  
;; CURRENT FILING DATE: 2001-03-21

;; PRIOR APPLICATION NUMBER: 60/191,078  
;; PRIOR FILING DATE: 2000-03-21  
;; PRIOR APPLICATION NUMBER: 60/206,848  
;; PRIOR FILING DATE: 2000-05-23  
;; PRIOR APPLICATION NUMBER: 60/207,727  
;; PRIOR FILING DATE: 2000-05-26  
;; PRIOR APPLICATION NUMBER: 60/242,578  
;; PRIOR FILING DATE: 2000-10-23  
;; PRIOR APPLICATION NUMBER: 60/253,625  
;; PRIOR FILING DATE: 2000-11-27  
;; PRIOR APPLICATION NUMBER: 60/257,931  
;; PRIOR FILING DATE: 2000-12-22  
;; PRIOR APPLICATION NUMBER: 60/269,308  
;; PRIOR FILING DATE: 2001-02-16  
;; NUMBER OF SEQ ID NOS: 14110  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 10647  
;; LENGTH: 464  
;; TYPE: prt  
;; ORGANISM: Enterococcus faecalis  
US-09-815-242-10647

Query Match  
Best Local Similarity 100.0%; Score 36; DB 10; Length 464;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 NMSWL 6  
|||||  
Db 422 NMSWL 426

RESULT 5  
US-09-815-242-4997  
;; Sequence 4997, Application US/09815242  
;; Patent No. US20020061569A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Haselbeck, Robert  
;; APPLICANT: Ohlsen, Karl L.  
;; APPLICANT: Zyskind, Judith W.  
;; APPLICANT: Wall, Daniel  
;; APPLICANT: Trawick, John D.  
;; APPLICANT: Carr, Grant J.  
;; APPLICANT: Yamamoto, Robert T.  
;; APPLICANT: Xu, H. Howard  
;; TITLE OF INVENTION: Identification of Essential Genes in  
;; TITLE OF INVENTION: Prokaryotes  
;; FILE REFERENCE: ELITRA.011A  
;; CURRENT APPLICATION NUMBER: US/09/815,242  
;; CURRENT FILING DATE: 2001-03-21  
;; PRIOR APPLICATION NUMBER: 60/191,078  
;; PRIOR FILING DATE: 2000-03-21  
;; PRIOR APPLICATION NUMBER: 60/206,848  
;; PRIOR FILING DATE: 2000-05-23  
;; PRIOR APPLICATION NUMBER: 60/207,727  
;; PRIOR FILING DATE: 2000-05-26  
;; PRIOR APPLICATION NUMBER: 60/242,578  
;; PRIOR FILING DATE: 2000-10-23  
;; PRIOR APPLICATION NUMBER: 60/253,625  
;; PRIOR FILING DATE: 2000-11-27  
;; PRIOR APPLICATION NUMBER: 60/257,931  
;; PRIOR FILING DATE: 2000-12-22  
;; PRIOR APPLICATION NUMBER: 60/269,308  
;; PRIOR FILING DATE: 2001-02-16  
;; NUMBER OF SEQ ID NOS: 14110  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 4997  
;; LENGTH: 467  
;; TYPE: prt  
;; ORGANISM: Enterococcus faecalis  
US-09-815-242-4997

Query Match  
Best Local Similarity 100.0%; Score 36; DB 10; Length 467;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LMSWL 6  
|||||  
Db 425 LMSWL 429

RESULT 6  
US-09-847-940B-2  
; Sequence 2, Application US/09847940B  
; Patent No. US20020156000A1  
; GENERAL INFORMATION:  
; APPLICANT: May, Michael J.  
; APPLICANT: Ghosh, Sankar  
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
; FILE REFERENCE: PPI-117CP  
; CURRENT APPLICATION NUMBER: US/09/847, 940B  
; CURRENT FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: 09/643,260  
; PRIOR FILING DATE: 2000-08-22  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:NBD mutants  
US-09-847-940B-2

Query Match 87.5%; Score 35; DB 9; Length 6;  
Best Local Similarity 83.3%; Pred. No. 3.4e+05;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSWL 6  
|||||  
Db 1 LMSWL 6

RESULT 7  
US-09-847-946A-2  
; Sequence 2, Application US/09847946A  
; Publication No. US20030054999A1  
; GENERAL INFORMATION:  
; APPLICANT: May, Michael J  
; APPLICANT: Ghosh, Sankar  
; APPLICANT: Findels, Mark A  
; APPLICANT: Phillips, Kathryn  
; APPLICANT: Hannig, Gerhard  
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
; FILE REFERENCE: PPI-119  
; CURRENT APPLICATION NUMBER: US/09/847, 946A  
; CURRENT FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: 60/201,261  
; PRIOR FILING DATE: 2000-05-02  
; PRIOR APPLICATION NUMBER: 09/643,260  
; PRIOR FILING DATE: 2000-08-22  
; NUMBER OF SEQ ID NOS: 160  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:NBD peptide  
US-09-847-946A-2

Query Match 87.5%; Score 35; DB 9; Length 6;  
Best Local Similarity 83.3%; Pred. No. 3.4e+05;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSWL 6  
|||||

Db 1 LMSWL 6

RESULT 8  
US-09-847-946A-33  
; Sequence 33, Application US/09847946A  
; Publication No. US20030054999A1  
; GENERAL INFORMATION:  
; APPLICANT: May, Michael J  
; APPLICANT: Ghosh, Sankar  
; APPLICANT: Findels, Mark A  
; APPLICANT: Phillips, Kathryn  
; APPLICANT: Hannig, Gerhard  
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
; FILE REFERENCE: PPI-119  
; CURRENT APPLICATION NUMBER: US/09/847, 946A  
; CURRENT FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: 60/201,261  
; PRIOR FILING DATE: 2000-05-02  
; PRIOR APPLICATION NUMBER: 09/643,260  
; PRIOR FILING DATE: 2000-08-22  
; NUMBER OF SEQ ID NOS: 160  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 33  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding  
US-09-847-946A-33

Query Match 87.5%; Score 35; DB 9; Length 6;  
Best Local Similarity 83.3%; Pred. No. 3.4e+05;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSWL 6  
|||||

Db 1 LMSWL 6

RESULT 9  
US-09-847-946A-37  
; Sequence 37, Application US/09847946A  
; Publication No. US20030054999A1  
; GENERAL INFORMATION:  
; APPLICANT: May, Michael J  
; APPLICANT: Ghosh, Sankar  
; APPLICANT: Findels, Mark A  
; APPLICANT: Phillips, Kathryn  
; APPLICANT: Hannig, Gerhard  
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
; FILE REFERENCE: PPI-119  
; CURRENT APPLICATION NUMBER: US/09/847, 946A  
; CURRENT FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: 60/201,261  
; PRIOR FILING DATE: 2000-05-02  
; PRIOR APPLICATION NUMBER: 09/643,260  
; PRIOR FILING DATE: 2000-08-22  
; NUMBER OF SEQ ID NOS: 160  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 37  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding  
US-09-847-946A-37

Query Match 87.5%; Score 35; DB 9; Length 7;  
Best Local Similarity 83.3%; Pred. No. 3.4e+05;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LNMWML 6  
1:||||  
Db 1 LDMWML 6

## RESULT 10

US-09-847-946A-30  
Sequence 30, Application US/09847946A  
Publication No. US20030054999A1  
GENERAL INFORMATION:  
APPLICANT: May, Michael J  
APPLICANT: Ghosh, Sankar  
APPLICANT: Pindels, Mark A  
APPLICANT: Phillips, Kathryn  
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
FILE REFERENCE: PPI-119  
CURRENT APPLICATION NUMBER: US/09/847,946A  
CURRENT FILING DATE: 2001-05-02  
PRIOR APPLICATION NUMBER: 60/201,261  
PRIOR FILING DATE: 2000-05-02  
PRIOR APPLICATION NUMBER: 09/643,260  
PRIOR FILING DATE: 2000-08-22  
NUMBER OF SEQ ID NOS: 160  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 30  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:NEMO binding  
US-09-847-946A-30

Query Match 87.5%; Score 35; DB 9; Length 8;  
Best Local Similarity 83.3%; Pred. No. 3.4e+05;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LNMWML 6  
1:||||  
Db 3 LDMWML 8

## RESULT 11

US-09-847-946A-38  
Sequence 38, Application US/09847946A  
Publication No. US20030054999A1  
GENERAL INFORMATION:  
APPLICANT: May, Michael J  
APPLICANT: Ghosh, Sankar  
APPLICANT: Pindels, Mark A  
APPLICANT: Phillips, Kathryn  
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
FILE REFERENCE: PPI-119  
CURRENT APPLICATION NUMBER: US/09/847,946A  
CURRENT FILING DATE: 2001-05-02  
PRIOR APPLICATION NUMBER: 60/201,261  
PRIOR FILING DATE: 2000-05-02  
PRIOR APPLICATION NUMBER: 09/643,260  
PRIOR FILING DATE: 2000-08-22  
NUMBER OF SEQ ID NOS: 160  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 38  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:NEMO binding  
US-09-847-946A-38

Query Match 87.5%; Score 35; DB 9; Length 8;  
Best Local Similarity 83.3%; Pred. No. 3.4e+05;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LNMWML 6  
1:||||  
Db 1 LDMWML 6

## RESULT 12

US-09-847-946A-29  
Sequence 29, Application US/09847946A  
Publication No. US20030054999A1  
GENERAL INFORMATION:  
APPLICANT: May, Michael J  
APPLICANT: Ghosh, Sankar  
APPLICANT: Pindels, Mark A  
APPLICANT: Phillips, Kathryn  
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
FILE REFERENCE: PPI-119  
CURRENT APPLICATION NUMBER: US/09/847,946A  
CURRENT FILING DATE: 2001-05-02  
PRIOR APPLICATION NUMBER: 60/201,261  
PRIOR FILING DATE: 2000-05-02  
PRIOR APPLICATION NUMBER: 09/643,260  
PRIOR FILING DATE: 2000-08-22  
NUMBER OF SEQ ID NOS: 160  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 29  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:NEMO binding  
US-09-847-946A-29

Query Match 87.5%; Score 35; DB 9; Length 9;  
Best Local Similarity 83.3%; Pred. No. 3.4e+05;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LNMWML 6  
1:||||  
Db 1 LDMWML 6

## RESULT 13

US-09-847-946A-32  
Sequence 32, Application US/09847946A  
Publication No. US20030054999A1  
GENERAL INFORMATION:  
APPLICANT: May, Michael J  
APPLICANT: Ghosh, Sankar  
APPLICANT: Pindels, Mark A  
APPLICANT: Phillips, Kathryn  
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
FILE REFERENCE: PPI-119  
CURRENT APPLICATION NUMBER: US/09/847,946A  
CURRENT FILING DATE: 2001-05-02  
PRIOR APPLICATION NUMBER: 60/201,261  
PRIOR FILING DATE: 2000-05-02  
PRIOR APPLICATION NUMBER: 09/643,260  
PRIOR FILING DATE: 2000-08-22  
NUMBER OF SEQ ID NOS: 160  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 32  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:NEMO binding

OTHER INFORMATION: sequence  
US-09-847-946A-32

Query Match  
Best Local Similarity 87.5%; Score 35; DB 9; Length 9;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNMSWL 6  
1:||||  
Db 1 LDMSWL 6

RESULT 14  
US-09-847-946A-35

Sequence 35; Application US/09847946A  
Publication No. US20030054999A1

GENERAL INFORMATION:

APPLICANT: May, Michael J

APPLICANT: Ghosh, Sankar

APPLICANT: Findels, Mark A

APPLICANT: Phillips, Kathryn

APPLICANT: Hannig, Gerhard

TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF

FILE REFERENCE: PFI-119

CURRENT APPLICATION NUMBER: US/09/847,946A

CURRENT FILING DATE: 2001-05-02

PRIOR APPLICATION NUMBER: 60/201,261

PRIOR FILING DATE: 2000-05-02

PRIOR APPLICATION NUMBER: 09/643,260

PRIOR FILING DATE: 2000-08-22

NUMBER OF SEQ ID NOS: 160

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 35

LENGTH: 9

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE: OTHER INFORMATION: Description of Artificial Sequence: NEMO binding

OTHER INFORMATION: sequence

US-09-847-946A-35

Query Match  
Best Local Similarity 87.5%; Score 35; DB 9; Length 9;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNMSWL 6  
1:||||  
Db 3 LDMSWL 8

RESULT 15  
US-09-847-946A-36

Sequence 36; Application US/09847946A  
Publication No. US20030054999A1

GENERAL INFORMATION:

APPLICANT: May, Michael J

APPLICANT: Ghosh, Sankar

APPLICANT: Findels, Mark A

APPLICANT: Phillips, Kathryn

APPLICANT: Hannig, Gerhard

TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF

FILE REFERENCE: PFI-119

CURRENT APPLICATION NUMBER: US/09/847,946A

CURRENT FILING DATE: 2001-05-02

PRIOR APPLICATION NUMBER: 60/201,261

PRIOR FILING DATE: 2000-05-02

PRIOR APPLICATION NUMBER: 09/643,260

PRIOR FILING DATE: 2000-08-22

NUMBER OF SEQ ID NOS: 160

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 36

LENGTH: 9

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: NEMO binding

OTHER INFORMATION: sequence

US-09-847-946A-36

Query Match  
Best Local Similarity 87.5%; Score 35; DB 9; Length 9;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNMSWL 6  
1:||||  
Db 2 LDMSWL 7

Search completed: May 30, 2003, 15:53:17  
Job time: 10.4605 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 30, 2003, 14:32:12 ; Search time 6.03947 Seconds  
(without alignments)  
29,231 Million cell updates/sec

Title: US-09-643-260-9  
Perfect score: 40  
Sequence: 1 LKMSWL 6

Scoring table: BLOSUM62  
Gapop 10.0, Gapept 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA:\*  
1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep:\*  
2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep:\*  
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/iaa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	36	90.0	117	4	US-09-149-476-360
2	35	87.5	745	2	US-08-887-518-3
3	35	87.5	745	2	US-09-023-321-3
4	35	87.5	745	2	US-08-890-853-4
5	35	87.5	745	2	US-09-032-475-3
6	35	87.5	745	2	US-09-099-125A-4
7	35	87.5	745	2	US-09-099-125A-4
8	35	87.5	745	2	US-09-032-476-4
9	35	87.5	745	4	US-08-890-854-4
10	35	87.5	745	4	US-09-023-324-4
11	35	87.5	745	4	US-09-168-629-2
12	35	87.5	745	4	US-08-910-820-10
13	35	87.5	745	4	US-08-810-131A-2
14	35	87.5	756	2	US-08-887-518-4
15	35	87.5	756	2	US-09-023-321-4
16	35	87.5	756	2	US-08-890-853-2
17	35	87.5	756	2	US-09-032-475-4
18	35	87.5	756	2	US-09-099-125A-2
19	35	87.5	756	2	US-09-099-124A-2
20	35	87.5	756	4	US-09-032-476-2
21	35	87.5	756	4	US-08-890-854-2
22	35	87.5	756	4	US-09-023-324-2
23	35	87.5	756	4	US-09-168-629-15
24	35	87.5	756	4	US-08-910-820-9
25	34	85.0	355	4	US-08-818-112-79
26	34	85.0	355	4	US-08-818-111-80
27	34	85.0	355	4	US-09-056-556-79

28	34	85.0	355	4	US-09-072-596-80	Sequence 80, Appl
29	33	82.5	396	2	US-09-134-001C-4443	Sequence 4443, Ap
30	33	82.5	455	2	US-08-272-255-14	Sequence 14, Appl
31	33	82.5	455	5	PCT-US95-08565-14	Sequence 14, Appl
32	32	80.0	122	3	US-08-722-126A-9	Sequence 9, Appl
33	32	80.0	122	5	PCT-US95-04258-9	Sequence 9, Appl
34	32	80.0	202	4	US-09-245-248B-30	Sequence 30, Appl
35	32	80.0	291	2	US-08-838-543-6	Sequence 6, Appl
36	32	80.0	298	4	US-08-838-543-5	Sequence 5, Appl
37	32	80.0	971	4	US-09-405-728-2	Sequence 2, Appl
38	31	77.5	58	4	US-09-227-357-549	Sequence 298, App
39	31	77.5	61	2	US-08-637-759B-298	Sequence 298, App
40	31	77.5	61	3	US-08-871-355A-298	Sequence 298, App
41	31	77.5	61	4	US-09-201-945-298	Sequence 298, App
42	31	77.5	100	1	US-08-241-853-28	Sequence 28, Appl
43	31	77.5	100	2	US-08-241-853-29	Sequence 28, Appl
44	31	77.5	100	2	US-08-850-917-28	Sequence 29, Appl
45	31	77.5	100	2	US-08-850-917-29	Sequence 29, Appl

## ALIGNMENTS

RESULT 1  
US-09-149-476-360  
Sequence 360, Application US/09149476  
Patent No. 6420526  
GENERAL INFORMATION:  
APPLICANT: Rosen et al.  
TITLE OR INVENTION: 186 Human Secreted proteins  
FILE REFERENCE: P2002P1  
CURRENT FILING DATE: 1998-09-08  
EARLIER APPLICATION NUMBER: US/09/149, 476  
EARLIER FILING DATE: 1998-03-06  
EARLIER APPLICATION NUMBER: 60/040, 162  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/040, 333  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/038, 621  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/040, 626  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/040, 334  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/040, 336  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/040, 163  
EARLIER FILING DATE: 1997-03-07  
EARLIER APPLICATION NUMBER: 60/047, 600  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047, 615  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047, 597  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047, 502  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047, 633  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047, 583  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047, 617  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047, 618  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047, 503  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047, 592  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047, 581  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047, 584  
EARLIER FILING DATE: 1997-05-23

[illegible][illegible]

EARLIER APPLICATION NUMBER: 60/057,669  
EARLIER FILING DATE: 1997-09-05  
EARLIER APPLICATION NUMBER: 60/049,610  
EARLIER FILING DATE: 1997-06-13  
EARLIER APPLICATION NUMBER: 60/061,060  
EARLIER FILING DATE: 1997-10-02

Query Match 90.0%; Score 36; DB 4; Length 117;  
Best Local Similarity 100.0%; Pred. No. 71;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNMWSL 5  
DB 30 LNMWSL 34

RESULT 2  
US-08-887-518-3  
Sequence 3, Application US/08887518

Patent No. 5843721

GENERAL INFORMATION:

APPLICANT: Roche, Mike

ATTORNEY/AGENT INFORMATION:

TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESSES:

ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP

STREET: 268 BUSH STREET, SUITE 3200

CITY: SAN FRANCISCO

STATE: CALIFORNIA

COUNTRY: USA

ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/887,518

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: OSMAN, RICHARD A

REGISTRATION NUMBER: 36,627

REFERENCE/DOCKET NUMBER: T97-008

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 343-4341

TELEFAX: (415) 343-4342

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 745 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-887-518-3

Query Match 87.5%; Score 35; DB 2; Length 745;  
Best Local Similarity 83.3%; Pred. No. 5,7e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNMWSL 6  
DB 738 LNMWSL 743

RESULT 3  
US-09-023-321-3  
Sequence 3, Application US/09033321

Patent No. 5844073

GENERAL INFORMATION:

APPLICANT: Roche, Mike

ATTORNEY/AGENT INFORMATION:

NAME: OSMAN, RICHARD A

TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESSES:

ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP

STREET: 268 BUSH STREET, SUITE 3200

CITY: SAN FRANCISCO

STATE: CALIFORNIA

COUNTRY: USA

ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/023,321

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/887,518

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: OSMAN, RICHARD A

REGISTRATION NUMBER: 36,627

REFERENCE/DOCKET NUMBER: T97-008

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 343-4341

TELEFAX: (415) 343-4342

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 745 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-09-023-321-3

Query Match 87.5%; Score 35; DB 2; Length 745;  
Best Local Similarity 83.3%; Pred. No. 5,7e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNMWSL 6  
DB 738 LNMWSL 743

RESULT 4  
US-08-890-853-4  
Sequence 4, Application US/08890853

Patent No. 5851812

GENERAL INFORMATION:

APPLICANT: Goeddel, David V.

ATTORNEY/AGENT INFORMATION:

TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESSES:

ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP

STREET: 268 BUSH STREET, SUITE 3200

CITY: SAN FRANCISCO

STATE: CALIFORNIA

COUNTRY: USA

ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/890,853

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: OSMAN, RICHARD A

REGISTRATION NUMBER: 36,627  
REFERENCE/DOCKET NUMBER: T97-006-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 343-4341  
TELEFAX: (415) 343-4342  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 745 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-890-853-4

Query Match 87.5%; Score 35; DB 2; Length 745;  
Best Local Similarity 83.3%; Pred. No. 5.7e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LNMWSL 6  
|:|||||  
DB 738 LDMWSL 743

RESULT 5  
US-09-032-475-3  
Sequence 3, Application US/09032475  
Patent No. 5854003  
GENERAL INFORMATION:  
APPLICANT: Rothe, Mike  
APPLICANT: Wu, Lin  
TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
STREET: 268 BUSH STREET, SUITE 3200  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94104

COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA: US/09/032.475  
APPLICATION NUMBER: US/09/032.475  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/887,518  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: OSMAN, RICHARD A  
REGISTRATION NUMBER: 36,627  
REFERENCE/DOCKET NUMBER: T97-008  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 343-4341  
TELEFAX: (415) 343-4342  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 745 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-032-475-3

Query Match 87.5%; Score 35; DB 2; Length 745;  
Best Local Similarity 83.3%; Pred. No. 5.7e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LNMWSL 6  
|:|||||

DB 738 LDMWSL 743

RESULT 6  
US-09-099-125A-4  
Sequence 4, Application US/09099125A  
Patent No. 5916760  
GENERAL INFORMATION:  
APPLICANT: Goedel, David V.  
APPLICANT: Moronicz, John  
TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
STREET: 268 BUSH STREET, SUITE 3200  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94104

COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA: US/09/099.125A  
APPLICATION NUMBER: US/09/099.125A  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/890,853  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: OSMAN, RICHARD A  
REGISTRATION NUMBER: 36,627  
REFERENCE/DOCKET NUMBER: T97-006-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 343-4341  
TELEFAX: (415) 343-4342  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 745 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-099-125A-4

Query Match 87.5%; Score 35; DB 2; Length 745;  
Best Local Similarity 83.3%; Pred. No. 5.7e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LNMWSL 6  
|:|||||  
DB 738 LDMWSL 743

RESULT 7  
US-09-099-124A-4  
Sequence 4, Application US/09099124A  
Patent No. 5939302  
GENERAL INFORMATION:  
APPLICANT: Goedel, David V.  
APPLICANT: Moronicz, John  
TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
STREET: 268 BUSH STREET, SUITE 3200  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/099,124A  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/890,853  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: OSMAN, RICHARD A  
REGISTRATION NUMBER: 36,627  
REFERENCE/DOCKET NUMBER: T97-006-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 343-4341  
TELEFAX: (415) 343-4342  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 745 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-099-124A-4

Query Match 87.5%; Score 35; DB 2; Length 745;  
Best Local Similarity 83.3%; Pred. No. 5.7e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNMWML 6  
|:||||  
DB 738 LDMWML 743

RESULT 8  
US-09-032-476-4  
Sequence 4, Application US/09032476  
Patent No. 6235492  
GENERAL INFORMATION:  
APPLICANT: Rothe, Mike  
APPLICANT: Cao, Zhaoan  
APPLICANT: R guier, Catherine  
TITLE OF INVENTION: IKK- $\gamma$  Proteins, Nucleic Acids and Methods  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
STREET: 268 BUSH STREET, SUITE 3200  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/032,476  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/890,854  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: OSMAN, RICHARD A  
REGISTRATION NUMBER: 36,627  
REFERENCE/DOCKET NUMBER: T97-006-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 343-4341  
TELEFAX: (415) 343-4342  
INFORMATION FOR SEQ ID NO: 4:  
GENERAL INFORMATION:

SEQUENCE CHARACTERISTICS:  
LENGTH: 745 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-032-476-4

Query Match 87.5%; Score 35; DB 4; Length 745;  
Best Local Similarity 83.3%; Pred. No. 5.7e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNMWML 6  
|:||||  
DB 738 LDMWML 743

RESULT 9  
US-08-890-854-4  
Sequence 4, Application US/08890854  
Patent No. 6235512  
GENERAL INFORMATION:  
APPLICANT: Rothe, Mike  
APPLICANT: Cao, Zhaoan  
APPLICANT: R guier, Catherine  
TITLE OF INVENTION: IKK- $\gamma$  Proteins, Nucleic Acids and Methods  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
STREET: 268 BUSH STREET, SUITE 3200  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/890,854  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: OSMAN, RICHARD A  
REGISTRATION NUMBER: 36,627  
REFERENCE/DOCKET NUMBER: T97-006-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 343-4341  
TELEFAX: (415) 343-4342  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 745 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-890-854-4

Query Match 87.5%; Score 35; DB 4; Length 745;  
Best Local Similarity 83.3%; Pred. No. 5.7e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNMWML 6  
|:||||  
DB 738 LDMWML 743

RESULT 10  
US-09-023-324-4  
Sequence 4, Application US/09023324  
Patent No. 6235513  
GENERAL INFORMATION:

APPLICANT: Rothe, Mike  
APPLICANT: Cao, Zhaoan  
APPLICANT: R gner, Catherine  
TITLE OF INVENTION: IKK- $\gamma$  Proteins, Nucleic Acids and Methods  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
STREET: 268 BUSH STREET, SUITE 3200  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/023,324  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/890,854  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: OSMAN, RICHARD A  
REGISTRATION NUMBER: 36,627  
REFERENCE/DOCKET NUMBER: T97-006-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 343-4341  
TELEFAX: (415) 343-4342  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 745 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-023-324-4

Query Match 87.5%; Score 35; DB 4; Length 745;  
Best Local Similarity 83.3%; Pred. No. 5.7e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNMWTL 6  
DB 738 LDMWTL 743

RESULT 11  
US-09-168-629-2  
Sequence 2, Application US/09168629  
Patent No. 6242253  
GENERAL INFORMATION:  
APPLICANT: Karin, Michael  
APPLICANT: Didonato, Joseph A.  
APPLICANT: Rothwarf, David M.  
APPLICANT: Hayakawa, Makio  
APPLICANT: Zandi, Ebrahim  
TITLE OF INVENTION: IKK Kinase, Subunits Thereof, and Methods of Using Same  
FILE REFERENCE: P-UD 3295  
CURRENT APPLICATION NUMBER: US/09/168,629  
EARLIER FILING DATE: 1998-10-08  
CURRENT FILING DATE: 1998-10-08  
NUMBER OF SEQ ID NOS: 20  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 2  
LENGTH: 745  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-168-629-2

Query Match 87.5%; Score 35; DB 4; Length 745;  
Best Local Similarity 83.3%; Pred. No. 5.7e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNMWTL 6  
DB 738 LDMWTL 743

RESULT 12  
US-08-910-820-10  
Sequence 10, Application US/08910820  
Patent No. 6258579  
GENERAL INFORMATION:  
APPLICANT: Mercutio, Frank  
APPLICANT: Zhu, Hengyi  
APPLICANT: Barbosa, Miguel  
APPLICANT: Li, Gan  
APPLICANT: Murray, Brian W.  
TITLE OF INVENTION: STIMULUS-INDUCIBLE PROTEIN KINASE  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SEED and BERRY LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/910,820  
FILING DATE: 12-AUG-1997  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: MAKI, David J.  
REGISTRATION NUMBER: 31,392  
REFERENCE/DOCKET NUMBER: 860098.413C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 745 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
US-08-910-820-10

Query Match 87.5%; Score 35; DB 4; Length 745;  
Best Local Similarity 83.3%; Pred. No. 5.7e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNMWTL 6  
DB 738 LDMWTL 743

RESULT 13  
US-08-810-131A-2  
Sequence 2, Application US/08810131A  
Patent No. 6268194  
GENERAL INFORMATION:  
APPLICANT: Karin, Michael  
APPLICANT: Didonato, Joseph A.  
APPLICANT: Rothwarf, David M.  
APPLICANT: Hayakawa, Makio  
APPLICANT: Zandi, Ebrahim  
TITLE OF INVENTION: I-kappa-B Kinase and Methods of Using

;; TITLE OF INVENTION: Same  
;; NUMBER OF SEQUENCES: 9  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Campbell & Flores LLP  
;; STREET: 4370 La Jolla Village Drive, Suite 700  
;; CITY: San Diego  
;; STATE: California  
;; COUNTRY: United States  
;; ZIP: 92122  
;;  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patentin Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/810,131A  
;; FILING DATE: 25-FEB-1997  
;; CLASSIFICATION: 435  
;;  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Campbell, Cathryn A.  
;; REGISTRATION NUMBER: 31,815  
;; REFERENCE/DOCKET NUMBER: P-UD 2408  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (619) 535-9001  
;; TELEFAX: (619) 535-8949  
;;  
;; INFORMATION FOR SEQ ID NO: 2:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 745 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
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US-08-810-131A-2

Query Match 87.5%; Score 35; DB 4; Length 745;  
Best Local Similarity 83.3%; Pred. No. 5.7e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNMSWL 6  
1:|||||  
DB 737 LDMSWL 743

RESULT 14  
US-08-887-518-4  
;; Sequence 4, Application US/08887518  
;; Patent No. 5843721  
;; GENERAL INFORMATION:  
;; APPLICANT: Roche, Mike  
;; APPLICANT: Wu, Lin  
;; TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods  
;; NUMBER OF SEQUENCES: 4  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
;; STREET: 268 BUSH STREET, SUITE 3200  
;; CITY: SAN FRANCISCO  
;; STATE: CALIFORNIA  
;; COUNTRY: USA  
;; ZIP: 94104  
;;  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; OPERATING SYSTEM: IBM PC compatible  
;; SOFTWARE: Patentin Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/887,518  
;; FILING DATE:  
;; CLASSIFICATION: 435  
;;  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: OSMAN, RICHARD A  
;; REGISTRATION NUMBER: 36,627  
;; REFERENCE/DOCKET NUMBER: T97-008  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (415) 343-4341  
;; TELEFAX: (415) 343-4342  
;;  
;; INFORMATION FOR SEQ ID NO: 4:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 756 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
;;  
US-09-023-321-4

;; TELEFAX: (415) 343-4342  
;; INFORMATION FOR SEQ ID NO: 4:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 756 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
;;  
US-08-887-518-4

Query Match 87.5%; Score 35; DB 2; Length 756;  
Best Local Similarity 83.3%; Pred. No. 5.8e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNMSWL 6  
1:|||||  
DB 737 LDMSWL 742

RESULT 15  
US-09-023-321-4  
;; Sequence 4, Application US/09023321  
;; Patent No. 5844073  
;; GENERAL INFORMATION:  
;; APPLICANT: Roche, Mike  
;; APPLICANT: Wu, Lin  
;; TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods  
;; NUMBER OF SEQUENCES: 4  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
;; STREET: 268 BUSH STREET, SUITE 3200  
;; CITY: SAN FRANCISCO  
;; STATE: CALIFORNIA  
;; COUNTRY: USA  
;; ZIP: 94104  
;;  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; OPERATING SYSTEM: IBM PC compatible  
;; SOFTWARE: Patentin Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/09/023,321  
;; FILING DATE:  
;; CLASSIFICATION: 435  
;;  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/887,518  
;; FILING DATE:  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: OSMAN, RICHARD A  
;; REGISTRATION NUMBER: 36,627  
;; REFERENCE/DOCKET NUMBER: T97-008  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (415) 343-4341  
;; TELEFAX: (415) 343-4342  
;;  
;; INFORMATION FOR SEQ ID NO: 4:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 756 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
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US-09-023-321-4

Query Match 87.5%; Score 35; DB 2; Length 756;  
Best Local Similarity 83.3%; Pred. No. 5.8e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNMSWL 6  
1:|||||  
DB 737 LDMSWL 742

Search completed: May 30, 2003, 14:41:26

Fri May 30 17:16:23 2003

us-09-643-260-9.ra1

Page 8

Job time : 6.03947 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 30, 2003, 14:32:12 ; Search time 19.6974 Seconds  
(without alignments)  
40.589 Million cell updates/sec

Title: US-09-643-260-9

Perfect score: 40

Sequence: 1 LMSWL 6

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 08  
Maximum Match 1008  
Listing first 45 summaries

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2: /SID52/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:\*  
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22: /SID52/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:\*  
23: /SID52/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40	100.0	6	23	ABB08731
2	40	100.0	6	23	AAW48514
3	40	100.0	295	23	ABB62034
4	40	100.0	756	23	ABB77304
5	38	95.0	135	20	AAV76530
6	37	92.5	130	22	AAW485139
7	37	92.5	130	22	AAW485139
8	36	90.0	464	22	AAW35054
9	36	90.0	467	22	AAW33501
10	35	87.5	6	23	ABB08725

11	35	87.5	6	23	AAW48530	Anti-inflammatory
12	35	87.5	6	23	AAW48530	NBD mutant peptide
13	35	87.5	7	23	AAW48534	Anti-inflammatory
14	35	87.5	8	23	AAW48527	Anti-inflammatory
15	35	87.5	8	23	AAW48535	Anti-inflammatory
16	35	87.5	9	20	AAW96182	IKK-alpha polypeptide
17	35	87.5	9	23	AAW48526	Anti-inflammatory
18	35	87.5	9	23	AAW48529	Anti-inflammatory
19	35	87.5	9	23	AAW48532	Anti-inflammatory
20	35	87.5	9	23	AAW48533	Anti-inflammatory
21	35	87.5	10	23	ABB77313	IKKbeta NEMO bindi
22	35	87.5	10	23	AAW48528	Anti-inflammatory
23	35	87.5	10	23	AAW48531	Anti-inflammatory
24	35	87.5	11	23	ABB77311	Human NBD peptide
25	35	87.5	11	23	AAW48506	Human IKKbeta pept
26	35	87.5	11	23	AAW48525	Anti-inflammatory
27	35	87.5	11	23	AAW48533	NBD peptide. Synt
28	35	87.5	13	23	AAW48640	Anti-inflammatory
29	35	87.5	13	23	AAW48641	Anti-inflammatory
30	35	87.5	13	23	AAW48642	Anti-inflammatory
31	35	87.5	13	23	AAW48645	Anti-inflammatory
32	35	87.5	17	23	AAW48638	Anti-inflammatory
33	35	87.5	17	23	AAW48639	Anti-inflammatory
34	35	87.5	17	23	AAW48643	Anti-inflammatory
35	35	87.5	17	23	AAW48644	Anti-inflammatory
36	35	87.5	18	23	AAW48628	Anti-inflammatory
37	35	87.5	18	23	AAW48629	Anti-inflammatory
38	35	87.5	18	23	AAW48632	Anti-inflammatory
39	35	87.5	18	23	AAW48633	Anti-inflammatory
40	35	87.5	22	23	AAW48630	Anti-inflammatory
41	35	87.5	22	23	AAW48631	Anti-inflammatory
42	35	87.5	22	23	AAW48634	Anti-inflammatory
43	35	87.5	22	23	AAW48635	Anti-inflammatory
44	35	87.5	22	23	AAW48636	Anti-inflammatory
45	35	87.5	22	23	AAW48637	Anti-inflammatory

#### ALIGNMENTS

RESULT 1	ABB08731	standard; peptide; 6 AA.
ID	ABB08731	
XX	AC	ABB08731:
XX	AC	14-JUN-2002 (first entry)
XX	DE	Mutated IKKbeta NEMO binding domain peptide SEQ ID NO 9.
XX	XX	IKKbeta: IKKalpha; NEMO; NEMO binding domain; NBD; NF-kappaB; NF-kB;
XX	KW	kinase activation; leukocyte; inflammation; E-selectin; osteoclast;
KW	KW	autoimmune disease; transplant rejection; osteoporosis; cancer;
KW	KW	Alzheimer's disease; viral; infection; asthma; anapylaxis; psoriasis;
KW	KW	rheumatoid arthritis; Crohn's disease; multiple sclerosis; HIV;
KW	KW	corticosteroid; immunosuppression; anti-inflammatory; immunosuppressive;
KW	KW	osteopathic; cytostatic; nootropic; neuroprotective; anti-HIV; human;
KW	KW	antiarteriosclerotic; virucide; antiparasitic; antiallergic;
KW	KW	dermatological; antibacterial; antiparasitic; antipneumatic;
KW	KW	antiarthritic; osteopathic; antiulcer; mutant; mutain.
XX	XX	
XX	OS	Homo sapiens.
XX	OS	Synthetic.
XX	XX	
XX	FT	Key
XX	FT	Misc-difference 2
XX	FT	Location/Qualifiers
XX	XX	W0200183547-A2.
XX	XX	W0200183547-A2.
XX	XX	08-NOV-2001.
XX	XX	02-MAY-2001; 2001MO-US40654.

XX 02-MAY-2000; 2000US-201261P.  
 PR 22-AUG-2000; 2000US-0643260.  
 XX (UYVA ) UNIV YALE.  
 PA May MJ, Ghosh S;  
 PI WPI: 2002-179350/23.  
 DR  
 XX Modulating NF-kappaB induction in a cell, useful for treating e.g.  
 PT inflammatory disorders, osteoporosis and cancer, comprises contacting a  
 PT cell with an anti-inflammatory compound comprising at least one NEMO  
 PT binding domain -  
 PS  
 XX Claim 23; Page 44; 82pp; English.  
 PS  
 XX The invention relates to modulating NF-kappaB (NF-KB) induction in a cell  
 CC comprises contacting a cell with an anti-inflammatory compound  
 CC (ABB08725-ABB08742) comprising at least one NEMO binding domain  
 CC (ABB77313). The compound has acts through selective inhibition of NEMO  
 CC cytokine-mediated NF-kB activation by blocking the interaction of NEMO  
 CC with IKKbeta at the NEMO binding domain. Blockage of IKKbeta-NEMO  
 CC interaction results in inhibition of IKKbeta kinase activation and  
 CC subsequent decreased phosphorylation of Ikbppa. The compound may also  
 CC act (directly or indirectly) by blocking the recruitment of leukocytes  
 CC into sites of acute and chronic inflammation, by down-regulating the  
 CC expression of E-selectin on leukocytes or by blocking osteoclast  
 CC differentiation. The compound is useful in treating NF-kB mediated  
 CC conditions, where the condition is an inflammatory disorder, an  
 CC autoimmune disease, transplant rejection, osteoporosis, cancer,  
 CC Alzheimer's disease, atherosclerosis, a viral infection or ataxia  
 CC telangiectasia. The inflammatory disorder is asthma, allergies,  
 CC urticaria, anaphylaxis, cutaneous inflammation, sepsis, psoriasis,  
 CC rheumatoid arthritis, osteoarthritis, psoriatic arthritis, inflammatory  
 CC bowel disease, chronic obstructive pulmonary disease, vasculitis and  
 CC bursitis. The inflammatory disorder may also be dermatitis, eczema,  
 CC psoriasis, osteoarthritis, psoriatic arthritis, lupus and  
 CC sporadic arthritis. Also for Crohn's disease, ulcerative colitis,  
 CC polymyalgia, scleroderma, Wegner's granulomatosis, temporal arteritis,  
 CC cryoglobulinemia or multiple sclerosis. For chronic viral infections  
 CC caused by Epstein-Barr, cytomegalovirus or herpes simplex. Other viral  
 CC diseases include HIV and influenza. The compound may also be useful for  
 CC treating anaphylaxis, drug and food sensitivity, contact dermatitis,  
 CC sunburn or aging. The compound may be used to replace corticosteroids in  
 CC any application in which corticosteroids are used, including  
 CC immunosuppression in transplants and cancer therapy. Also for identifying  
 CC anti-inflammatory compounds and for diagnosis of an inflammatory disorder.  
 CC The compound may be administered alone or in combination with other known  
 CC anti-inflammatory agents. The present sequence is that of a mutated NEMO  
 CC binding domain of IKKbeta.  
 XX  
 SQ Sequence 6 AA;  
 QY Query Match 100.0%; Score 40; DB 23; Length 6;  
 DB Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LNMSWL 6  
 DB 1 LNMSWL 6  
 RESULT 2  
 AAM48514  
 ID AAM48514 standard; Peptide: 6 AA.  
 XX  
 AC AAM48514;  
 XX  
 DT 20-MAR-2002 (first entry)  
 XX  
 DE NBD mutant peptide SEQ ID NO 9.  
 XX

KW Antinflammatory; antiasthmatic; cytostatic; antipsoriatic; neutrotic;  
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;  
 KW immunosuppressive; dermatologic; neuroprotective; antithrombotic;  
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;  
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;  
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
 KW autoimmune disorder; multiple sclerosis; transplant rejection;  
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.  
 OS  
 XX Synthetic.  
 XX  
 PN WO200183554-A2.  
 XX  
 XX 08-NOV-2001.  
 PD  
 XX  
 XX 02-MAY-2001; 2001WO-US14346.  
 PF  
 XX  
 XX 02-MAY-2000; 2000US-201261P.  
 PR 22-AUG-2000; 2000US-0643260.  
 XX  
 XX (PRAE-) PRAECIS PHARM INC.  
 PA (UYVA ) UNIV YALE.  
 XX  
 PI May MJ, Ghosh S, Findeis MA, Phillips K;  
 XX  
 DR WPI: 2002-121889/16.  
 XX  
 XX Novel antinflammatory compound comprising membrane translocation  
 PT domain fused to NEMO binding sequence, useful for blocking nuclear  
 PT factor kappaB activation, and for treating asthma, lung inflammation,  
 PT psoriasis -  
 PS  
 XX Example 6; Page 47; 88pp; English.  
 PS  
 XX The invention relates to an antinflammatory compound (especially  
 CC AAM48628-AAM48645), comprising a membrane translocation domain  
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15  
 CC amino acid residues, fused to a NEMO binding sequence  
 CC (AAM48525-AAM48619). The antinflammatory compounds have antiasthmatic,  
 CC cytotatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,  
 CC antibacterial, immunosuppressive, dermatologic, neuroprotective,  
 CC neutrotic, antithrombotic, virucide and antiallergic activity. The  
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB  
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at  
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase  
 CC activation and subsequent decreased phosphorylation of IkappaB. The  
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,  
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,  
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,  
 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,  
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;  
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia  
 CC telangiectasia. The compounds are also useful for treating  
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,  
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and  
 CC arthritis.  
 CC  
 XX  
 SQ Sequence 6 AA;  
 QY Query Match 100.0%; Score 40; DB 23; Length 6;  
 DB Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LNMSWL 6  
 DB 1 LNMSWL 6  
 RESULT 3  
 ABB62034  
 ID ABB62034 standard; Protein: 295 AA.  
 XX

AC ABB62034;  
 XX 26-MAR-2002 (first entry)  
 DT  
 XX Drosophila melanogaster polypeptide SEQ ID NO 12894.  
 DE  
 XX Drosophila: developmental biology; cell signalling; insecticide;  
 KW pharmaceutical.  
 KM  
 XX Drosophila melanogaster.  
 OS  
 XX WO200171042-A2.  
 PN  
 XX 27-SEP-2001.  
 PD  
 XX 23-MAR-2001; 2001WO-US09231.  
 PF  
 XX 23-MAR-2000; 2000US-191637P.  
 PR 11-JUL-2000; 2000US-0614150.  
 XX  
 XX (PEKE ) PE CORP NY.  
 PA  
 XX Venter JC, Adams M, Li PMD, Myers EW;  
 PI  
 XX WPI: 2001-656860/75.  
 DR N-PSDB: ABL06137.  
 DR  
 XX New isolated nucleic acid detection reagent for detecting 1000 or more  
 PT genes from Drosophila and for elucidating cell signalling and cell-cell  
 PT interactions -  
 XX  
 XX Disclosure: SEQ ID NO 12894; 21pp + Sequence Listing; English.  
 PS  
 XX The invention relates to an isolated nucleic acid detection reagent  
 CC capable of detecting 1000 or more genes from Drosophila. The invention is  
 CC useful in developmental biology and in elucidating cell signalling and  
 CC cell-cell interactions in higher eukaryotes for the development of  
 CC insecticides, therapeutics and pharmaceutical drugs. The invention  
 CC discloses genomic DNA sequences (AB16176-AB130511), expressed DNA  
 CC sequences (AB101840-AB16175) and the encoded proteins  
 CC (AB57737-AB72072).  
 CC The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences.  
 CC  
 CC Sequence 295 AA:  
 SQ  
 Query Match 100.0%; Score 40; DB 22; Length 295;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 LNMWTL 6  
 DB 286 LNMWTL 291  
 AB77304  
 ID ABB77304 standard; protein; 756 AA.  
 XX  
 AC ABB77304;  
 XX  
 XX 14-JUN-2002 (first entry)  
 DT  
 XX Human IKKbeta mutant D738N.  
 DE  
 XX IKKbeat; IKKalpha; NEMO; NEMO binding domain; NBD; NF-kappaB; NF-kB;  
 KW kinase activation; leukocyte; inflammation; E-selectin; osteoclast;  
 KW autoimmune disease; transplant rejection; osteoporosis; cancer;  
 KW Alzheimer's disease; viral; infection; asthma; anaphylaxis; psoriasis;  
 KW rheumatoid arthritis; Crohn's disease; multiple sclerosis; HIV;  
 KW corticosteroid; immunosuppression; antiinflammatory; immunosuppressive;  
 KW osteopathic; cytostatic; neutrophic; neuroprotective; anti-HIV; human.

KW antiarteriosclerotic; virucide; antiasthmatic; anti-allergic;  
 KW dermatological; antibacterial; antipsoriatic; antirheumatic;  
 KW antiarthritic; osteopathic; antiulcer; mutant; mutein.  
 OS  
 XX Homo sapiens.  
 OS  
 XX Synthetic.  
 FH  
 XX Key Location/Qualifiers  
 FT Misc-difference 738  
 FT /note- "Wildtype Asp substituted by Asn"  
 XX  
 XX WO200183547-A2.  
 PN  
 XX 08-NOV-2001.  
 PD  
 XX 02-MAY-2001; 2001WO-US40654.  
 PF  
 XX 02-MAY-2000; 2000US-201261P.  
 PR 22-AUG-2000; 2000US-0643260.  
 XX  
 XX (UYVA ) UNIV YALE.  
 PA  
 XX May MJ, Ghosh S;  
 PI  
 XX WPI: 2002-179350/23.  
 DR  
 XX Modulating NF-kappaB induction in a cell, useful for treating e.g.  
 PT inflammatory disorders, osteoporosis and cancer, comprises contacting a  
 PT cell with an anti-inflammatory compound comprising at least one NEMO  
 PT binding domain -  
 XX  
 XX Example 11; Page -; 82pp; English.  
 PS  
 XX The invention relates to modulating NF-kappaB (NF-kB) induction in a cell  
 CC comprises contacting a cell with an anti-inflammatory compound  
 CC (ABB08725-ABB08742) comprising at least one NEMO binding domain  
 CC (ABB77313). The compound has acts through selective inhibition of  
 CC cytokine-mediated NF-kB activation by blocking the interaction of NEMO  
 CC with IKKbeta at the NEMO binding domain. Blockage of IKKbeta-NEMO  
 CC interaction results in inhibition of IKKbeta kinase activation and  
 CC subsequent decreased phosphorylation of Ikbap. The compound may also  
 CC act (directly or indirectly) by blocking the recruitment of leukocytes  
 CC into sites of acute and chronic inflammation, by down-regulating the  
 CC expression of E-selectin on leukocytes or by blocking osteoclast  
 CC differentiation. The compound is useful in treating NF-kB mediated  
 CC conditions, where the condition is an inflammatory disorder, an  
 CC autoimmune disease, transplant rejection, osteoporosis, cancer,  
 CC Alzheimer's disease, atherosclerosis, a viral infection or ataxia  
 CC telangiectasia. The inflammatory disorder is asthma, allergies,  
 CC urticaria, anaphylaxis, cutaneous inflammation, sepsis, psoriasis,  
 CC rheumatoid arthritis, osteoarthritis, psoriatic arthritis, inflammatory  
 CC bowel disease, chronic obstructive pulmonary disease, vasculitis and  
 CC bursitis. The inflammatory disorder may also be dermatitis, eczema,  
 CC psoriasis, osteoarthritis, psoriatic arthritis, lupus and  
 CC spondylarthritis. Also for Crohn's disease, ulcerative colitis,  
 CC polymyalgia, scleroderma, Wegner's granulomatosis, temporal arteritis,  
 CC cryoglobulinemia or multiple sclerosis. For chronic viral infections  
 CC caused by Epstein-Barr, cytomegalovirus or herpes simplex. Other viral  
 CC diseases include HIV and influenza. The compound may also be useful for  
 CC treating anaphylaxis, drug and food sensitivity, contact dermatitis,  
 CC sunburn or aging. The compound may be used to replace corticosteroids in  
 CC any application in which corticosteroids are used, including  
 CC immunosuppression in transplants and cancer therapy. Also for identifying  
 CC anti-inflammatory compounds and for diagnosis of an inflammatory disorder.  
 CC The compound may be administered alone or in combination with other known  
 CC anti-inflammatory agents. The present sequence is that of an IKKbeta  
 CC mutant, useful in examples of the invention.  
 CC Note: The present sequence is not given in the specification but is  
 CC derived from GenBank Accession No. 014920 (ABB77294).  
 XX  
 SO Sequence 756 AA:  
 Query Match 100.0%; Score 40; DB 23; Length 756;

Best Local Similarity 100.0%; Pred. No. 3.2e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LNMSWL 6  
DB 737 LNMSWL 742

## RESULT 5

AAV76530 standard; Protein; 135 AA.

AC AAY76530;

DT 10-APR-2000 (first entry)

DE Human ovarian tumor EST fragment encoded protein 26.

KW Expressed sequence tag; EST; human; ovarian tumor; anticancer;  
gene therapy; treatment.

OS Homo sapiens.

PN DE19817557-A1.

PD 21-OCT-1999.

PF 09-APR-1998; 98DE-1017557.

PR 09-APR-1998; 98DE-1017557.

PA (META-) METAGEN GES GENOMFORSCHUNG MEH.

PI Rosenthal A, Specht T, Hinzmann B, Schmitt A, Pilarsky C, Dahl E;

DR WPI: 1999-591920/51.

XX N-PSDB; AA277461.

PT New nucleic acid sequences expressed in ovarian, and some other, cancer  
tissues, and derived polypeptides, for treatment of ovarian cancer and  
identification of therapeutic agents

PS Claim 25; Page 254; 310pp; German.

CC This invention describes novel nucleic acid (cDNA) sequences (A) which  
have anticancer activity and are highly expressed in ovarian tumor  
tissue (and some also in testis and breast cancer tissue). The products  
of the invention can be used for gene therapy. (A) are used (i) for  
recombinant expression of polypeptides (B) and (ii) to isolate complete  
genes. (B) are used (i) to identify agents suitable for treatment of  
ovarian cancer; (ii) directly for treating this form of cancer  
CC (including expression from gene therapy vectors) and (iii) for generation  
of specific antibodies. (A) are identified by assembling ESTs (expressed  
sequence tags) from a particular tissue type before comparison of  
expression patterns. This allows a significantly longer fragment of the  
gene to be revealed, so should reduce the number of failures associated  
with the fact that ESTs from different libraries may represent different  
parts of the same unknown gene, distorting the estimated frequency of  
occurrence in a particular tissue. AAY76505-Y76638 represent protein  
CC fragments encoded by the human ovarian tumor CDNA library derived EST  
fragments represented in AA277450-277572.

SO Sequence 135 AA;

Query Match 95.0%; Score 38; DB 20; Length 135;

Best Local Similarity 83.3%; Pred. No. 1.1e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LNMSWL 6

DB 69 LNMSWI 74

RESULT 6  
AAAB85139 standard; Protein; 130 AA.

AC AAAB85139;

DT 07-NOV-2001 (first entry)

DE Human immune/haematopoietic antigen SEQ ID NO:12732.

KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;  
cytostatic; gene therapy; vaccine; metastasis.

OS Homo sapiens.

PN WO200157182-A2.

PD 09-AUG-2001.

PF 17-JAN-2001; 2001WO-US01354.

PR 31-JAN-2000; 2000US-0179065.

PR 04-FEB-2000; 2000US-0180628.

PR 24-FEB-2000; 2000US-0184664.

PR 02-MAR-2000; 2000US-0186350.

PR 16-MAR-2000; 2000US-0189874.

PR 17-MAR-2000; 2000US-0190076.

PR 18-APR-2000; 2000US-0198123.

PR 19-MAY-2000; 2000US-0205515.

PR 07-JUN-2000; 2000US-0209467.

PR 28-JUN-2000; 2000US-0214886.

PR 30-JUN-2000; 2000US-0215135.

PR 07-JUL-2000; 2000US-0216647.

PR 11-JUL-2000; 2000US-0216880.

PR 11-JUL-2000; 2000US-0217487.

PR 14-JUL-2000; 2000US-0217496.

PR 26-JUL-2000; 2000US-0218290.

PR 26-JUL-2000; 2000US-0220963.

PR 14-AUG-2000; 2000US-0220964.

PR 14-AUG-2000; 2000US-0224518.

PR 14-AUG-2000; 2000US-0224519.

PR 14-AUG-2000; 2000US-0225213.

PR 14-AUG-2000; 2000US-0225214.

PR 14-AUG-2000; 2000US-0225266.

PR 14-AUG-2000; 2000US-0225267.

PR 14-AUG-2000; 2000US-0225268.

PR 14-AUG-2000; 2000US-0225270.

PR 14-AUG-2000; 2000US-0225447.

PR 14-AUG-2000; 2000US-0225757.

PR 14-AUG-2000; 2000US-0225758.

PR 14-AUG-2000; 2000US-0225759.

PR 18-AUG-2000; 2000US-0226279.

PR 22-AUG-2000; 2000US-0226681.

PR 22-AUG-2000; 2000US-0226686.

PR 22-AUG-2000; 2000US-0227182.

PR 23-AUG-2000; 2000US-0227009.

PR 30-AUG-2000; 2000US-0228924.

PR 01-SEP-2000; 2000US-0229287.

PR 01-SEP-2000; 2000US-0229343.

PR 01-SEP-2000; 2000US-0229344.

PR 01-SEP-2000; 2000US-0229345.

PR 05-SEP-2000; 2000US-0229509.

PR 05-SEP-2000; 2000US-0229513.

PR 06-SEP-2000; 2000US-0230437.

PR 06-SEP-2000; 2000US-0230438.

PR 08-SEP-2000; 2000US-0231242.

PR 08-SEP-2000; 2000US-0231243.

PR 08-SEP-2000; 2000US-0231244.

PR 08-SEP-2000; 2000US-0231413.

PR 08-SEP-2000; 2000US-0231414.

PR 08-SEP-2000; 2000US-0232080.

PR 08-SEP-2000; 2000US-0232081.

PR 12-SEP-2000; 2000US-0231966.



PN	MO200028040-A2.
XX	18-MAY-2000.
PD	
XX	05-NOV-1999; 99WO-US26260.
XX	06-NOV-1998; 98US-0107507.
XX	20-NOV-1998; 98US-0109409.
PR	(UYOR-) UNIV OREGON HEALTH SCI.
PA	
XX	Wong SM, Athelme MK, Searles RP.
PI	WPI; 2000-376552/32.
DR	
XX	
XX	New rhesus rhadno virus for producing non-human primate model useful
PT	for testing potential treatments and efficacy of the candidate vaccine
PT	for conditions associated with RRV infection
XX	
PS	Claim 5; Page 128-129; 141pp; English.
XX	
CC	The present invention describes a novel rhesus macaque rhadinovirus
CC	called macaca mulatta rhadinovirus 17577 (RRV). AAC64754 represents the
CC	RRV genome sequence, and AAB53123 to AAB53204 represent the proteins
CC	encoded by the genome sequence. The present invention also specifically
CC	claims the individual open reading frame (ORF) nucleotide sequences from
CC	the genome which encode the individual proteins, but these sequences are
CC	not given. A non-human animal infected with RRV can be used for testing
CC	the efficacy of drug in the treatment of condition associated with
CC	infection with RRV such as Kaposi's sarcoma, lymphoproliferative
CC	disorders, B-cell hyperplasia, lymphadenopathy, splenomegaly,
CC	hypergammaglobulinemia or autoimmune haemolytic anaemia, by
CC	administering the drug to a immuno-compromised non-human primate
CC	preferably Rhesus macaque monkey obtained by as a result of infection
CC	by Simian Immunodeficiency Virus (SIV). RRV is useful for producing
CC	non-human primate model for testing potential treatments for conditions
CC	associated with RRV infection. It is also useful for testing the
CC	efficacy of the candidate vaccine against RRV infection or conditions
CC	associated with its infection by administering the vaccine to the
CC	subject capable of infection with RRV, inoculating the subject with RRV
CC	and observing the effect of vaccine. AAC64755 to AAC64765 and AAB53205
CC	to AAB53213 represent sequence used in the exemplification of the
CC	present invention.
XX	
SO	Sequence 464 AA;
Query Match	92.5%; Score 37; DB 21; Length 464;
Best Local Similarity	83.3%; Pred. No. 5.3e+02;
Matches	5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY	1 LNMWML 6
DB	397 VNMSWL 402
RESULT 8	
AAU35054	AAU35054 standard; Protein: 464 AA.
AC	AAU35054;
XX	
DT	13-FEB-2002 (first entry)
XX	
DE	Enterococcus faecalis cellular proliferation protein #341.
KW	Antisense; prokaryotic cellular proliferation protein;
KW	antibiotic; antibacterial; drug design.
XX	
OS	Enterococcus faecalis.
XX	
PN	MO200170955-A2.
XX	
DD	27-SEP-2001.

```

XX 21-MAR-2001; 2001WO-US09180.
PR 21-MAR-2000; 2000US-191078P.
PR 23-MAY-2000; 2000US-206848P.
PR 26-MAY-2000; 2000US-207272P.
PR 23-OCT-2000; 2000US-242578P.
PR 27-NOV-2000; 2000US-253625P.
PR 22-DEC-2000; 2000US-257931P.
PR 16-FEB-2001; 2001US-269308P.
XX
XX (ELIT-).ELITRA PHARM INC.
XX
XX Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GT;
XX Yamamoto RT, Xu HH;
XX WPI; 2001-611495/70.
XX DR N-PSDB; AAS52913.
XX
XX New polynucleotides for the identification and development of
XX antibiotics, comprise sequences of antisense nucleic acids -
XX
XX Example 3; Seq ID No 10647; 51pp; English.
XX
XX The invention relates to antisense inhibitors of genes essential to
XX prokaryotic cellular proliferation, their use in identifying the
XX genes, their use in the discovery of novel antibiotics, the essential
XX genes themselves and the encoded proteins. The prokaryotes used are
XX Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella
XX pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The
XX invention is also useful for the identification of potential new targets
XX for antibiotic development. The antisense nucleic acids can also be used
XX to identify proteins used in proliferation, to express these proteins,
XX and to obtain antibodies capable of binding to the expressed proteins.
XX The proteins can be used to screen compounds in rational drug discovery
XX programmes. The antisense nucleic acid sequence is also useful to screen
XX for homologous nucleic acids which are required for cell proliferation in
XX a wide variety of organisms. The present sequence represents an
XX essential prokaryotic cellular proliferation protein.
XX Note: The sequence data for this patent did not form part
XX of the printed specification, but was obtained in electronic
XX format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 464 AA;
XX
XX Query Match 90.0%; Score 36; DB 22; Length 464;
XX Best Local Similarity 100.0%; Pred. No. 7.4e+02;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0
XX
XX 2.NMSWL 6
XX |||||
XX
XX Db 422 NMSWL 426
XX
XX RESULT 9
XX ID AU033501
XX AU033501 standard; Protein: 467 AA.
XX
XX AAU033501;
XX
XX 14-FEB-2002 (first entry)
XX
XX Enterococcus faecalis cellular proliferation protein #137.
XX
XX Antisense; prokaryotic cellular proliferation protein;
XX antibiotic; antibacterial; drug design.
XX
XX Enterococcus faecalis.
XX
XX WO200170955-A2.
XX
XX 27-SEP-2001.
XX

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XX 21-MAR-2001; 2001MO-US09180.  
 PF  
 XX 21-MAR-2000; 2000US-191078P.  
 PR 23-MAY-2000; 2000US-206848P.  
 PR 26-MAY-2000; 2000US-207727P.  
 PR 23-OCT-2000; 2000US-242578P.  
 PR 27-NOV-2000; 2000US-253625P.  
 PR 22-DEC-2000; 2000US-257931P.  
 PR 16-FEB-2001; 2001US-269308P.  
 XX  
 PA (ELIT-) ELITRA PHARM INC.  
 XX  
 PI Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;  
 PI Yamamoto RT, Xu HH;  
 XX  
 DR WPI: 2001-611495/70.  
 DR N-PSDB; NMS51360.  
 XX  
 PT New polynucleotides for the identification and development of  
 PT antibiotics, comprise sequences of antisense nucleic acids -  
 PS  
 PS Example 3; Seq ID No 4997; 511pp; English.  
 CC The invention relates to antisense inhibitors of genes essential to  
 CC prokaryotic cellular proliferation, their use in identifying the  
 CC genes, their use in the discovery of novel antibiotics, the essential  
 CC genes themselves and the encoded proteins. The prokaryotes used are  
 CC Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella  
 CC pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The  
 CC invention is also useful for the identification of potential new targets  
 CC for antibiotic development. The antisense nucleic acids can also be used  
 CC to identify proteins used in proliferation, to express these proteins,  
 CC and to obtain antibodies capable of binding to the expressed proteins.  
 CC The proteins can be used to screen compounds in rational drug discovery  
 CC programmes. The antisense nucleic acid sequence is also useful to screen  
 CC for homologous nucleic acids which are required for cell proliferation in  
 CC a wide variety of organisms. The present sequence represents an  
 CC essential prokaryotic cellular proliferation protein.  
 CC Note: The sequence data for this patent did not form part  
 CC of the printed specification, but was obtained in electronic  
 CC format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences.  
 CC  
 XX  
 SQ Sequence 467 AA;  
 Query Match 90.0%; Score 36; DB 22; Length 467;  
 Best Local Similarity 100.0%; Pred. No. 7.5e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 NMSWL 6  
 |||||  
 DB 425 NMSWL 429

RESULT 10  
 ABB08725  
 ID ABB08725 standard; peptide; 6 AA.  
 XX  
 AC ABB08725;  
 XX  
 DT 14-JUN-2002 (first entry)  
 XX  
 DE IKKbeta NEMO binding domain peptide SEQ ID NO 2.  
 XX  
 XX IKKbeta; IKKalpha; NEMO; NEMO binding domain; NBD; NF-kappaB; NF-kB;  
 KW kinase activation; leukocyte; inflammation; E-selectin; osteoclast;  
 KW autoimmune disease; transplant rejection; osteoporosis; cancer;  
 KW Alzheimer's disease; viral; infection; asthma; anaphylaxis; psoriasis;  
 KW rheumatoid arthritis; Crohn's disease; multiple sclerosis; HIV;  
 KW corticosteroid; immunosuppression; antiinflammatory; immunosuppressive;  
 KW osteopathic; cytostatic; nootropic; neuroprotective; anti-HIV; human;  
 KW antiarteriosclerotic; virucide; antiaesthetic; antiallergic;

KW dermatological; antibacterial; antipsoriatic; antirheumatic;  
 KW antiarthritic; osteopathic; antitumor.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200183547-A2.  
 XX  
 PD 08-NOV-2001.  
 XX  
 PF 02-MAY-2001; 2001MO-US40654.  
 XX  
 PR 02-MAY-2000; 2000US-201261P.  
 PR 22-AUG-2000; 2000US-0643260.  
 XX  
 PA (UYVA ) UNIV YALE.  
 XX  
 PI May MJ, Ghosh S;  
 XX  
 DR WPI: 2002-179350/23.  
 XX  
 PT Modulating NF-kappaB induction in a cell, useful for treating e.g.  
 PT inflammatory disorders, osteoporosis and cancer, comprises contacting a  
 PT cell with an anti-inflammatory compound comprising at least one NEMO  
 PT binding domain -  
 PS  
 PS Claim 23; Page 44; 82pp; English.  
 CC The invention relates to modulating NF-kappaB (NF-kB) induction in a cell  
 CC comprising contacting a cell with an anti-inflammatory compound  
 CC (ABB08725-ABB08742) comprising at least one NEMO binding domain  
 CC (ABB77313). The compound has acts through selective inhibition of  
 CC cytokine-mediated NF-kB activation by blocking the interaction of NEMO  
 CC with IKKbeta at the NEMO binding domain. Blockage of IKKbeta-NEMO  
 CC interaction results in inhibition of IKKbeta kinase activation and  
 CC subsequent decreased phosphorylation of Ikbpp. The compound may also  
 CC act (directly or indirectly) by blocking the recruitment of leukocytes  
 CC into sites of acute and chronic inflammation, by down-regulating the  
 CC expression of E-selectin on leukocytes or by blocking osteoclast  
 CC differentiation. The compound is useful in treating NF-kB mediated  
 CC conditions, where the condition is an inflammatory disorder, an  
 CC autoimmune disease, transplant rejection, osteoporosis, cancer,  
 CC Alzheimer's disease, atherosclerosis, a viral infection or ataxia  
 CC telangiectasia. The inflammatory disorder is asthma, allergies,  
 CC urticaria, anaphylaxis, cutaneous inflammation, sepsis, psoriasis,  
 CC rheumatoid arthritis, osteoarthritis, psoriatic arthritis, inflammatory  
 CC bowel disease, chronic obstructive pulmonary disease, vasculitis and  
 CC bursitis. The inflammatory disorder may also be dermatitis, eczema,  
 CC psoriasis, osteoarthritis, psoriatic arthritis, lupus and  
 CC spondylarthritis. Also for Crohn's disease, ulcerative colitis,  
 CC polymyalgia, scleroderma, Wegner's granulomatosis, temporal arteritis,  
 CC cryoglobulinaemia or multiple sclerosis. For chronic viral infections  
 CC caused by Epstein-Barr, cytomegalovirus or herpes simplex. Other viral  
 CC diseases include HIV and influenza. The compound may also be useful for  
 CC treating anaphylaxis, drug and food sensitivity, contact dermatitis,  
 CC sunburn or aging. The compound may be used to replace corticosteroids in  
 CC any application in which corticosteroids are used, including  
 CC immunosuppression in transplants and cancer therapy. Also for identifying  
 CC antiinflammatory compounds and for diagnosis of an inflammatory disorder.  
 CC The compound may be administered alone or in combination with other known  
 CC anti-inflammatory agents. The present sequence is that of the NEMO  
 CC binding domain of IKKbeta.  
 CC  
 XX  
 SQ Sequence 6 AA;  
 Query Match 87.5%; Score 35; DB 23; Length 6;  
 Best Local Similarity 83.3%; Pred. No. 7.8e+05;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LNMSWL 6  
 |||||  
 DB 1 LDMSWL 6

RESULT 11  
 AAM48530  
 ID AAM48530 standard; Peptide: 6 AA.  
 AC AAM48530;  
 XX  
 DT 20-MAR-2002 (first entry)  
 XX  
 DE Anti-Inflammatory peptide SEQ ID NO 33.  
 XX  
 DE Antiinflammatory; antiasthmatic; cytosolic; antipsoriatic; nootropic;  
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;  
 KW immunosuppressive; dermatological; neuroprotective; antithrombotic;  
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;  
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;  
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
 KW autoimmune disorder; multiple sclerosis; transplant rejection;  
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200183554-A2.  
 XX  
 PD 08-NOV-2001.  
 XX  
 PE 02-MAY-2001; 2001WO-US14346.  
 XX  
 PR 02-MAY-2000; 2000US-201261P.  
 XX  
 PR 22-AUG-2000; 2000US-0643260.  
 XX  
 PA (PRAE-) PRAECIS PHARM INC.  
 XX  
 PI (UYVA ) UNIV YALE.  
 XX  
 PI May MJ, Ghosh S, Flindeis MA, Phillips K;  
 XX  
 DR WPI: 2002-121889/16.  
 XX  
 PT Novel antiinflammatory compound comprising membrane translocation  
 PT domain fused to NEMO binding sequence, useful for blocking nuclear  
 PT factor kappab activation, and for treating asthma, lung inflammation,  
 PT psoriasis  
 XX  
 PS Claim 6; Page 61; 88pp; English.  
 XX  
 CC The invention relates to an antiinflammatory compound (especially  
 CC AAM48628-AAM48645), comprising a membrane translocation domain  
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15  
 CC amino acid residues, fused to a NEMO binding sequence  
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,  
 CC cytosolic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,  
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,  
 CC nootropic, antithrombotic, virucide and antiallergic activity. The  
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB  
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at  
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase  
 CC activation and subsequent decreased phosphorylation of IkappaB. The  
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,  
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,  
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,  
 CC burstitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,  
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;  
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia  
 CC telangiectasia. The compounds are also useful for treating  
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,  
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and  
 CC arthritis.  
 CC  
 SO Sequence 6 AA.  
 XX  
 Query Match 87.5%; Score 35; DB 23; Length 6;  
 Best Local Similarity 83.3%; Pred. No. 7.8e+05;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNWSWL 6  
 DB 1 LDMSWL 6  
 XX  
 DE  
 ID AAM48655 standard; Peptide: 6 AA.  
 XX  
 AC AAM48655;  
 XX  
 DT 20-MAR-2002 (first entry)  
 XX  
 DE NBD mutant peptide SEQ ID NO 2.  
 XX  
 DE Antiinflammatory; antiasthmatic; cytosolic; antipsoriatic; nootropic;  
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;  
 KW immunosuppressive; dermatological; neuroprotective; antithrombotic;  
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;  
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;  
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
 KW autoimmune disorder; multiple sclerosis; transplant rejection;  
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200183554-A2.  
 XX  
 PD 08-NOV-2001.  
 XX  
 PE 02-MAY-2001; 2001WO-US14346.  
 XX  
 PR 02-MAY-2000; 2000US-201261P.  
 XX  
 PR 22-AUG-2000; 2000US-0643260.  
 XX  
 PA (PRAE-) PRAECIS PHARM INC.  
 XX  
 PI (UYVA ) UNIV YALE.  
 XX  
 PI May MJ, Ghosh S, Flindeis MA, Phillips K;  
 XX  
 DR WPI: 2002-121889/16.  
 XX  
 PT Novel antiinflammatory compound comprising membrane translocation  
 PT domain fused to NEMO binding sequence, useful for blocking nuclear  
 PT factor kappab activation, and for treating asthma, lung inflammation,  
 PT psoriasis  
 XX  
 PS Example 6; Page 47; 88pp; English.  
 XX  
 CC The invention relates to an antiinflammatory compound (especially  
 CC AAM48628-AAM48645), comprising a membrane translocation domain  
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15  
 CC amino acid residues, fused to a NEMO binding sequence  
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,  
 CC cytosolic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,  
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,  
 CC nootropic, antithrombotic, virucide and antiallergic activity. The  
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB  
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at  
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase  
 CC activation and subsequent decreased phosphorylation of IkappaB. The  
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,  
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,  
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,  
 CC burstitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,  
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;  
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia  
 CC telangiectasia. The compounds are also useful for treating  
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,  
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and  
 CC arthritis.

XX Sequence 6 AA;  
 SQ Query Match 87.5%; Score 35; DB 23; Length 6;  
 Best Local Similarity 83.3%; Pred. No. 7.8e+05;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LNMSTL 6  
 1:|||||  
 DB 1 LDMSTL 6

RESULT 13  
 AAM48534  
 ID AAM48534 standard; Peptide; 7 AA.  
 XX AAM48534;  
 AC  
 XX 20-MAR-2002 (first entry)  
 DT  
 XX Anti-inflammatory peptide SEQ ID NO 37.  
 DE  
 XX Anti-inflammatory; antiallergic; cytosolic; antipsoriatic; neurotropic;  
 KM antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;  
 KM immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;  
 KM antiallergic; membrane translocation domain; NEMO binding domain; eczema;  
 KM cytokine; NF-kappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;  
 KM rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
 KM autoimmune disorder; multiple sclerosis; transplant rejection;  
 KM osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
 KM ataxia telangiectasia; allergy; anaphylaxis; arthritis.  
 XX  
 OS Synthetic.  
 XX WO200183554-A2.  
 PN  
 XX 08-NOV-2001.  
 PD  
 XX 02-MAY-2001; 2001WO-US14346.  
 PF  
 XX 02-MAY-2000; 2000US-201261P.  
 PR 22-AUG-2000; 2000US-0643260.  
 XX  
 PA (PRAE-) PRAECIS PHARM INC.  
 PA (UYVA ) UNIV YALE.  
 PI  
 XX May MJ, Ghosh S, Finkel MA, Phillips K;  
 PI WPI; 2002-121889/16.  
 DR  
 XX Novel anti-inflammatory compound comprising membrane translocation  
 PT domain fused to NEMO binding sequence, useful for blocking nuclear  
 PT factor kappaB activation, and for treating asthma, lung inflammation,  
 PT psoriasis -  
 PS  
 XX Claim 6; Page 61; 88pp; English.  
 PS  
 XX The invention relates to an anti-inflammatory compound (especially  
 CC AAM48628-AAM48645), comprising a membrane translocation domain  
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15  
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 CC (AAM48525-AAM48619). The anti-inflammatory compounds have antiallergic,  
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 CC neurotropic, antiatherosclerotic, virucide and antiallergic activity. The  
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 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at  
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase  
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 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,  
 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,

CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;  
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia  
 CC telangiectasia. The compounds are also useful for treating  
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,  
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and  
 CC arthritis.  
 XX  
 SQ Sequence 7 AA;  
 OY Query Match 87.5%; Score 35; DB 23; Length 7;  
 Best Local Similarity 83.3%; Pred. No. 7.8e+05;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LNMSTL 6  
 1:|||||  
 DB 1 LDMSTL 6

RESULT 14  
 AAM48527  
 ID AAM48527 standard; Peptide; 8 AA.  
 XX AAM48527;  
 AC  
 XX 20-MAR-2002 (first entry)  
 DT  
 XX Anti-inflammatory peptide SEQ ID NO 30.  
 DE  
 XX Anti-inflammatory; antiallergic; cytosolic; antipsoriatic; neurotropic;  
 KM antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;  
 KM immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;  
 KM antiallergic; membrane translocation domain; NEMO binding domain; eczema;  
 KM cytokine; NF-kappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;  
 KM rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
 KM autoimmune disorder; multiple sclerosis; transplant rejection;  
 KM osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
 KM ataxia telangiectasia; allergy; anaphylaxis; arthritis.  
 XX  
 OS Synthetic.  
 XX WO200183554-A2.  
 PN  
 XX 08-NOV-2001.  
 PD  
 XX 02-MAY-2001; 2001WO-US14346.  
 PF  
 XX 02-MAY-2000; 2000US-201261P.  
 PR 22-AUG-2000; 2000US-0643260.  
 XX  
 PA (PRAE-) PRAECIS PHARM INC.  
 PA (UYVA ) UNIV YALE.  
 PI  
 XX May MJ, Ghosh S, Finkel MA, Phillips K;  
 PI WPI; 2002-121889/16.  
 DR  
 XX Novel anti-inflammatory compound comprising membrane translocation  
 PT domain fused to NEMO binding sequence, useful for blocking nuclear  
 PT factor kappaB activation, and for treating asthma, lung inflammation,  
 PT psoriasis -  
 PS  
 XX Claim 6; Page 61; 88pp; English.  
 PS  
 XX The invention relates to an anti-inflammatory compound (especially  
 CC AAM48628-AAM48645), comprising a membrane translocation domain  
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15  
 CC amino acid residues, fused to a NEMO binding sequence  
 CC (AAM48525-AAM48619). The anti-inflammatory compounds have antiallergic,  
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 CC neurotropic, antiatherosclerotic, virucide and antiallergic activity. The  
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 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at

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 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;  
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia  
 CC telangiectasia. The compounds are also useful for treating  
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,  
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and  
 CC arthritis.

XX Sequence 8 AA;  
 SQ

Query Match 87.5%; Score 35; DB 23; Length 8;  
 Best Local Similarity 83.3%; Pred. No. 7.8e+05;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNMSTL 6  
 1:11111  
 DB 3 LDMSTL 8

RESULT 15  
 AAM48535  
 ID AAM48535 standard; Peptide: 8 AA.  
 XX  
 AC AAM48535;  
 XX  
 DT 20-MAR-2002 (first entry)  
 XX  
 DE Anti-inflammatory peptide SEQ ID NO 38.  
 XX  
 KW Anti-inflammatory; antiasthmatic; cytostatic; antipsoriatic; neotropic;  
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;  
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;  
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;  
 KW cytokine; NFkappaB; Ikkappa kinase beta; IKKbeta; cancer; psoriasis;  
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
 KW autoimmune disorder; multiple sclerosis; transplant rejection;  
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.

XX OS Synthetic.  
 XX  
 PN WO200183554-A2.  
 XX  
 PD 08-NOV-2001.  
 XX  
 PF 02-MAY-2001; 2001WO-US14346.  
 XX  
 PR 02-MAY-2000; 2000US-201261P.  
 PR 22-AUG-2000; 2000US-0643260.  
 XX  
 PA (PRAE-) PRAECIS PHARM INC.  
 PA (UYVA) UNIV YALE.  
 XX  
 PI May MJ, Ghosh S, Flindels MA, Phillips K;  
 XX  
 DR WPI; 2002-121889/16.  
 XX  
 PT Novel antiinflammatory compound comprising membrane translocation  
 PT domain fused to NEMO binding sequence, useful for blocking nuclear  
 PT factor kappab activation, and for treating asthma, lung inflammation,  
 PT psoriasis  
 XX  
 PS Claim 6; Page 61; 88pp; English.  
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 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;  
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia  
 CC telangiectasia. The compounds are also useful for treating  
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,  
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and  
 CC arthritis.

SQ Sequence 8 AA;

Query Match 87.5%; Score 35; DB 23; Length 8;

Best Local Similarity 83.3%; Pred. No. 7.8e+05;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNMSTL 6  
 1:11111

DB 1 LDMSTL 6

Search completed: May 30, 2003, 14:49:54  
 Job time : 19.7529 secs



RP SEQUENCE FROM N.A.  
 RC STRATIN-TN;  
 RX MEDLINE-21128732; PubMed-11234002;  
 RA Cole S.T., Elgmeler K., Parkhill J., James K.D., Thomson N.R.,  
 RA Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,  
 RA Mungall K., Basham D., Brown D., Chillingworth T., Connor R.,  
 RA Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N.,  
 RA Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,  
 RA Murphy L., Oliver K., Quail M.A., Rajadream M.A., Rutherford K.M.,  
 RA Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,  
 RA Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,  
 RA Barrett B.G.;  
 RT "Massive gene decay in the leprosy bacillus";  
 RL Nature 409:1007-1011(2001).  
 CC -1- FUNCTION: CATALYZES THE BIOSYNTHESIS OF DEOXYRIBONUCLEOTIDES FROM  
 THE CORRESPONDING RIBONUCLEOTIDES, PRECURSORS THAT ARE NECESSARY  
 FOR DNA SYNTHESIS (BY SIMILARITY).  
 CC -1- CATALYTIC ACTIVITY: 2'-deoxyribonucleoside diphosphate + oxidized  
 thioedoxin + H(2)O -> ribonucleoside diphosphate + reduced  
 thioedoxin.  
 CC -1- COFACTOR: BINDS 2 IRON IONS (BY SIMILARITY).  
 CC -1- PATHWAY: FIRST REACTION IN THE DNA REPLICATION PATHWAY.  
 CC -1- SUBUNIT: Tetramer of two alpha and two beta chains  
 (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE RIBONUCLEOSIDE DIPHOSPHATE REDUCTASE  
 SMALL CHAIN FAMILY. MORE SIMILAR TO ENTEROBACTERIAL NRDF THAN TO  
 NRDF.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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 the European Bioinformatics Institute. There are no restrictions on its  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL: AL583923; CAC30684.1; -  
 DR HSSP: P17424; 2RZF.  
 DR Leptoma; ML1731;  
 DR InterPro: IPR000358; RibonucL\_redctse.  
 DR Pfam: PF00268; ribonuc\_red\_sm; 1.  
 DR PROSITE: PS00368; RIBORED\_SMALL; 1.  
 KW Oxidoreductase; DNA replication; Iron; Complete proteome.  
 FT METAL 73 73  
 FT METAL 104 104 IRON 1 AND 2 (BY SIMILARITY).  
 FT METAL 107 107 IRON 1 (BY SIMILARITY).  
 FT METAL 164 164 IRON 2 (BY SIMILARITY).  
 FT METAL 198 198 IRON 2 (BY SIMILARITY).  
 FT METAL 201 201 IRON 2 (BY SIMILARITY).  
 FT ACT SITE 111 111 BY SIMILARITY.  
 SQ SEQUENCE 325 AA; 37316 MW; A80D29751183358B CRC64;

Query Match 87.5%; Score 35; DB 1; Length 325;  
 Best Local Similarity 66.7%; Pred. No. 81;  
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 LMSWL 6  
 DB 15 INMNL 20

RESULT 3  
 ID IKKA\_HUMAN STANDARD; PRT; 745 AA.  
 AC 01511; 014666; 013132; 092467;  
 DT 16-OCT-2001 (Rel. 40; Created)  
 DT 16-OCT-2001 (Rel. 40; Last sequence update)  
 DT 15-JUN-2002 (Rel. 41; Last annotation update)  
 DE Inhibitor of nuclear factor kappa-B kinase alpha subunit (EC 2.7.1.1-)  
 DE (I kappa-B kinase alpha) (IKK-alpha) (IKK-A) (Ikkappa kinase)  
 DE (I kappa-B kinase 1) (IKK1) (Conserved helix-loop-helix ubiquitons  
 kinase) (Nuclear factor NFkappaB inhibitor kinase alpha) (NFKBIA).  
 GN IKKA OR CHUK.

OS Homo sapiens (human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-44.  
 RC TISSUE-T-cell;  
 RX MEDLINE-97386461; PubMed-9244310;  
 RA Regnier C.H., Song H.Y., Gao X., Goeddel D.V., Cao Z., Rothe M.;  
 RT "Identification and characterization of an IkappaB kinase";  
 RL Cell 90:373-383(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
 RX MEDLINE-97394468; PubMed-9252186;  
 RA Didonato J.A., Hayakawa M., Rothwarf D.M., Zandi E., Karin M.;  
 RT "A cytokine-responsive IkappaB kinase that activates the transcription  
 factor NF-kappaB";  
 RL Nature 388:548-554(1997).  
 RN [3]  
 RP SEQUENCE FROM N.A., PARTIAL SEQUENCE, AND MUTAGENESIS OF LYS-44 AND  
 RP SER-176.  
 RC TISSUE-Cervical carcinoma;  
 RX MEDLINE-98008813; PubMed-9346484;  
 RA Mercurio F., Zhu H., Murray B.W., Shevchenko A., Bennett B.L.,  
 RA Li J.W., Young D.B., Barbosa M., Mann M., Manning A., Rao A.;  
 RT "IKK-1 and IKK-2: cytokine-activated IkappaB kinases essential for  
 NF-kappaB activation";  
 RL Science 278:860-866(1997).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-Heart;  
 RX MEDLINE-99032998; PubMed-9813230;  
 RA Hu M.C.-T., Wang Y.-P.;  
 RT "IkappaB kinase-alpha and -beta genes are coexpressed in adult and  
 RT embryonic tissues but localized to different human chromosomes";  
 RL Gene 223:31-40(1998).  
 RN [5]  
 RP SEQUENCE OF 32-745 FROM N.A.  
 RC TISSUE-Cervical carcinoma;  
 RX MEDLINE-96258427; PubMed-8777433;  
 RA Connelly M.A., Marcu K.B.;  
 RT "CHUK, a new member of the helix-loop-helix and leucine zipper  
 RT families of interacting proteins, contains a serine-threonine kinase  
 RT catalytic domain";  
 RL Cell. Mol. Biol. Res. 41:537-549(1995).  
 RN [6]  
 RP PHOSPHORYLATION BY MAP3K14/NIK, AND MUTAGENESIS OF S-176; T-179 AND  
 RP S-180.  
 RX MEDLINE-98188283; PubMed-9520446;  
 RA Ling L., Cao Z., Goeddel D.V.;  
 RT "NF-kappaB-inducing kinase activates IKK-alpha by phosphorylation of  
 RT Ser-176";  
 RL Proc. Natl. Acad. Sci. U.S.A. 95:3792-3797(1998).  
 RN [7]  
 RP PHOSPHORYLATION BY AKT, AND MUTAGENESIS OF THR-23.  
 RX MEDLINE-99413720; PubMed-10485710;  
 RA Donner D.B.;  
 RT "NF-kappaB activation by tumour necrosis factor requires the Akt  
 RT serine-threonine kinase";  
 RL Nature 401:82-85(1999).  
 RN [8]  
 RP IKKA-IKKB BINDING.  
 RX MEDLINE-99212141; PubMed-10195894;  
 RA Delhase M., Hayakawa M., Chen Y., Karin M.;  
 RT "Positive and negative regulation of IkappaB kinase activity through  
 RT IkappaB subunit phosphorylation";  
 RL Science 284:309-313(1999).  
 RN [9]  
 RP IKK PHOSPHORYLATION.  
 RX MEDLINE-99038238; PubMed-9819420;  
 RA Nemoto S., Didonato J.A., Lin A.;  
 RT "Coordinate regulation of IkappaB kinases by mitogen-activated protein

RT kinase kinase kinase 1 and NF-kappaB-inducing kinase.";  
 RL Mol. Cell. Biol. 18:7336-7343(1998).  
 RN [10]  
 RP MEDLINE-20178139; PubMed-10712233;  
 RA Jobin C., Sartor R.B.;  
 RT "The I kappa B/NF-kappa B system: a key determinant of mucosal  
 inflammation and protection.";  
 RL Am. J. Physiol. 278:C451-C462(2000).  
 CC -1- FUNCTION: PHOSPHORYLATES INHIBITORS OF NF-KAPPA-B THUS LEADING TO  
 THE DISSOCIATION OF THE INHIBITOR/NF-KAPPA-B COMPLEX AND  
 ULTIMATELY THE DEGRADATION OF THE INHIBITOR.  
 CC -1- ENZYME REGULATION: ACTIVATED WHEN PHOSPHORYLATED AND INACTIVATED  
 WHEN DEPHOSPHORYLATED.  
 CC -1- SUBUNIT: PREFERENTIALLY FOUND AS A HETERODIMER WITH IKK-BETA BUT  
 ALSO AS AN HOMODIMER. DIRECTLY INTERACTS WITH IKK-GAMMA/NEMO.  
 CC HETERODIMERS FORM THE ACTIVE COMPLEX. THE TRIPARTITE COMPLEX CAN  
 ALSO BIND TO MAPK14/NIK, MEK1, IKAP AND IKK-ALPHA-P55-P50  
 COMPLEX. A WEAK INTERACTION WITH TRAF2 CANNOT BE EXCLUDED.  
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.  
 CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED.  
 CC -1- PTM: PHOSPHORYLATED BY MAPK14/NIK, AKT AND TO A LESSER EXTENT BY  
 MEK1, AND DEPHOSPHORYLATED BY PP2A. AUTOPHOSPHORYLATED.  
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 CC IKAPAB KINASE SUBFAMILY.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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 the European Bioinformatics Institute. There are no restrictions on its  
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 or send an email to [license@sb-sib.ch](mailto:license@sb-sib.ch)).  
 CC -----  
 DR EMBL: AF012890; AAC51662.1; -  
 DR EMBL: AF009225; AAC51671.1; -  
 DR EMBL: AF080157; AAD08996.1; -  
 DR HSSP: U22512; AAC50713.1; -  
 DR HSSP: Q63450; 1A06.  
 DR Genew: HGNC:1974; CHUK.  
 DR MIM: 600664; -  
 DR InterPro: IPR000719; Euk\_Pkinase.  
 DR InterPro: IPR002290; Ser\_thr\_Pkinase.  
 DR Pfam: PF00069; Pkinase; 1.  
 DR PRODOM: PD000001; Euk\_Pkinase; 1.  
 DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE: PS00108; PROTEIN\_KINASE\_SF; 1.  
 DR PROSITE: PS00111; PROTEIN\_KINASE\_DOM; 1.  
 KW Transferase; Serine/threonine-protein kinase; ATP-binding;  
 phosphorylation.  
 KW DOMAIN 15 302  
 FT DOMAIN 455 476  
 FT DOMAIN 738 743  
 FT NP\_BIND 21 29  
 FT BINDING 44 44  
 FT ACT\_SITE 144 144  
 FT MOD\_RES 23 23  
 FT MOD\_RES 176 176  
 FT MOD\_RES 23 23  
 FT MUTAGEN 44 44  
 FT MUTAGEN 44 44  
 FT MUTAGEN 176 176  
 FT MUTAGEN 176 176  
 FT MUTAGEN 179 179  
 FT MUTAGEN 180 180  
 FT CONFLICT 543 543  
 FT CONFLICT 604 604  
 FT CONFLICT 679 680  
 FT CONFLICT 684 684  
 FT CONFLICT 686 687  
 SQ SEQUENCE 745 AA; 84653 MW; 7A90B539C9A56C2 CRC64;

Query Match 87.5%; Score 35; DB 1; Length 745;  
 Best Local Similarity 83.3%; Pred. No. 1.8e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Oy 1 LNMSWL 6  
 Db 738 LDMSWL 743  
 RESULT 4  
 IKKA\_MOUSE STANDARD; PRT; 745 AA.  
 ID IKKA\_MOUSE  
 AC 060680; Q9D2X3;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Inhibitor of nuclear factor kappa-B kinase alpha subunit (BC 2.7.1.-)  
 DE (I kappa-B kinase alpha) (IKKA) (IKK-alpha) (IKK-A) (IkappaB kinase  
 DE (I-kappa-B kinase 1) (IKK1) (Conserved helix-loop-helix ubiquitons  
 DE kinase) (Nuclear factor NFkappaB inhibitor kinase alpha) (NFKB1KA).  
 GN IKKA OR CHUK. (Mouse).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RC STRAIN-BALB/C;  
 RX MEDLINE=96044444; PubMed=7558004;  
 RA Mock B.A., Connolly M.A., McBride O.W., Kozak C.A., Marcu K.B.;  
 RT "CHUK, a conserved helix-loop-helix ubiquitons kinase, maps to human  
 RT chromosome 10 and mouse chromosome 19.";  
 RL Genomics 27:348-351(1995).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RC STRAIN-BALB/C;  
 RX MEDLINE=96258427; PubMed=8777433;  
 RA Connolly M.A., Marcu K.B.;  
 RT "CHUK, a new member of the helix-loop-helix and leucine zipper  
 RT families of interacting proteins, contains a serine-threonine kinase  
 RT catalytic domain.";  
 RL Cell. Mol. Biol. Res. 41:537-549(1996).  
 RN [3]  
 RP SEQUENCE FROM N.A. (ISOFORM 3).  
 RC STRAIN=C57BL/6J; TISSUE=COLON;  
 RX MEDLINE=21085660; PubMed=11217851;  
 RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
 RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K.I.,  
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,  
 RA Schirral L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
 RA Blake J., Boffelli D., Bojunga N., Carlini P., de Bonaldo M.F.,  
 RA Brownstein S., Hill D., Holtmann M., Hume D.A., Kamiya M., Lee N.H.,  
 RA Gustincich S., Hill D., Holtmann M., Hume D.A., Kamiya M., Lee N.H.,  
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,  
 RA Wyszynski-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,  
 RA Hayashizaki Y.,  
 RT "Functional annotation of a full-length mouse cDNA collection.";  
 RL Nature 409:685-690(2001).  
 RN [4]  
 RP ALTERNATIVE SPLICING.  
 RX MEDLINE=20198447; PubMed=10733566;  
 RA McKenzie F.R., Connolly M.A., Balzarano D., Mueller J.R.,  
 RA Gelezinas R., Marcu K.B.;  
 RT "Functional isoforms of IkappaB kinase alpha (IKKalpha) lacking

leucine zipper and helix-loop-helix domains reveal that IKKalpha and IKKbeta have different activation requirements.";  
 Mol. Cell. Biol. 20:2635-2649(2000).  
 [5]  
 PHOSPHORYLATION BY MAP3K14/NIK.  
 NAKANO H., SHINDO M., SAKON S., NISHINAKA S., MIHARA M., YAGITA H., OKUMURA K.;  
 Mol. Cell. Biol. 20:2635-2649(2000).  
 "Differential regulation of IkappaB kinase alpha and beta by two upstream kinases, NF-kappaB-inducing kinase and mitogen-activated protein kinase/ERK kinase-1.";  
 Proc. Natl. Acad. Sci. U.S.A. 95:3537-3542(1998).  
 [6]  
 IKK-ALPHA BINDING.  
 MEDLINE-99212141; PubMed-10195894;  
 Delnase M., Hayakawa M., Chen Y., Karin M.;  
 "Positive and negative regulation of IkappaB kinase activity through IKKbeta subunit phosphorylation.";  
 Science 284:309-313(1999).  
 [7]  
 IKK PHOSPHORYLATION.  
 MEDLINE-99038238; PubMed-9819420;  
 Nemoto S., DiDonato J.A., Lin A.;  
 "Coordinate regulation of IkappaB kinases by mitogen-activated protein kinase kinase kinase 1 and NF-kappaB-inducing kinase.";  
 Mol. Cell. Biol. 18:7336-7343(1998).  
 [8]  
 REVIEW.  
 MEDLINE-20178139; PubMed-10712233;  
 Jobin C., Sartor R.B.;  
 "The I kappa B/NF-kappa B system: a key determinant of mucosal inflammation and protection.";  
 Am. J. Physiol. 278:C451-C462(2000).  
 -1- FUNCTION: PHOSPHORYLATES INHIBITORS OF NF-KAPPA-B THUS LEADING TO ULTIMATELY THE DEGRADATION OF THE INHIBITOR.  
 -1- ENZYME REGULATION: ACTIVATED WHEN PHOSPHORYLATED AND INACTIVATED WHEN DEPHOSPHORYLATED.  
 -1- SUBUNIT: PREFERENTIALLY FOUND AS A HETERODIMER WITH IKK-BETA BUT ALSO AS A HOMODIMER. DIRECTLY INTERACTS WITH IKK-GAMMA/NEMO. HETERODIMERS FORM THE ACTIVE COMPLEX. THE TRIPARTITE COMPLEX CAN ALSO BIND TO MAP3K14/NIK, MEK1, IKAP AND IKK-ALPHA-P65-P50 COMPLEX. A WEAK INTERACTION WITH TRAF2 CANNOT BE EXCLUDED.  
 -1- SUBCELLULAR LOCATION: Cytoplasmic.  
 -1- ALTERNATIVE PRODUCTS: 3 ISOFORMS: 1 (SHOWN HERE), 2/DELTA LH AND 3/DELTA H; ARE PRODUCED BY ALTERNATIVE SPLICING.  
 -1- TISSUE SPECIFICITY: UBIQUITOUS ONLY FOR ISOFORM 1, ISOFORMS 2 AND 3 ARE EXPRESSED PREDOMINANTLY IN BRAIN AND T-LYMPHOCYTES.  
 -1- DEVELOPMENTAL STAGE: MAXIMALLY EXPRESSED AT E7 DAY FOLLOWED BY E11, E15 AND E17 DAYS. IN THE LIMB DEVELOPMENT, ITS EXPRESSION PREDOMINATES IN THE LIMB BUDS AT E12.5 DAY.  
 -1- PFM: PHOSPHORYLATED BY MAP3K14/NIK, AKT AND TO A LESSER EXTENT BY MEK1, AND DEPHOSPHORYLATED BY PP2A. AUTOPHOSPHORYLATED.  
 -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES. IKAPAB KINASE SUBFAMILY.  
 -----  
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 EMBL: U12473; AAC52589.1;  
 EMBL: AK018671; BAB31335.1;  
 DR HSP: 063450; 1A06.  
 DR MGI: 99484; Chuk.  
 DR InterPro: IPR000719; Euk\_pkinase.  
 DR InterPro: IPR002290; Ser\_thr\_pkinase.  
 DR Pfam: PF00069; pkinase; 1.  
 DR Prodom: PD000001; Euk\_pkinase; 1.  
 DR PROSITE, PS00107; PROTEIN\_KINASE\_ATP; 1.

PROSITE, PS00108; PROTEIN\_KINASE\_ST; 1.  
 DR PROSITE, PS50011; PROTEIN\_KINASE\_DOM; 1.  
 DR Transferrase: Serine/threonine-protein kinase; ATP-binding;  
 KM Phosphorylation: Alternative splicing.  
 FT DOMAIN 15 300  
 FT PROTEIN KINASE.  
 FT LEUCINE-ZIPPER (POTENTIAL).  
 FT NEMO-BINDING.  
 FT ATP (BY SIMILARITY).  
 FT ATP (BY SIMILARITY).  
 FT BY SIMILARITY.  
 FT PHOSPHORYLATION (BY PKB/AKT) (BY SIMILARITY).  
 FT PHOSPHORYLATION (BY MAP3K14) (BY SIMILARITY).  
 FT MULTISUBSTRATE/INTEGRIN-LIKE -> IFRKVKMERGRKGH SLE (IN ISOFORM 2).  
 FT MISSING (IN ISOFORM 2).  
 FT DHXSDST -> GKTIQSDY (IN ISOFORM 3).  
 FT MISSING (IN ISOFORM 3).  
 FT K -> E (IN REF. 3).  
 FT S -> Y (IN REF. 3).  
 FT SEQUENCE 745 AA; 84728 MW; 3FEF582AF92233 CRC64;  
 Query Match 87.5%; Score 35; DB 1; Length 745;  
 Best Local Similarity 83.3%; Pred. No. 1; 8e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LNMWML 6  
 DB 738 LDMWML 743  
 RESULT 5  
 IKRB\_HUMAN STANDARD; PRT; 756 AA.  
 AC 014920; 075327.  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Inhibitor of nuclear factor kappa B kinase beta subunit (I-kappa-B) (I-kappa-B kinase beta) (IKKB) (IKK-beta) (I-kappa-B kinase 2) (IKK2) (Nuclear factor NF-kappa-B inhibitor kinase beta) (NFKB1K2).  
 GN IKKB OR IKKB2.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-44; SER-177 AND SER-181.  
 RC TISSUE=Cervical carcinoma;  
 RX MEDLINE-98008813; PubMed-9346484;  
 RA Mercurio F., Zhu H., Murray B.W., Shevchenko A., Bennett B.L., Li J.W., Young D.B., Barbosa M., Mann M., Manning A., Rao A.;  
 "IKK-1 and IKK-2: cytokine-activated IkappaB kinases essential for NF-kappaB activation.";  
 Science 278:866-869(1997).  
 RL [2]  
 RP SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-44.  
 RC MEDLINE-98008814; PubMed-9346485;  
 RX Woronicz J.D., Gao X., Cao Z., Rothe M., Goeddel D.V.;  
 "IkappaB kinase-beta: NF-kappaB activation and complex formation with IkappaB kinase-alpha and NIK.";  
 Science 278:866-869(1997).  
 RL [3]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Heart;  
 RX MEDLINE-99032998; PubMed-9813230;  
 RA Hu M.C.-T., Wang Y.-P.;  
 "IkappaB kinase-alpha and -beta genes are coexpressed in adult and embryonic tissues but localized to different human chromosomes.";  
 Gene 222:31-40(1998).  
 RL [4]  
 RP SEQUENCE FROM N.A., AND GENE MAPPING.

RX MEDLINE-98438415; PubMed-9763654;  
 RA Shindo M., Nakano H., Sakon S., Yagita H., Mihara M., Okumura K.;  
 RT "Assignment of Ikappab kinase beta (IKKB) to human chromosome band  
 RT 8p12-->p11 by in situ hybridization.";  
 RL Cytogenet. Cell Genet. 82:32-33(1998).  
 RN [5]  
 RP SEQUENCE OF 1-256 FROM N.A.  
 RC TISSUE-LUNG;  
 RA Strausberg R.;  
 RL Submitted (Apr-2001) to the EMBL/GenBank/DBJ databases.  
 RN [6]  
 RP IKK PHOSPHORYLATION;  
 RX MEDLINE-99038238; PubMed-9819420;  
 RA Nemoto S., DiDonato J.A., Lin A.;  
 RT "Coordinate regulation of Ikappab kinases by mitogen-activated protein  
 RT kinase kinase kinase 1 and NF-kappaB-inducing kinase.";  
 RL Mol. Cell. Biol. 18:7336-7343(1998).  
 RN [7]  
 RP REVIEW;  
 RX MEDLINE-20178139; PubMed-10712233;  
 RA Jobin C., Sartor R.B.;  
 RT "The I kappa B/NF-kappa B system: a key determinant of  
 RT mucosal inflammation and protection.";  
 RL Am. J. Physiol. 278:C451-C462(2000).  
 CC -1- FUNCTION: PHOSPHORYLATES INHIBITORS OF NF-KAPPA-B THUS LEADING TO  
 CC THE DISSOCIATION OF THE INHIBITOR/NF-KAPPA-B COMPLEX AND  
 CC ULTIMATELY THE DEGRADATION OF THE INHIBITOR.  
 CC -1- SUBUNIT: PREFERENTIALLY FOUND AS A HETERODIMER WITH IKK-ALPHA BUT  
 CC ALSO AS A HOMODIMER. DIRECTLY INTERACTS WITH IKK-GAMMA/IKK-  
 CC HETERODIMERS FORM THE ACTIVE COMPLEX. THE TRIPARTITE COMPLEX CAN  
 CC ALSO BIND TO MEK1, MAP3K14/NIK, IKAP AND IKK-ALPHA-P65-P50  
 CC COMPLEX. PHOSPHORYLATED IKK-ALPHA IS FURTHER RELEASED FROM THE  
 CC COMPLEX.  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC TISSUE SPECIFICITY: HIGHLY EXPRESSED IN HEART, PLACENTA, SKELETAL  
 CC MUSCLE, KIDNEY, PANCREAS, SPLEEN, THYMUS, PROSTATE, TESTIS AND  
 CC PERIPHERAL BLOOD.  
 CC -1- PTM: PHOSPHORYLATED BY MEK1 AND PROBABLY ALSO BY MAP3K14/NIK.  
 CC WEAKLY AUTOPHOSPHORYLATED.  
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 CC IKAPPAB KINASE SUBFAMILY.  
 CC  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; AF029684; AAC51860.1; -;  
 DR EMBL; AF080158; AAD08997.1; -;  
 DR EMBL; AF031416; AAC64675.1; -;  
 DR EMBL; BC006231; AAH06231.1; -;  
 DR HSSP; O63450; 1A06.  
 DR geneW; HGNC:3960; IKKB.  
 DR MIM; 603258; -;  
 DR InterPro; IPR000719; Euk\_pkinase.  
 DR InterPro; IPR002290; Ser\_thr\_pkinase.  
 DR InterPro; IPR001245; Tyr\_pkinase.  
 DR Pfam; PF00069; pkinase; 1.  
 DR Pfam; PF00240; tyk1kinase; 1.  
 DR PRINTS; PR00109; YBIK1INASE.  
 DR PROSITE; PD000001; Euk\_pkinase; 1.  
 DR PROSITE; PD000107; PROTEIN\_KINASE\_ATP; FALSE\_NEG.  
 DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
 DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
 DR Transfaser; Serine/threonine-protein kinase; ATP-binding;  
 KW Phosphorylation.  
 FT DOMAIN 15 300 PROTEIN KINASE.  
 FT DOMAIN 458 479 LEUCINE-ZIPPER (POTENTIAL).  
 FT DOMAIN 737 742 NEMO-BINDING.  
 FT NP\_BIND 21 29 ATP (BY SIMILARITY).  
 RP REVIEW.

FT BINDING 44 44 ATP (BY SIMILARITY).  
 FT ACT\_SITE 145 145 BY SIMILARITY.  
 FT MOD\_RES 23 23 PHOSPHORYLATION (BY SIMILARITY).  
 FT MOD\_RES 177 177 PHOSPHORYLATION.  
 FT MOD\_RES 181 181 PHOSPHORYLATION.  
 FT MOD\_RES 181 181 PHOSPHORYLATION.  
 FT MOTAGEN 44 44 K->A: LOSS OF KINASE ACTIVITY AND NO  
 FT MOTAGEN 177 177 EFFECT ON BINDING TO NIK.  
 FT MOTAGEN 177 177 S->A: DECREASE OF ACTIVITY.  
 FT MOTAGEN 181 181 S->E: FULL ACTIVATION.  
 FT MOTAGEN 181 181 S->A: DECREASE OF ACTIVITY.  
 FT CONFLICT 231 255 S->E: FULL ACTIVATION.  
 FT CONFLICT 231 255 WSKVRKRSVDIVSEDLNGTVKF -> CVRMKPGTVAKS  
 FT CONFLICT 231 255 CNPSTIGGRGRMI (IN REF. 5).  
 FT CONFLICT 231 255 Q -> H (IN REF. 1).  
 SQ SEQUENCE 756 AA: 86563 MW: P9CADF671AE9E14E CRG64;  
 Query Match 87.5%; Score: 35; DB 1; Length 756;  
 Best Local Similarity 83.3%; Pred. No. 1; 8e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Oy 1 LNM5WL 6  
 Db 737 LNM5WL 742  
 RESULT 6  
 ID IKKB\_MOUSE STANDARD; PRT; 757 AA.  
 AC 088351; 09RJ6.  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Inhibitor of nuclear factor kappa B kinase beta subunit (EC 2.7.1.-)  
 DE (I-kappa-B-kinase beta) (IKKB) (IKK-beta) (I-kappa-B kinase  
 DE 2) (IKK2) (nuclear factor NF-kappa B inhibitor kinase beta) (NFKB2).  
 GN IKKB OR IKKB2.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_Taxid=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND PHOSPHORYLATION BY MEK1.  
 RC STRAIN=C57BL/6; TISSUE=Spleen;  
 RX MEDLINE-98188238; PubMed-9520401;  
 RA Nakano H., Shindo M., Sakon S., Nishinaka S., Mihara M., Yagita H.,  
 RA Okumura K.;  
 RT "Coordinate regulation of Ikappab kinase alpha and beta by two  
 RT upstream kinases, NF-kappaB-inducing kinase and mitogen-activated  
 RT protein kinase/ERK kinase kinase-1.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 95:3537-3542(1998).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Hu M.C.-T., Wang Y.-P., Qiu W.R.;  
 RT "Murine Ikb kinase-B, a developmentally regulated protein kinase that  
 RT constitutively phosphorylates serine residues of Ikb.";  
 RL Submitted (Aug-1998) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP DEVELOPMENTAL STAGE.  
 RX MEDLINE-99455228; PubMed-10523828;  
 RA Hu M.C.-T., Wang Y.-P., Qiu W.R., Mikhail A., Meyer C.F., Tan T.-H.;  
 RT "Hematopoietic progenitor kinase-1 (HPK1) stress response signaling  
 RT pathway activates Ikappab kinases (IKK-alpha/beta) and IKK-beta is a  
 RT developmentally regulated protein kinase.";  
 RL Oncogene 18:5514-5524(1999).  
 RN [4]  
 RP IKK PHOSPHORYLATION;  
 RX MEDLINE-99038238; PubMed-9819420;  
 RA Nemoto S., DiDonato J.A., Lin A.;  
 RT "Coordinate regulation of Ikappab kinases by mitogen-activated protein  
 RT kinase kinase kinase 1 and NF-kappaB-inducing kinase.";  
 RL Mol. Cell. Biol. 18:7336-7343(1998).  
 RN [5]  
 RP REVIEW.

RA MEDLINE-20178139; PubMed-10712233;  
 RA Jobin C., Sartor R.B.;  
 RT "The Ikkapab/NF-kappaB system: a key determinant of mucosal  
 RT inflammation and protection."  
 RT Am. J. Physiol. 278:C451-C462(2000).  
 CC -1- FUNCTION: PHOSPHORYLATES INHIBITORS OF NF-KAPPA-B THUS LEADING TO  
 CC THE DISSOCIATION OF THE INHIBITOR/NF-KAPPA-B COMPLEX AND  
 CC ULTIMATELY THE DEGRADATION OF THE INHIBITOR.  
 CC -1- SUBUNIT: PREFERENTIALLY FOUND AS A HETERODIMER WITH IKK-ALPHA BUT  
 CC ALSO AS A HOMODIMER. DIRECTLY INTERACTS WITH IKK-GAMMA/NEMO.  
 CC HETERODIMERS FORM THE ACTIVE COMPLEX. THE TRIPARTITE COMPLEX CAN  
 CC ALSO BIND TO MEK1, MAP3K14/NIK, IKAP AND IKK-ALPHA-P65-P50  
 CC COMPLEX. PHOSPHORYLATED IKK-ALPHA IS FURTHER RELEASED FROM THE  
 CC COMPLEX.  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN LIVER, KIDNEY AND SPLEEN.  
 CC -1- DEVELOPMENTAL STAGE: WHILE IT IS EXPRESSED UBICITOUSLY THROUGHOUT  
 CC THE MOUSE EMBRYO, AT E9.5 DAY ITS EXPRESSION BEGINS TO BE  
 CC LOCALIZED TO THE BRAIN, NEURAL GANGLIA, NEURAL TUBE, AND IN LIVER  
 CC AT E12.5 DAY. AT E15.5 DAY, THE EXPRESSION IS FURTHER RESTRICTED  
 CC TO SPECIFIC TISSUES OF THE EMBRYO.  
 CC -1- PTM: PHOSPHORYLATED BY MEK1 AND PROBABLY ALSO BY MAP3K14/NIK.  
 CC WEAKLY AUTOPHOSPHORYLATED.  
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 CC IKAPAB KINASE SUBFAMILY.  
 CC -----  
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 CC -----  
 DR EMBL: AF026524; AAC23557.1; -  
 DR EMBL: AF088910; AAD52095.1; -  
 DR HSSP: 063450; 1A06.  
 DR MGD: MGI:138071; Ikabk.  
 DR InterPro: IPR000719; Euk\_pkinase.  
 DR InterPro: IPR002290; Ser\_thr\_pkinase.  
 DR Pfam: PF00069; pkinase; 1.  
 DR ProDom: PD000001; Euk\_pkinase; 1.  
 DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP; FALSE\_NEG.  
 DR PROSITE: PS00108; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE: PS50011; PROTEIN\_KINASE\_ST; 1.  
 DR Transferrase: Serine/threonine-protein kinase; ATP-binding;  
 KW Phosphorylation.  
 KW DOMAIN 15 300  
 FT DOMAIN 15 300 PROTEIN KINASE.  
 FT DOMAIN 458 479 LEUCINE-ZIPPER (POTENTIAL).  
 FT DOMAIN 737 742 NEMO-BINDING.  
 FT NP\_BIND 21 29 ATP (BY SIMILARITY).  
 FT BINDING 44 44 ATP (BY SIMILARITY).  
 FT ACT\_SITE 145 145 BY SIMILARITY.  
 FT MOD\_RES 23 23 PHOSPHORYLATION (BY SIMILARITY).  
 FT MOD\_RES 177 177 PHOSPHORYLATION (BY SIMILARITY).  
 FT MOD\_RES 181 181 PHOSPHORYLATION (BY SIMILARITY).  
 FT CONFLICT 56 56 N -> D (IN REF. 2).  
 FT CONFLICT 343 343 N -> D (IN REF. 2).  
 FT CONFLICT 356 356 L -> E (IN REF. 2).  
 FT CONFLICT 390 390 L -> F (IN REF. 2).  
 FT CONFLICT 406 406 P -> Q (IN REF. 2).  
 FT CONFLICT 573 573 K -> R (IN REF. 2).  
 FT CONFLICT 736 757 TIDMSWLDQWEDERKSLQACD -> VTA (IN REF.  
 FT CONFLICT 757 757 2).  
 SQ SEQUENCE 757 AA; 86690 MW; FED962F095449C5E CRC64;  
 QY Query Match 87.5%; Score 35. DB 1; Length 757;  
 DB Best Local Similarity 83.3%; Pred. No. 1.8e+02;  
 DB Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 DB 1 LNMWTL 6  
 DB 737 LDMWTL 742

RESULT 7  
 ID IKKB RAT STANDARD: PRT; 757 AA.  
 AC 09078;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Inhibitor of nuclear factor kappa B kinase beta subunit (EC 2.7.1.-)  
 DE (I-kappa-B kinase beta) (IKKb) (IKK-beta) (I-kappa-B kinase  
 DE 2) (IKK2) (Nuclear factor NF-kappa-B inhibitor kinase beta) (NFKB1K2).  
 GN IKKB OR IKKb.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Zhang Y., Sun S., Ravid K.;  
 RT "IKK beta in megakaryocyte differentiation."  
 RT submitted (DEC-1998) to the EMBL/Genbank/DBJ databases.  
 RN [2]  
 RP IKK PHOSPHORYLATION.  
 RX MEDLINE-9038238; PubMed-9819420;  
 RA Nemoto S., Didonato J.A., Iln A.;  
 RT "Coordinate regulation of Ikkapab kinases by mitogen-activated protein  
 RT kinase kinase kinase 1 and NF-kappaB-inducing kinase."  
 RL Mol. Cell. Biol. 18:7336-7343(1998).  
 RN [3]  
 RP REVIEW.  
 RX MEDLINE-20178139; PubMed-10712233;  
 RA Jobin C., Sartor R.B.;  
 RT "The I kappa B/NF-kappa B system: a key determinant of  
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 RT Am. J. Physiol. 278:C451-C462(2000).  
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 CC THE DISSOCIATION OF THE INHIBITOR/NF-KAPPA-B COMPLEX AND  
 CC ULTIMATELY THE DEGRADATION OF THE INHIBITOR.  
 CC -1- SUBUNIT: PREFERENTIALLY FOUND AS A HETERODIMER WITH IKK-ALPHA BUT  
 CC ALSO AS A HOMODIMER. DIRECTLY INTERACTS WITH IKK-GAMMA/NEMO.  
 CC HETERODIMERS FORM THE ACTIVE COMPLEX. THE TRIPARTITE COMPLEX CAN  
 CC ALSO BIND TO MEK1, MAP3K14/NIK, IKAP AND IKK-ALPHA-P65-P50  
 CC COMPLEX. PHOSPHORYLATED IKK-ALPHA IS FURTHER RELEASED FROM THE  
 CC COMPLEX.  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -1- PTM: PHOSPHORYLATED BY MEK1 AND PROBABLY ALSO BY MAP3K14/NIK.  
 CC WEAKLY AUTOPHOSPHORYLATED.  
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 CC IKAPAB KINASE SUBFAMILY.  
 CC -----  
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 CC -----  
 DR EMBL: AF115282; AAF21978.1; -  
 DR HSSP: 063450; 1A06.  
 DR InterPro: IPR000719; Euk\_pkinase.  
 DR InterPro: IPR002290; Ser\_thr\_pkinase.  
 DR InterPro: IPR001245; Tyr\_pkinase.  
 DR Pfam: PF00069; pkinase; 1.  
 DR PRINTS: PR00109; TYRKINASE.  
 DR ProDom: PD000001; Euk\_pkinase; 1.  
 DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP; FALSE\_NEG.  
 DR PROSITE: PS00108; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE: PS50011; PROTEIN\_KINASE\_ST; 1.  
 DR Transferrase: Serine/threonine-protein kinase; ATP-binding;  
 KW Phosphorylation.  
 KW DOMAIN 15 300 PROTEIN KINASE.  
 FT DOMAIN 15 300

FT DOMAIN 458 479 LECICINE-21PPER (POTENTIAL).  
 FT BIND 737 742 NEMO-BINDING.  
 FT BIND 21 29 ATP (BY SIMILARITY).  
 FT BIND 44 44 ATP (BY SIMILARITY).  
 FT ACT SITE 145 145 BY SIMILARITY.  
 FT MOD\_RES 23 23 PHOSPHORYLATION (BY SIMILARITY).  
 FT MOD\_RES 177 177 PHOSPHORYLATION (BY SIMILARITY).  
 FT MOD\_RES 181 181 PHOSPHORYLATION (BY SIMILARITY).  
 SQ SEQUENCE 757 AA: 86866 MW: 3AFPE46A7DF91F9C CRC64;

Query Match 87.5%; Score 35; DB 1; Length 757;  
 Best Local Similarity 83.3%; Pred. No. 1.8e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LNMSWL 6  
 DB 737 LDMSWL 742

RESULT 8  
 ID Y451\_SYNY3 STANDARD; PRT; 154 AA.  
 AC P74676;  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Hypothetical protein sll0451.  
 GN Sll0451.  
 OS Synechocystis sp. (strain PCC 6803).  
 OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.  
 OX NCBI\_Taxid=1148;  
 RN [1]

RP SEQUENCE FROM N.A.  
 RX MEDLINE=97061201; Pubmed=8905231;  
 RA Kaneo T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,  
 RA Miyajima N., Hirosewa M., Sugita M., Sasamoto S., Kimura T.,  
 RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naito K.,  
 RA Okumura S., Shimo S., Takeuchi C., Wada T., Watanabe A.,  
 RA Yamada M., Yasuda M., Tabata S.;  
 RT "Sequence analysis of the genome of the unicellular cyanobacterium  
 Synechocystis sp. strain PCC6803. II. Sequence determination of the  
 RT entire genome and assignment of potential protein-coding regions.";  
 RL DNA Res. 3:109-136(1996).  
 CC -1- SIMILARITY: BELONGS TO THE UPF0039 (ELAA) FAMILY.  
 CC  
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 CC  
 DR EMBL: D90917; BAA18794.1; -  
 DR InterPro: IPR000182; GCN5acetyltransf.  
 DR Pfam: PF00583; Acetyltransf. 1.  
 KW Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 154 AA: 17612 MW: C8A777660627F9C2 CRC64;

Query Match 85.0%; Score 34; DB 1; Length 154;  
 Best Local Similarity 80.0%; Pred. No. 57;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LNMSWL 5  
 DB 3 LNMSWL 7

RESULT 9  
 ID NO08\_PARDE STANDARD; PRT; 345 AA.  
 AC P29920;  
 DT 01-APR-1993 (Rel. 25, Created)

DT 01-APR-1993 (Rel. 25, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE NADH-ubiquinone oxidoreductase chain 8 (EC 1.6.5.3) (NADH  
 DE dehydrogenase 1, chain 8) (NDH-1, chain 8).  
 GN NO08.  
 OS Paracoccus denitrificans.  
 OC Bacteria; Proteobacteria; alpha subdivision; Rhodobacter group;  
 OC Paracoccus.  
 OX NCBI\_Taxid=266;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC 13543;  
 RX MEDLINE=93136200; Pubmed=8422400;  
 RA Xu X., Matsuno-Yagi A., Yagi T.;  
 RT "DNA sequencing of the seven remaining structural genes of the gene  
 RT cluster encoding the energy-transducing NADH-quinone oxidoreductase  
 RT of Paracoccus denitrificans.";  
 RL Biochemistry 32:968-981(1993).  
 CC -1- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.  
 CC -1- SUBUNIT: COMPOSED OF 14 DIFFERENT SUBUNITS. SUBUNIT NO07-14  
 CC CONSTITUTE THE MEMBRANE SECTOR OF THE COMPLEX.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- SIMILARITY: BELONGS TO THE COMPLEX I SUBUNIT 1 FAMILY.  
 CC  
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 CC  
 DR EMBL: L02354; AAA25592.1; -  
 DR PIR: C45456; C45456.  
 DR InterPro: IPR001694; Resp\_NADH\_dhl.  
 DR Pfam: PF00146; NADHdh. 1.  
 DR PROSITE: PS00667; COMPLEX1\_ND1\_1; 1.  
 DR PROSITE: PS00668; COMPLEX1\_ND1\_2; 1.  
 KW Oxidoreductase; NAD; Ubiquinone; Transmembrane.  
 FT TRANSMEM 15 35 POTENTIAL.  
 FT TRANSMEM 82 102 POTENTIAL.  
 FT TRANSMEM 115 135 POTENTIAL.  
 FT TRANSMEM 161 181 POTENTIAL.  
 FT TRANSMEM 190 210 POTENTIAL.  
 FT TRANSMEM 253 273 POTENTIAL.  
 FT TRANSMEM 278 298 POTENTIAL.  
 FT TRANSMEM 309 329 POTENTIAL.  
 SQ SEQUENCE 345 AA: 38751 MW: E33B667E569506B4 CRC64;

Query Match 85.0%; Score 34; DB 1; Length 345;  
 Best Local Similarity 83.3%; Pred. No. 1.2e+02;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 LNMSWL 6  
 DB 191 LNMYWL 196

RESULT 10  
 ID NU0H\_RHOCA STANDARD; PRT; 345 AA.  
 AC P42032;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE NADH dehydrogenase I chain H (EC 1.6.5.3) (NADH-ubiquinone  
 DE oxidoreductase chain H).  
 GN NU0H OR NDHA.  
 OS Rhodobacter capsulatus (Rhodospirillum rubrum).  
 OC Bacteria; Proteobacteria; alpha subdivision; Rhodobacter group;  
 OC Rhodobacter.  
 OX NCBI\_Taxid=1061;  
 RN [1]

RP SEQUENCE FROM N.A.  
 RC STRAIN-ATCC 33303 / B10;  
 RX MEDLINE-92233948; PubMed-1568483;  
 RA Dupuis A.;  
 RT Identification of two genes of Rhodobacter capsulatus coding for  
 proteins homologous to the ND1 and 23 kDa subunits of the  
 mitochondrial Complex I.;  
 RL FEBS Lett. 301:215-218(1992).  
 CC -1- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- SIMILARITY: BELONGS TO THE COMPLEX I SUBUNIT 1 FAMILY.  
 CC  
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 CC  
 DR EMBL: AF029365; AAC2497.1; -  
 DR EMBL: Z11611; CAAT7684.1; -  
 DR InterPro: IPR001694; Resp\_NADH\_dhl.  
 DR Pfam: PF00146; NADHdh: 1.  
 DR PROSITE: PS00667; COMPLEX1\_ND1\_1; 1.  
 DR PROSITE: PS00668; COMPLEX1\_ND1\_2; 1.  
 KW Oxidoreductase; NAD; Ubiquinone; Transmembrane.  
 FT TRANSMEM 14 34  
 FT TRANSMEM 84 104 POTENTIAL.  
 FT TRANSMEM 115 135 POTENTIAL.  
 FT TRANSMEM 161 181 POTENTIAL.  
 FT TRANSMEM 190 210 POTENTIAL.  
 FT TRANSMEM 248 268 POTENTIAL.  
 FT TRANSMEM 277 297 POTENTIAL.  
 FT TRANSMEM 309 329 POTENTIAL.  
 SO SEQUENCE 345 AA; 37852 MW; 5F9E9D640D911854 CRC64;  
 Query Match Best Local Similarity 85.0%; Score 34; DB 1; Length 345;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 OY 1 LNMSWL 6  
 DB 191 LNMYWL 196  
 RESULT 11  
 ID T1SD\_ECOLI STANDARD; PRT; 444 AA.  
 AC P06991;  
 DT 01-APR-1988 (Rel. 07, Created)  
 DT 01-APR-1988 (Rel. 07, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Type I restriction enzyme EcodI specificity protein (s protein)  
 DE (S. EcodI).  
 GN HSDB OR HSB.  
 OS Escherichia coli.  
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
 OC Escherichia.  
 OX NCBI\_TaxID=562;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-D / E166;  
 RA MEDLINE-83216118; PubMed-6304321;  
 RA Gough J.A., Murray N.E.;  
 RT "Sequence diversity among related genes for recognition of specific  
 targets in DNA molecules";  
 RL J. Mol. Biol. 166:1-19(1983).  
 CC -1- FUNCTION: THE M AND S SUBUNITS TOGETHER FORM A METHYLTRANSFERASE  
 CC (MTASE) THAT METHYLATES TWO ADENINE RESIDUES IN COMPLEMENTARY  
 CC STRANDS OF BIPARTITE DNA RECOGNITION SEQUENCE. IN THE PRESENCE OF  
 CC THE R SUBUNIT THE COMPLEX CAN ALSO ACT AS AN ENDONUCLEASE, BINDING  
 CC TO THE SAME TARGET SEQUENCE BUT CUTTING THE DNA SOME DISTANCE FROM

CC THIS SITE. WHETHER THE DNA IS CUT OR MODIFIED DEPENDS ON THE  
 CC METHYLATION STATE OF THE TARGET SEQUENCE. WHEN THE TARGET SITE IS  
 CC UNMODIFIED, THE DNA IS CUT. WHEN THE TARGET SITE IS  
 CC METHYLATED, THE COMPLEX ACTS AS A MAINTENANCE MTASE MODIFYING  
 CC THE DNA SO THAT BOTH STRANDS BECOME METHYLATED. SUBUNIT S DICTATES  
 CC DNA SEQUENCES SPECIFICITY. THE ECODI ENZYME RECOGNIZES 5'-  
 CC TTA(N7)GTCT-3'.  
 CC -1- SUBUNIT: THE TYPE I RESTRICTION/MODIFICATION SYSTEM IS COMPOSED  
 CC OF THREE POLYPEPTIDES R,M AND S.  
 CC -1- DOMAIN: CONTAINS TWO DNA RECOGNITION DOMAINS, EACH SPECIFYING  
 CC RECOGNITION OF ONE OF THE TWO DEFINED COMPONENTS OF THE TARGET  
 CC SEQUENCE.  
 CC -1- SIMILARITY: BELONGS TO THE TYPE-I RESTRICTION SYSTEM S METHYLASE  
 CC FAMILY.  
 CC  
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 CC  
 DR EMBL: V00287; CA23553.1; -  
 DR REBASE: 3640; S.EcodI.  
 DR InterPro: IPR000055; Methylase\_S.  
 DR Pfam: PF01420; Methylase\_S; 2.  
 KW Restriction system; DNA-binding.  
 SO SEQUENCE 444 AA; 49893 MW; 14BE17B5325294F0 CRC64;  
 Query Match Best Local Similarity 85.0%; Score 34; DB 1; Length 444;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 OY 2 NMSWL 6  
 DB 215 NMSWM 219  
 RESULT 12  
 ID YAMD\_SCHPO STANDARD; PRT; 612 AA.  
 AC Q10187;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Hypothetical protein C3F10.13 in chromosome I.  
 GN SPAC3F10.13.  
 GN Schizosaccharomyces pombe (Fission yeast).  
 OS Schizosaccharomyces pombe (Fission yeast).  
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;  
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;  
 OC Schizosaccharomycetes.  
 OX NCBI\_TaxID=4896;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=972;  
 RX MEDLINE-21848401; PubMed-11859360;  
 RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,  
 RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,  
 RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,  
 RA Collins M., Connor R., Cronin A., Davis P., Fellwell T., Fraser A.,  
 RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,  
 RA Holtroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,  
 RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,  
 RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,  
 RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinovitch E.,  
 RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,  
 RA Skelton J., Stimmings M., Squares R., Squares S., Stevens K.,  
 RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,  
 RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,  
 RA Welteens I., Vanstreels E., Rieger M., Schaefer M., Wellert-Auer S.,  
 RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,  
 RA Borzym K., Langer I., Beck A., Lehnach H., Reinhardt R., Pohl T.M.,

RA Eger P., Zimmermann W., Medler H., Wandt R., Purnelle B.,  
 RA Goffeau A., Cadieu E., Diano S., Lelaire V., Mottier S.,  
 RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,  
 RA Lucas M., Rochet M., Gallardin C., Tallada V.A., Garzon A., Thode G.,  
 RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,  
 RA Dominguez A., Revelante J., Moreno S., Armstrong J., Forsburg S.L.,  
 RA Cerritelli L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,  
 RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;  
 RT "The genome sequence of *Schizosaccharomyces pombe*.";  
 RL Nature 415:871-880(2002).  
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 CC -----  
 CC EMBL: Z69369; CAA93311.1; -  
 DR InterPro: IPR000449; UBA\_domain.  
 DR Pfam: PF00627; UBA; 1.  
 DR SMART: SM00165; UBA; 1.  
 KM Hypothetical protein: Glycoprotein; Transmembrane.  
 FT TRANSMEM 91 111  
 FT TRANSMEM 437 457  
 FT CARBOHYD 128 128  
 FT CARBOHYD 220 220  
 FT CARBOHYD 296 296  
 FT CARBOHYD 315 315  
 FT CARBOHYD 416 416  
 SQ SEQUENCE 612 AA; 68720 MW; 3FBDF3808F554CD CRC64;  
 Query Match 85.0%; Score 34; DB 1; Length 612;  
 Best Local Similarity 80.0%; Pred. No. 2.1e+02;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 NMSWL 6  
 DB 296 NMSWI 300  
 RESULT 13  
 AT8 ASPRE STANDARD; PRT; 54 AA.  
 ID Q33822;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE ATP synthase protein 8 (EC 3.6.3.14) (ATPase subunit 8) (A6L).  
 GN MTAP8 OR ATP8.  
 OS Asterina pectinifera (Starfish).  
 OC Mitochondrion.  
 CC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Asterozoa;  
 CC Asteroidea; Valvatacea; Valvatida; Asterinidae; Asterina.  
 OX NCBI\_TaxId=7594;  
 RN NCB1  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-Ovary;  
 RX MEDLINE=95402698; PubMed=7672576;  
 RA Asakawa S., Himeno H., Miura K.-I., Watanabe K.;  
 RT "Nucleotide sequence and gene organization of the starfish *Asterina*  
 RT *pectinifera* mitochondrial genome.";  
 RL Genetics 140:1047-1060(1995).  
 CC -1- FUNCTION: THIS IS ONE OF THE CHAINS OF THE NONENZYMATIC COMPONENT  
 CC (CF0) SUBUNIT OF THE MITOCHONDRIAL ATPASE COMPLEX.  
 CC -1- CATALYTIC ACTIVITY: ATP + H(2)O + H(+) (in) -> ADP + phosphate +  
 CC H(+) (out).  
 CC -1- SUBCELLULAR LOCATION: Membrane-bound.  
 CC -1- SIMILARITY: BELONGS TO THE ATPASE PROTEIN 8 FAMILY.  
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 CC -----  
 CC EMBL: D16387; BAA03883.1; -  
 DR InterPro: IPR001421; ATPase8\_mt.  
 DR Pfam: PF00895; ATP-synt\_8; 1.  
 KM Hydrogen ion transport; CF(0); Mitochondrion; Transmembrane.  
 FT TRANSMEM 8 28  
 FT TRANSMEM 47 47  
 SQ SEQUENCE 54 AA; 6241 MW; 9EABDACB9CDE5F1 CRC64;  
 Query Match 82.5%; Score 33; DB 1; Length 54;  
 Best Local Similarity 80.0%; Pred. No. 30;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LNMSW 5  
 DB 49 LNMTW 53  
 RESULT 14  
 PKBS\_BOVIN STANDARD; PRT; 169 AA.  
 ID P30535;  
 DT 01-APR-1993 (Rel. 25, Created)  
 DT 01-APR-1993 (Rel. 25, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE Peripheral-type benzodiazepine receptor (PBR) (PKBS) (isoguinoline-  
 DE binding protein) (IBP).  
 GN BZRP.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovinae; Bovinae; Bos.  
 OX NCBI\_TaxId=9913;  
 RN NCB1  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=91310699; PubMed=1649835;  
 RA Parola A.L., Stump D.G., Pepper J.D., Krueger K.E., Regan J.W.,  
 RA Laird H.E. II;  
 RT "Cloning and expression of a pharmacologically unique bovine  
 RT peripheral-type benzodiazepine receptor isoguinoline binding  
 RT protein.";  
 RL J. Biol. Chem. 266:14082-14087(1991).  
 CC -1- FUNCTION: RESPONSIBLE FOR THE MANIFESTATION OF PERIPHERAL-TYPE  
 CC BENZODIAZEPINE RECOGNITION SITES AND IS MOST LIKELY TO COMPRISE  
 CC BINDING DOMAINS FOR BENZODIAZEPINES AND ISOQUINOLINE CARBOXAMIDES.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- SIMILARITY: SEGMENTS TML, TM4, AND TM5 SHOW SIMILARITY WITH THE  
 CC TRANSMEMBRANE SEGMENTS M1, M2, AND M4 FROM SUBUNITS OF THE  
 CC GABA(A)/BENZODIAZEPINE RECEPTOR FAMILY, RESPECTIVELY.  
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 CC -----  
 CC EMBL: M64520; AAA30686.1; -  
 DR PIR: A39473; A39473.  
 DR InterPro: IPR004307; Tspo\_MBR.  
 DR Pfam: PF03073; Tspo\_MBR; 1.  
 KM Receptor; Transmembrane.  
 FT TRANSMEM 6 26  
 FT TRANSMEM 47 67  
 FT TRANSMEM 80 100  
 FT TRANSMEM 106 126  
 FT TRANSMEM 135 155  
 SQ SEQUENCE 169 AA; 18927 MW; 70E71E5B4CBA4C CRC64;



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OM protein - protein search, using sw model

Run on: May 30, 2003, 14:32:12 ; Search time 6.5921 Seconds  
(without alignments)  
87.500 Million cell updates/sec

Title: US-09-643-260-9  
Perfect score: 40  
Sequence: 1 LMMSWL 6

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues  
Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_73:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	37	92.5	204	2	C83748
2	37	92.5	337	2	C98336
3	37	92.5	337	2	AG2946
4	36	90.0	204	2	T15295
5	36	90.0	380	2	T11041
6	36	90.0	460	2	AG0965
7	36	90.0	590	2	C83491
8	36	90.0	744	2	T10035
9	35	87.5	116	2	T03472
10	35	87.5	321	2	T24773
11	35	87.5	325	2	E87125
12	35	87.5	745	1	I49101
13	35	87.5	777	2	T09056
14	34	85.0	154	2	S76882
15	34	85.0	345	2	C45456
16	34	85.0	345	2	S22368
17	34	85.0	355	2	F70983
18	34	85.0	612	2	T38714
19	34	85.0	685	1	A48289
20	34	85.0	903	3	E88221
21	34	85.0	919	2	T37062
22	34	85.0	980	2	T24336
23	34	85.0	1147	2	T35781
24	33	82.5	52	2	D90532
25	33	82.5	54	2	S70600
26	33	82.5	72	2	AD2464
27	33	82.5	169	2	I38724
28	33	82.5	169	2	JC1393
29	33	82.5	169	2	I57953

30	33	82.5	169	2	A53405	peripheral-type be
31	33	82.5	169	2	S14257	benzodiazepine rec
32	33	82.5	169	2	A39473	peripheral-type be
33	33	82.5	169	2	JE0149	peripheral benzod
34	33	82.5	275	2	AB2466	ABC transporter su
35	33	82.5	281	2	AF2161	cation-efflux syst
36	33	82.5	289	2	A82953	ATP synthase A cha
37	33	82.5	310	2	C84701	hypothetical prote
38	33	82.5	315	2	A86710	transposase of IS9
39	33	82.5	315	2	G86712	transposase of IS9
40	33	82.5	315	2	D86741	transposase of IS9
41	33	82.5	315	2	G86787	transposase of IS9
42	33	82.5	315	2	G86794	transposase of IS9
43	33	82.5	315	2	C86814	transposase of IS9
44	33	82.5	315	2	B86837	transposase of IS9
45	33	82.5	315	2	E86860	transposase of IS9

## ALIGNMENTS

## RESULT 1

C83748  
hypothetical protein BH0787 [Imported] - Bacillus halodurans (strain C-125)  
C/Species: Bacillus halodurans  
C/Date: 01-Dec-2000 #sequence\_revision 01-Dec-2000 #text\_change 15-Jun-2001  
C/Accession: C83748  
R/Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; H  
Nucleic Acids Res. 28, 4317-4331, 2000  
A/Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans a  
A/Reference number: A83650; MUID:20512582; PMID:11058132  
A/Accession: C83748  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-204 <SNO>  
A/Cross-references: GB:AP001509; GB:BA000004; NID:g10173176; PIDN:BA04506.1; GSPDB:G  
A/Experimental source: strain C-125  
C/Genetics:  
A/Genes: BH0787  
C/Superfamily: Bacillus subtilis conserved hypothetical protein yeast

Query Match 92.5% Score 37; DB 2; Length 204;  
Best Local Similarity 83.3% Pred. No. 49;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LMMSWL 6  
DB 22 LMMSWL 27

## RESULT 2

C98336  
probable integral membrane transport protein (t41665) [Imported] - Agrobacterium tume  
C/Species: Agrobacterium tumefaciens  
C/Date: 22-Oct-2001 #sequence\_revision 22-Oct-2001 #text\_change 11-Jan-2002  
C/Accession: C98336  
R/Goodner, B.; Hinkle, G.; Gatlung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldm  
A.; Liu, F.; Wollam, C.; Allinger, M.; Dougherty, D.; Scott, C.; Lappas, C.; Markelz,  
Science 294, 2323-2328, 2001  
A/Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium  
A/Reference number: A97359; PMID:11743194  
A/Accession: C98336  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-337 <KUR>  
A/Cross-references: GB:AE007870; PIDN:AAK90213.1; PID:g15160224; GSPDB:GN00170  
C/Genetics:  
A/Genes: AGR\_L\_3272  
A/Map position: linear chromosome  
C/Superfamily: inner membrane protein upga  
Query Match 92.5% Score 37; DB 2; Length 337;  
Best Local Similarity 83.3% Pred. No. 81;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LNMSWL 6  
 |||||  
 Db 164 LNMAWL 169

## RESULT 3

AG2946  
 hypothetical protein Atcu3173 [Imported] - Agrobacterium tumefaciens (strain C58, Dupont)  
 C:Species: Agrobacterium tumefaciens  
 C>Date: 11-Jan-2002 #sequence\_revision 11-Jan-2002 #text\_change 01-Feb-2002  
 C:Accession: AG2946  
 R:Wood, D.W.; Sebuel, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.  
 erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavlin, T.; Levy, R.; Li, M.; McClell  
 ; Karp, P.; Romero, P.; Zhang, S.  
 Science 294, 2317-2323, 2001  
 A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,  
 ster, E.W.  
 A>Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.  
 A:Reference number: AB2577; PMID:11743193  
 A:Accession: AG2946  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-337 <KUR>  
 A:Cross-references: GB:AE008689; PIDN:AAI43989.1; PID:g17741546; GSPDB:GN00187  
 A:Experimental source: strain C58 (Dupont)  
 C:Genetics:  
 A:Gene: Atcu3173  
 A:Map position: linear chromosome  
 C:Superfamily: inner membrane protein ugpa

Query Match 92.5%; Score 37; DB 2; Length 337;  
 Best Local Similarity 83.3%; Pred. No. 81;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNMSWL 6  
 |||||  
 Db 164 LNMAWL 169

## RESULT 4

T15295  
 hypothetical protein B0252.6 - Caenorhabditis elegans  
 C:Species: Caenorhabditis elegans  
 C>Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 23-Mar-2001  
 C:Accession: T15295  
 R:Du, Z.  
 submitted to the EMBL Data Library, July 1995  
 A:Description: The sequence of C. elegans cosmid B0252.  
 A:Reference number: S59415  
 A:Accession: T15295  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-204 <DUZ>  
 A:Cross-references: EMBL:U23453; NID:g733572; PID:g733579; PIDN:AAI46760.1; CESP:B0252.6  
 A:Experimental source: strain Bristol N2  
 C:Genetics:  
 A:Gene: CESP:B0252.6  
 A:Introns: 149/3; 182/2  
 C:Superfamily: Caenorhabditis elegans hypothetical protein B0252.6

Query Match 90.0%; Score 36; DB 2; Length 204;  
 Best Local Similarity 100.0%; Pred. No. 70;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NMSWL 6  
 |||||  
 Db 96 NMSWL 100

## RESULT 5

T11041

ubiquinol-cytochrome-c reductase (EC 1.10.2.2) cytochrome b - Chlamydomonas eugametos  
 C:Species: Chlamydomonas eugametos  
 C>Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 03-Jun-2002  
 C:Accession: T11041  
 R:Denovan-Wright, E.M.; Nedelcu, A.M.; Lee, R.W.

Plant Mol. Biol. 36, 285-295, 1998  
 A>Title: Complete sequence of the mitochondrial DNA of Chlamydomonas eugametos.  
 A:Reference number: Z17244; MOID:98145434; PMID:9484440  
 A:Accession: T11041  
 A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA  
 A:Residues: 1-380 <DEN>  
 A:Cross-references: EMBL:AF08237; NID:92865233; PID:g2865267; PIDN:AAI393350.1

C:Genetics:  
 A:Gene: mitochondrion  
 A:Introns: 131/3  
 A:Note: cob

C:Superfamily: cytochrome b; cytochrome b homology; cytochrome b6 homology; plastocyt  
 C:Keywords: electron transfer; heme; iron; metalloprotein; mitochondrion; oxidative p  
 F:10-340/Domain: cytochrome b homology <CB>  
 F:10-210/Domain: cytochrome b6 homology <CB6>  
 F:222-340/Domain: plastocytin-plastocyanin reductase 17K protein homology <17K>  
 F:82-183/Binding site: heme iron (His) (axial ligands) (low potential) #status predic  
 F:96-197/Binding site: heme iron (His) (axial ligands) (high potential) #status predi

Query Match 90.0%; Score 36; DB 2; Length 380;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNMSW 5  
 |||||  
 Db 26 LNMSW 30

## RESULT 6

AG0965  
 probable glycosyl hydrolase STY4009 [Imported] - Salmonella enterica subsp. enterica  
 C:Species: Salmonella enterica subsp. enterica serovar Typhi  
 A:Note: this species has also been called Salmonella typhi  
 C>Date: 09-Nov-2001 #sequence\_revision 09-Nov-2001 #text\_change 27-Nov-2001  
 C:Accession: AG0965

R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Church  
 th, T.; Conerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farr  
 S.; Moule, S.; O'Gaora, P.

Nature 413, 848-852, 2001  
 A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens,  
 A>Title: Complete genome sequence of a multiple drug resistant Salmonella enterica se  
 A:Reference number: AB0502; PMID:11677608

A:Accession: AG0965  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-460 <PAR>  
 A:Cross-references: GB:AL513382; PIDN:CAD03219.1; PID:g16504848; GSPDB:GN00176

A:Gene: STY4009  
 C:Superfamily: Agrobacterium beta-glucosidase

Query Match 90.0%; Score 36; DB 2; Length 460;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NMSWL 6  
 |||||  
 Db 418 NMSWL 422

## RESULT 7

C83491  
 hypothetical protein PA1242 [Imported] - Pseudomonas aeruginosa (strain PA01)

C:Species: Pseudomonas aeruginosa  
 C>Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 31-Dec-2000  
 C:Accession: C83491  
 R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.;

adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lardig, K.; Lim,  
 .; Lory, S.; Olson, M.V.  
 Nature 406, 959-964, 2000  
 A:Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic patho  
 A:Reference number: A82950; MUID:20437337; PMID:10984043  
 A:Accession: C83491  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-590 <STO>  
 A:Cross-references: GB:AE004553; GB:AE004091; NID:9947164; PIDN:AG04631.1; GSPDB:GN001  
 A:Experimental source: strain PA01  
 C:Genetics:  
 A:Gene: PA1242

Query Match 90.0%; Score 36; DB 2; Length 590;  
 Best Local Similarity 100.0%; Pred. No. 2e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LNMSW 5  
 |||||  
 Db 360 LNMSW 364

RESULT 8  
 T10035  
 hypothetical protein MLCB628.16c - *Mycobacterium leprae*  
 C:Species: *Mycobacterium leprae*  
 C:Date: 13-Aug-1999 #sequence\_revision 13-Aug-1999 #text\_change 21-Jul-2000  
 C:Accession: T10035  
 R:Eligmeier, K.; Honore, N.; Woods, S.A.; Caudron, B.; Cole, S.T.  
 Mol. Microbiol. 7, 197-206, 1993  
 A:Title: Use of an ordered cosmid library to deduce the genomic organization of *Mycobact*  
 A:Reference number: Z16917; MUID:93188700; PMID:8446027  
 A:Accession: T10035  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-744 <ETG>  
 A:Cross-references: EMBL:Y14967; NID:92370268; PIDN:CAA75203.1; PID:92370283  
 C:Genetics:  
 A:Note: MLCB628.16c

Query Match 90.0%; Score 36; DB 2; Length 744;  
 Best Local Similarity 100.0%; Pred. No. 2.6e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 NMSWL 6  
 |||||  
 Db 265 NMSWL 269

RESULT 9  
 T03472  
 conserved hypothetical protein - *Rhodobacter capsulatus*  
 C:Species: *Rhodobacter capsulatus*  
 C:Date: 24-Mar-1999 #sequence\_revision 24-Mar-1999 #text\_change 08-Oct-1999  
 C:Accession: T03472  
 R:Vitek, C.; Paces, V.; Maltsev, N.; Paces, J.; Haselkorn, R.; Feinstein, M.  
 Proc. Natl. Acad. Sci. U.S.A. 94, 9384-9388, 1997  
 A:Title: Sequence of a 189-kb segment of the chromosome of *Rhodobacter capsulatus* SBI003  
 A:Reference number: Z14955; MUID:97404404; PMID:9256491  
 A:Accession: T03472  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-116 <VIC>  
 A:Cross-references: EMBL:AF010496; NID:93128256; PIDN:AA016125.1; PID:93128273  
 C:Genetics:  
 A:Map position: 1

Query Match 87.5%; Score 35; DB 2; Length 116;  
 Best Local Similarity 83.3%; Pred. No. 56;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LNMSWL 6

Db 63 LMSWL 68

RESULT 10  
 T24773  
 hypothetical protein T10B10.8 - *Caenorhabditis elegans*  
 C:Species: *Caenorhabditis elegans*  
 C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 18-Feb-2000  
 C:Accession: T24773  
 R:Sim, M.  
 submitted to the EMBL Data Library, May 1996  
 A:Reference number: Z1934  
 A:Accession: T24773  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-321 <NTL>  
 A:Cross-references: EMBL:Z72514; PIDN:CAA96680.1; GSPDB:GN00028; CESP:T10B10.8  
 A:Experimental source: clone T10B10  
 C:Genetics:  
 A:Gene: CESP:T10B10.8  
 A:Map position: X  
 A:Introns: 40/3; 54/2; 64/3; 123/3; 229/2; 262/3

Query Match 87.5%; Score 35; DB 2; Length 321;  
 Best Local Similarity 83.3%; Pred. No. 1.6e+02;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 LNMSWL 6  
 |||||  
 Db 221 LNMSWL 226

RESULT 11  
 E87125  
 ribonucleotide reductase small subunit [imported] - *Mycobacterium leprae*  
 C:Species: *Mycobacterium leprae*  
 C:Date: 20-Apr-2001 #sequence\_revision 20-Apr-2001 #text\_change 10-May-2001  
 C:Accession: E87125  
 R:Cole, S.T.; Elgimeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.;  
 R.; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holro  
 cam, M.A.; Rutherford, K.M.  
 Nature 409, 1007-1011, 2001  
 A:Authors: Rutherford, S.; Seeger, K.; Simon, S.; Simmons, M.; Skelton, J.; Squares, R.;  
 A:Title: Massive gene decay in the leprosy bacillus.  
 A:Reference number: A86909; MUID:21128732; PMID:11234002  
 A:Accession: E87125  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-325 <STO>  
 A:Cross-references: GB:AL450380; NID:G13093483; PIDN:CAC30684.1; GSPDB:GN00147  
 C:Genetics:  
 A:Gene: nrdr  
 C:Superfamily: ribonucleoside-diphosphate reductase beta

Query Match 87.5%; Score 35; DB 2; Length 325;  
 Best Local Similarity 66.7%; Pred. No. 1.6e+02;  
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 LNMSWL 6  
 |||||  
 Db 15 LNMSWL 20

RESULT 12  
 I49101  
 conserved helix-loop-helix ubiquitous kinase (EC 2.7.1.-) CHUK - mouse  
 C:Species: *Mus musculus* (house mouse)  
 C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
 C:Accession: I49101  
 R:Mock, B.A.; Connelly, M.A.; McBride, O.W.; Kozak, C.A.; Marcu, K.B.  
 Genomics 27, 348-351, 1995  
 A:Title: CHUK, a conserved helix-loop-helix ubiquitous kinase, maps to human chromoso

A:Reference number: I49101; MWID:96044444; PMID:7558004  
 A:Accession: I49101  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-745 <RES>  
 A:Cross-references: EMBL:U12473; NID:g1079492; PIDN:AAC52589.1; PID:g1079493  
 C:Genetics:  
 A:Gene: CLKK  
 C:Superfamily: mouse conserved helix-loop-helix ubiquitons kinase; protein kinase homolog  
 C:Keywords: ATP; phosphotransferase  
 F:13-283/Domain: protein kinase homology <KIN>

Query Match 87.5%; Score 35; DB 1; Length 745;  
 Best Local Similarity 83.3%; Pred. No. 3.6e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LNMSWL 6  
 :|||||  
 DB 738 LDMRWL 743

RESULT 13  
 T09056  
 glucan 1,3-beta-glucosidase (EC 3.2.1.58) - *Ampelomyces quisqualis*  
 N:Alternate names: exo-beta-1,3-glucanase  
 C:Species: *Ampelomyces quisqualis*  
 C>Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 20-Sep-1999  
 C:Accession: T09056  
 R:Rotem, Y.; Yarden, O.; Szejnberg, A.  
 submitted to the EMBL Data Library, October 1997  
 A:Reference number: Z16541  
 A:Accession: T09056  
 A:Status: translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-777 <ROT>  
 A:Cross-references: EMBL:AF029354; NID:g3004862; PID:g3004863  
 A:Experimental source: strain AQ10  
 C:Genetics:  
 A:Gene: exga  
 C:Function:  
 A:Description: catalyzes the hydrolysis of beta-D-glucose units from the non-reducing en  
 C:Keywords: glycosidase; hydrolase

Query Match 87.5%; Score 35; DB 2; Length 777;  
 Best Local Similarity 66.7%; Pred. No. 3.8e+02;  
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 LNMSWL 6  
 :|||||  
 DB 266 MNMWWL 271

RESULT 14  
 S76882  
 hypothetical protein - *Synechocystis* sp. (strain PCC 6803)  
 C:Species: *Synechocystis* sp.  
 A:Variety: PCC 6803  
 C>Date: 25-Apr-1997 #sequence\_revision 25-Apr-1997 #text\_change 20-Jun-2000  
 C:Accession: S76882  
 R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;  
 O. K.; Okumura, S.; Shlomo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda  
 DNA Res. 3, 109-136, 1996  
 A>Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis*  
 S.  
 A:Reference number: S74322; MWID:97061201; PMID:8905231  
 A:Accession: S76882  
 A:Status: nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-154 <KAN>  
 A:Cross-references: EMBL:D90917; GB:AB001339; NID:g1653836; PIDN:BA18794.1; PID:g165388  
 C:Genetics:  
 A>Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996  
 A:Start codon: GTG

C:Superfamily: hypothetical protein b2267

Query Match 85.0%; Score 34; DB 2; Length 154;  
 Best Local Similarity 80.0%; Pred. No. 1.1e+02;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LNMSW 5  
 :|||||  
 DB 3 LNMSW 7

RESULT 15  
 C45456  
 NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 1 - *Paracoccus denitrificans*  
 N:Alternate names: NADH-quinone oxidoreductase chain I  
 C:Species: *Paracoccus denitrificans*  
 C>Date: 24-Feb-1994 #sequence\_revision 15-Oct-1994 #text\_change 03-Jun-2002  
 C:Accession: C45456  
 R:Xu, X.; Matsuno-Yagi, A.; Yagi, T.  
 Biochemistry 32, 968-981, 1993  
 A>Title: DNA sequencing of the seven remaining structural genes of the gene cluster e  
 A:Reference number: A45456; MWID:93136200; PMID:8422400  
 A:Accession: C45456  
 A:Molecule type: DNA  
 A:Residues: 1-345 <XU1>  
 A:Cross-references: GB:L02354; NID:g150606; PIDN:AA25592.1; PID:g150608  
 A>Note: sequence extracted from NCBI backbone (NCBIN:123409, NCBI:123413)  
 C:Genetics:  
 A:Gene: NQ08  
 C:Superfamily: NADH dehydrogenase (ubiquinone) chain 1  
 C:Keywords: membrane-associated complex; NAD; oxidative phosphorylation; oxidoreducta

Query Match 85.0%; Score 34; DB 2; Length 345;  
 Best Local Similarity 83.3%; Pred. No. 2.4e+02;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 LNMSWL 6  
 :|||||  
 DB 191 LNMYWL 196

Search completed: May 30, 2003, 14:52:50  
 Job time: 7.5921 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 30, 2003, 14:50:13 ; Search time 10.4605 Seconds  
(without alignments)  
58.060 Million cell updates/sec

Title: US-09-643-260-8

Perfect score: 39

Sequence: 1 LEWSWL 6

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 383519 seqs, 101223694 residues

Total number of hits satisfying chosen parameters: 383519

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published\_Applications\_AA.\*

1: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*  
2: /cgn2\_6/ptodata/1/pubpaa/PTCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*  
6: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*  
7: /cgn2\_6/ptodata/1/pubpaa/PTCT\_PUBCOMB.pep.\*  
8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*  
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11: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*  
12: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB.pep.\*  
13: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*  
14: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	39	100.0	6	9	US-09-847-940B-8
2	39	100.0	6	9	US-09-847-946A-8
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4	36	92.3	6	9	US-09-847-946A-2
5	36	92.3	6	9	US-09-847-946A-33
6	36	92.3	7	9	US-09-847-946A-37
7	36	92.3	8	9	US-09-847-946A-30
8	36	92.3	8	9	US-09-847-946A-38
9	36	92.3	9	9	US-09-847-946A-29
10	36	92.3	9	9	US-09-847-946A-32
11	36	92.3	9	9	US-09-847-946A-35
12	36	92.3	9	9	US-09-847-946A-36
13	36	92.3	10	9	US-09-847-946A-31
14	36	92.3	10	9	US-09-847-946A-34
15	36	92.3	11	9	US-09-847-946A-28
16	36	92.3	11	9	US-09-847-946A-132
17	36	92.3	11	9	US-09-847-946A-140
18	36	92.3	13	9	US-09-847-946A-143
19	36	92.3	13	9	US-09-847-946A-144

20	36	92.3	13	9	US-09-847-946A-145	Sequence 145, App
21	36	92.3	13	9	US-09-847-946A-148	Sequence 148, App
22	36	92.3	17	9	US-09-847-946A-141	Sequence 141, App
23	36	92.3	17	9	US-09-847-946A-142	Sequence 142, App
24	36	92.3	17	9	US-09-847-946A-146	Sequence 146, App
25	36	92.3	17	9	US-09-847-946A-147	Sequence 147, App
26	36	92.3	18	9	US-09-847-946A-131	Sequence 131, App
27	36	92.3	18	9	US-09-847-946A-135	Sequence 135, App
28	36	92.3	18	9	US-09-847-946A-136	Sequence 136, App
29	36	92.3	22	9	US-09-847-946A-133	Sequence 133, App
30	36	92.3	22	9	US-09-847-946A-134	Sequence 134, App
31	36	92.3	22	9	US-09-847-946A-137	Sequence 137, App
32	36	92.3	22	9	US-09-847-946A-138	Sequence 138, App
33	36	92.3	22	9	US-09-847-946A-139	Sequence 139, App
34	36	92.3	28	9	US-09-847-940B-18	Sequence 18, App
35	36	92.3	28	9	US-09-847-946A-18	Sequence 18, App
36	36	92.3	22	10	US-09-771-161A-141	Sequence 141, App
37	36	92.3	745	9	US-09-844-988-10	Sequence 10, App
38	36	92.3	745	9	US-10-243-408-4	Sequence 4, App
39	36	92.3	745	9	US-10-059-585-35	Sequence 35, App
40	36	92.3	745	10	US-09-796-872-2	Sequence 2, App
41	36	92.3	745	10	US-09-844-908-10	Sequence 10, App
42	36	92.3	756	9	US-09-844-988-9	Sequence 9, App
43	36	92.3	756	9	US-10-243-408-2	Sequence 2, App
44	36	92.3	756	10	US-09-796-872-15	Sequence 15, App
45	36	92.3	756	10	US-09-771-161A-232	Sequence 232, App

#### ALIGNMENTS

RESULT 1  
US-09-847-940B-8  
Sequence 8, Application US/09847940B  
Patent No. US2002015600A1  
GENERAL INFORMATION:  
APPLICANT: May, Michael J.  
APPLICANT: Ghosh, Sankar  
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
FILE REFERENCE: PFI-117CP  
CURRENT APPLICATION NUMBER: US/09/847, 940B  
CURRENT FILING DATE: 2001-05-02  
PRIOR APPLICATION NUMBER: 09/643, 260  
PRIOR FILING DATE: 2000-08-22  
NUMBER OF SEQ ID NOS: 27  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 8  
LENGTH: 6  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: NBD mutants  
US-09-847-940B-8

Query Match 100.0%; Score 39; DB 9; Length 6;  
Best Local Similarity 100.0%; Pred. No. 3.4e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEWSWL 6  
DB 1 LEWSWL 6

RESULT 2  
US-09-847-946A-8  
Sequence 8, Application US/09847946A  
Publication No. US2003005499A1  
GENERAL INFORMATION:  
APPLICANT: May, Michael J  
APPLICANT: Ghosh, Sankar  
APPLICANT: Flindels, Mark A  
APPLICANT: Phillips, Kathryn  
APPLICANT: Hannig, Gernard

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; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NBD peptide
US-09-847-946A-8

Query Match
Best Local Similarity 100.0%; Score 39; DB 9; Length 6;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEWSWL 6
Db 1 LDMSWL 6

RESULT 3
US-09-847-940B-2
; Sequence 2, Application US/09847940B
; Patent No. US20020156000A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J.
; APPLICANT: Ghosh, Sankar
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-117CP
; CURRENT APPLICATION NUMBER: US/09/847,940B
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NBD mutants
US-09-847-940B-2

Query Match
Best Local Similarity 92.3%; Score 36; DB 9; Length 6;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEWSWL 6
Db 1 LDMSWL 6

RESULT 4
US-09-847-946A-2
; Sequence 2, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02

; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NBD peptide
US-09-847-946A-2

Query Match
Best Local Similarity 92.3%; Score 36; DB 9; Length 6;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEWSWL 6
Db 1 LDMSWL 6

RESULT 5
US-09-847-946A-33
; Sequence 33, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
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; SEQ ID NO 33
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NBD binding
US-09-847-946A-33

Query Match
Best Local Similarity 92.3%; Score 36; DB 9; Length 6;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEWSWL 6
Db 1 LDMSWL 6

RESULT 6
US-09-847-946A-37
; Sequence 37, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
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; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 37
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-37
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Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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OY      1 LEMSWL 6
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Db      1 LDMSWL 6
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; US-09-847-946A-30
; Sequence 30, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Ghosh, Sankar
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 30
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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-30
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Best Local Similarity 83.3%; Pred. No. 3.4e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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OY      1 LEMSWL 6
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Db      3 LDMSWL 8
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RESULT 8
; US-09-847-946A-38
; Sequence 38, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Ghosh, Sankar
; APPLICANT: Phillips, Mark A
; APPLICANT: Phillips, Kathryn
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; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
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; LENGTH: 8
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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-38
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Best Local Similarity 83.3%; Pred. No. 3.4e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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Db      1 LDMSWL 6
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; US-09-847-946A-29
; Sequence 29, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Ghosh, Sankar
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 29
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-29
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Query Match          92.3%; Score 36; DB 9; Length 9;
Best Local Similarity 83.3%; Pred. No. 3.4e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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```
OY      1 LEMSWL 6
        |:||||
Db      1 LDMSWL 6
```

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RESULT 10
; US-09-847-946A-32
; Sequence 32, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
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APPLICANT: Ghosh, Sankar  
APPLICANT: Flindels, Mark A  
APPLICANT: Phillips, Kathryn  
APPLICANT: Hannig, Gerhard  
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
FILE REFERENCE: PPI-119  
CURRENT APPLICATION NUMBER: US/09/847,946A  
CURRENT FILING DATE: 2001-05-02  
PRIOR APPLICATION NUMBER: 60/201,261  
PRIOR FILING DATE: 2000-05-02  
PRIOR APPLICATION NUMBER: 09/643,260  
PRIOR FILING DATE: 2000-08-22  
NUMBER OF SEQ ID NOS: 160  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 32  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:NEMO binding  
US-09-847-946A-32

Query Match 92.3%; Score 36; DB 9; Length 9;  
Best Local Similarity 83.3%; Pred. No. 3.4e+05;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEWSWL 6  
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DB 1 LDMSWL 6

RESULT 11  
US-09-847-946A-35  
Sequence 35, Application US/09847946A  
Publication No. US20030054999A1  
GENERAL INFORMATION:  
APPLICANT: May, Michael J  
APPLICANT: Ghosh, Sankar  
APPLICANT: Flindels, Mark A  
APPLICANT: Phillips, Kathryn  
APPLICANT: Hannig, Gerhard  
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
FILE REFERENCE: PPI-119  
CURRENT APPLICATION NUMBER: US/09/847,946A  
CURRENT FILING DATE: 2001-05-02  
PRIOR APPLICATION NUMBER: 60/201,261  
PRIOR FILING DATE: 2000-05-02  
PRIOR APPLICATION NUMBER: 09/643,260  
PRIOR FILING DATE: 2000-08-22  
NUMBER OF SEQ ID NOS: 160  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 35  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:NEMO binding  
US-09-847-946A-35

Query Match 92.3%; Score 36; DB 9; Length 9;  
Best Local Similarity 83.3%; Pred. No. 3.4e+05;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEWSWL 6  
|:||||  
DB 3 LDMSWL 8

RESULT 12  
US-09-847-946A-36  
Sequence 36, Application US/09847946A

Publication No. US20030054999A1  
GENERAL INFORMATION:  
APPLICANT: May, Michael J  
APPLICANT: Ghosh, Sankar  
APPLICANT: Flindels, Mark A  
APPLICANT: Phillips, Kathryn  
APPLICANT: Hannig, Gerhard  
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
FILE REFERENCE: PPI-119  
CURRENT APPLICATION NUMBER: US/09/847,946A  
CURRENT FILING DATE: 2001-05-02  
PRIOR APPLICATION NUMBER: 60/201,261  
PRIOR FILING DATE: 2000-05-02  
PRIOR APPLICATION NUMBER: 09/643,260  
PRIOR FILING DATE: 2000-08-22  
NUMBER OF SEQ ID NOS: 160  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 36  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:NEMO binding  
US-09-847-946A-36

Query Match 92.3%; Score 36; DB 9; Length 9;  
Best Local Similarity 83.3%; Pred. No. 3.4e+05;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEWSWL 6  
|:||||  
DB 2 LDMSWL 7

RESULT 13  
US-09-847-946A-31  
Sequence 31, Application US/09847946A  
Publication No. US20030054999A1  
GENERAL INFORMATION:  
APPLICANT: May, Michael J  
APPLICANT: Ghosh, Sankar  
APPLICANT: Flindels, Mark A  
APPLICANT: Phillips, Kathryn  
APPLICANT: Hannig, Gerhard  
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
FILE REFERENCE: PPI-119  
CURRENT APPLICATION NUMBER: US/09/847,946A  
CURRENT FILING DATE: 2001-05-02  
PRIOR APPLICATION NUMBER: 60/201,261  
PRIOR FILING DATE: 2000-05-02  
PRIOR APPLICATION NUMBER: 09/643,260  
PRIOR FILING DATE: 2000-08-22  
NUMBER OF SEQ ID NOS: 160  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 31  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:NEMO binding  
US-09-847-946A-31

Query Match 92.3%; Score 36; DB 9; Length 10;  
Best Local Similarity 83.3%; Pred. No. 18;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEWSWL 6  
|:||||  
DB 2 LDMSWL 7

Db 3 LDMSWL 8  
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Job time : 11.4605 secs

RESULT 14  
US-09-847-946A-34  
Sequence 34, Application US/09847946A  
Publication No. US20030054999A1  
GENERAL INFORMATION:  
APPLICANT: May, Michael J  
APPLICANT: Ghosh, Sankar  
APPLICANT: Findels, Mark A  
APPLICANT: Phillips, Kathryn  
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
FILE REFERENCE: PPI-119  
CURRENT APPLICATION NUMBER: US/09/847,946A  
CURRENT FILING DATE: 2001-05-02  
PRIOR APPLICATION NUMBER: 60/201,261  
PRIOR FILING DATE: 2000-05-02  
PRIOR APPLICATION NUMBER: 09/643,260  
PRIOR FILING DATE: 2000-08-22  
NUMBER OF SEQ ID NOS: 160  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 34  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:NEMO binding  
OTHER INFORMATION: sequence  
US-09-847-946A-34

Query Match 92.3%; Score 36; DB 9; Length 10;  
Best Local Similarity 83.3%; Pred. No. 18;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSWL 6  
1:||||  
Db 3 LDMSWL 8

RESULT 15  
US-09-847-946A-28  
Sequence 28, Application US/09847946A  
Publication No. US20030054999A1  
GENERAL INFORMATION:  
APPLICANT: May, Michael J  
APPLICANT: Ghosh, Sankar  
APPLICANT: Findels, Mark A  
APPLICANT: Phillips, Kathryn  
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
FILE REFERENCE: PPI-119  
CURRENT APPLICATION NUMBER: US/09/847,946A  
CURRENT FILING DATE: 2001-05-02  
PRIOR APPLICATION NUMBER: 60/201,261  
PRIOR FILING DATE: 2000-05-02  
PRIOR APPLICATION NUMBER: 09/643,260  
PRIOR FILING DATE: 2000-08-22  
NUMBER OF SEQ ID NOS: 160  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 28  
LENGTH: 11  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:NEMO binding  
OTHER INFORMATION: sequence  
US-09-847-946A-28

Query Match 92.3%; Score 36; DB 9; Length 11;  
Best Local Similarity 83.3%; Pred. No. 20;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSWL 6  
1:||||



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Title: US-09-643-260-8

Perfect score: 39

Sequence: 1 LEWSWL 6

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Listing first 45 summaries

Database : Issued\_Patents\_AA:\*

1: /cgn2\_6/ptodata/1/1aa/5A.COMB.pep:\*\n2: /cgn2\_6/ptodata/1/1aa/5B.COMB.pep:\*\n3: /cgn2\_6/ptodata/1/1aa/6A.COMB.pep:\*\n4: /cgn2\_6/ptodata/1/1aa/6B.COMB.pep:\*\n5: /cgn2\_6/ptodata/1/1aa/PCITUS.COMB.pep:\*\n6: /cgn2\_6/ptodata/1/1aa/Backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	36	92.3	745	2	US-08-887-518-3
2	36	92.3	745	2	US-09-023-321-3
3	36	92.3	745	2	US-08-890-853-4
4	36	92.3	745	2	US-09-032-475-3
5	36	92.3	745	2	US-09-099-125A-4
6	36	92.3	745	2	US-09-099-124A-4
7	36	92.3	745	2	US-09-032-476-4
8	36	92.3	745	4	US-08-890-854-4
9	36	92.3	745	4	US-09-023-324-4
10	36	92.3	745	4	US-09-168-629-2
11	36	92.3	745	4	US-08-910-820-10
12	36	92.3	745	2	US-08-810-131A-2
13	36	92.3	756	2	US-08-887-518-4
14	36	92.3	756	2	US-09-023-321-4
15	36	92.3	756	2	US-08-890-853-2
16	36	92.3	756	2	US-09-032-475-4
17	36	92.3	756	2	US-09-099-125A-2
18	36	92.3	756	2	US-09-099-124A-2
19	36	92.3	756	4	US-09-032-476-2
20	36	92.3	756	4	US-08-890-854-2
21	36	92.3	756	4	US-09-023-324-2
22	36	92.3	756	4	US-09-168-629-15
23	36	92.3	756	4	US-08-910-820-9
24	36	89.7	137	1	US-08-392-419-2
25	35	89.7	140	3	US-08-836-561-27
26	35	89.7	140	3	US-08-836-561-63
27	35	89.7	140	3	US-08-836-561-74

28	35	89.7	140	3	US-08-836-561-78	Sequence 78, Appl
29	35	89.7	140	3	US-08-836-561-83	Sequence 83, Appl
30	35	89.7	140	4	US-08-579-378A-4	Sequence 4, Appl
31	35	89.7	140	5	PCT-US93-11612-4	Sequence 61, Appl
32	34	87.2	12	3	US-08-603-024-9	Sequence 9, Appl
33	34	87.2	117	2	US-08-822-028-2	Sequence 2, Appl
34	34	87.2	117	2	US-08-479-285-2	Sequence 2, Appl
35	34	87.2	133	2	US-08-822-028-6	Sequence 6, Appl
36	34	87.2	133	2	US-08-822-028-30	Sequence 30, Appl
37	34	87.2	133	4	US-08-718-323A-8	Sequence 8, Appl
38	34	87.2	133	4	US-08-479-285-6	Sequence 6, Appl
39	34	87.2	133	4	US-08-479-285-30	Sequence 30, Appl
40	34	87.2	133	4	US-09-587-526-8	Sequence 8, Appl
41	34	87.2	133	6	5219996-17	Sequence 17, Appl
42	34	87.2	134	2	US-08-822-028-4	Sequence 4, Appl
43	34	87.2	134	2	US-08-822-028-8	Sequence 8, Appl
44	34	87.2	134	2	US-08-822-028-10	Sequence 10, Appl
45	34	87.2	134	2	US-08-822-028-10	Sequence 10, Appl

## ALIGNMENTS

RESULT 1  
US-08-887-518-3  
Sequence 3, Application US/08887518

Patent No. 5843721

GENERAL INFORMATION:

APPLICANT: Roche, Mike

APPLICANT: Wu, Lin

TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP

STREET: 268 BUSH STREET, SUITE 3200

CITY: SAN FRANCISCO

STATE: CALIFORNIA

COUNTRY: USA

ZIP: 94104

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/887,518

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: OSMAN, RICHARD A

REGISTRATION NUMBER: 36,627

REFERENCE/DOCKET NUMBER: T97-008

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 343-4341

TELEFAX: (415) 343-4342

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 745 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-887-518-3

Query Match

Best Local Similarity 92.3%

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEWSWL 6

DB 738 LDMSWL 743

RESULT 2  
US-09-023-321-3  
; Sequence 3, Application US/09023321  
; Patent No. 5844073  
; GENERAL INFORMATION:  
; APPLICANT: Rothe, Mike  
; APPLICANT: Wu, Lin  
; TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
; STREET: 268 BUSH STREET, SUITE 3200  
; CITY: SAN FRANCISCO  
; STATE: CALIFORNIA  
; COUNTRY: USA  
; ZIP: 94104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/023.321  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/887.518  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: OSMAN, RICHARD A  
; REGISTRATION NUMBER: 36.627  
; REFERENCE/DOCKET NUMBER: T97-008  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 343-4341  
; TELEFAX: (415) 343-4342  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 745 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-09-023-321-3

Query Match 92.3%; Score 36; DB 2; Length 745;  
Best Local Similarity 83.3%; Pred. NO. 4.3e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LEWSWL 6  
|:||||  
Db 738 LDMSWL 743

RESULT 3  
US-08-890-853-4  
; Sequence 4, Application US/08890853  
; Patent No. 5851812  
; GENERAL INFORMATION:  
; APPLICANT: Goeddel, David V.  
; APPLICANT: Moronicz, John  
; TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
; STREET: 268 BUSH STREET, SUITE 3200  
; CITY: SAN FRANCISCO  
; STATE: CALIFORNIA  
; COUNTRY: USA  
; ZIP: 94104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30

SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/890.853  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: OSMAN, RICHARD A  
; REGISTRATION NUMBER: 36.627  
; REFERENCE/DOCKET NUMBER: T97-006-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 343-4341  
; TELEFAX: (415) 343-4342  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 745 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-08-890-853-4

Query Match 92.3%; Score 36; DB 2; Length 745;  
Best Local Similarity 83.3%; Pred. NO. 4.3e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LEWSWL 6  
|:||||  
Db 738 LDMSWL 743

RESULT 4  
US-09-032-475-3  
; Sequence 3, Application US/09032475  
; Patent No. 5854003  
; GENERAL INFORMATION:  
; APPLICANT: Rothe, Mike  
; APPLICANT: Wu, Lin  
; TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
; STREET: 268 BUSH STREET, SUITE 3200  
; CITY: SAN FRANCISCO  
; STATE: CALIFORNIA  
; COUNTRY: USA  
; ZIP: 94104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/032.475  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/887.518  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: OSMAN, RICHARD A  
; REGISTRATION NUMBER: 36.627  
; REFERENCE/DOCKET NUMBER: T97-008  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 343-4341  
; TELEFAX: (415) 343-4342  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 745 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-09-032-475-3

Query Match 92.3%; Score 36; DB 2; Length 745;  
Best Local Similarity 83.3%; Pred. No. 4.3e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEMSWL 6  
|:||||  
DB 738 LDMWSL 743

RESULT 5  
US-09-099-125A-4  
; Sequence 4, Application US/09099125A  
; Patent No. 5916760  
; GENERAL INFORMATION:  
; APPLICANT: Goeddel, David V.  
; APPLICANT: Moronicz, John  
; TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
; STREET: 268 BUSH STREET, SUITE 3200  
; CITY: SAN FRANCISCO  
; STATE: CALIFORNIA  
; COUNTRY: USA  
; ZIP: 94104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/099,125A  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/890,853  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: OSMAN, RICHARD A  
; REGISTRATION NUMBER: 36,627  
; REFERENCE/DOCKET NUMBER: T97-006-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 343-4341  
; TELEFAX: (415) 343-4342  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 745 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-09-099-125A-4

Query Match 92.3%; Score 36; DB 2; Length 745;  
Best Local Similarity 83.3%; Pred. No. 4.3e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEMSWL 6  
|:||||  
DB 738 LDMWSL 743

RESULT 6  
US-09-099-124A-4  
; Sequence 4, Application US/09099124A  
; Patent No. 5939302  
; GENERAL INFORMATION:  
; APPLICANT: Goeddel, David V.  
; APPLICANT: Moronicz, John  
; TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:

ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
; STREET: 268 BUSH STREET, SUITE 3200  
; CITY: SAN FRANCISCO  
; STATE: CALIFORNIA  
; COUNTRY: USA  
; ZIP: 94104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/099,124A  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/890,853  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: OSMAN, RICHARD A  
; REGISTRATION NUMBER: 36,627  
; REFERENCE/DOCKET NUMBER: T97-006-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 343-4341  
; TELEFAX: (415) 343-4342  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 745 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-09-099-124A-4

Query Match 92.3%; Score 36; DB 2; Length 745;  
Best Local Similarity 83.3%; Pred. No. 4.3e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEMSWL 6  
|:||||  
DB 738 LDMWSL 743

RESULT 7  
US-09-032-476-4  
; Sequence 4, Application US/09032476  
; Patent No. 6235492  
; GENERAL INFORMATION:  
; APPLICANT: Rothe, Mike  
; APPLICANT: Cao, Zhaodan  
; APPLICANT: R guier, Catherine  
; TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
; STREET: 268 BUSH STREET, SUITE 3200  
; CITY: SAN FRANCISCO  
; STATE: CALIFORNIA  
; COUNTRY: USA  
; ZIP: 94104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/032,476  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/890,854  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:

NAME: OSMAN, RICHARD A  
REGISTRATION NUMBER: 36,627  
REFERENCE/DOCKET NUMBER: T97-006-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 343-4341  
TELEFAX: (415) 343-4342  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 745 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-032-476-4

Query Match 92.3%; Score 36; DB 4; Length 745;  
Best Local Similarity 83.3%; Pred. No. 4.3e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEWSWL 6  
1:|||||  
DB 738 LDMSWL 743

RESULT 8  
US-08-890-854-4  
Sequence 4, Application US/08890854  
Patent No. 6235512  
GENERAL INFORMATION:  
APPLICANT: Rothe, Mike  
APPLICANT: Cao, Zhaodan  
APPLICANT: R gnier, Catherine  
TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
STREET: 268 BUSH STREET, SUITE 3200  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/890,854  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: OSMAN, RICHARD A  
REGISTRATION NUMBER: 36,627  
REFERENCE/DOCKET NUMBER: T97-006-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 343-4341  
TELEFAX: (415) 343-4342  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 745 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-890-854-4

Query Match 92.3%; Score 36; DB 4; Length 745;  
Best Local Similarity 83.3%; Pred. No. 4.3e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEWSWL 6  
1:|||||  
DB 738 LDMSWL 743

RESULT 9  
US-09-023-324-4  
Sequence 4, Application US/09023324  
Patent No. 6235513  
GENERAL INFORMATION:  
APPLICANT: Rothe, Mike  
APPLICANT: Cao, Zhaodan  
APPLICANT: R gnier, Catherine  
TITLE OF INVENTION: IKK- Proteins, Nucleic Acids and Methods  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
STREET: 268 BUSH STREET, SUITE 3200  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/023,324  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/890,854  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: OSMAN, RICHARD A  
REGISTRATION NUMBER: 36,627  
REFERENCE/DOCKET NUMBER: T97-006-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 343-4341  
TELEFAX: (415) 343-4342  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 745 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-023-324-4

Query Match 92.3%; Score 36; DB 4; Length 745;  
Best Local Similarity 83.3%; Pred. No. 4.3e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEWSWL 6  
1:|||||  
DB 738 LDMSWL 743

RESULT 10  
US-09-168-629-2  
Sequence 2, Application US/09168629  
Patent No. 6242253  
GENERAL INFORMATION:  
APPLICANT: Karlin, Michael  
APPLICANT: Didonato, Joseph A.  
APPLICANT: Rothwarf, David M.  
APPLICANT: Hayakawa, Makio  
APPLICANT: Zandi, Ebrahim  
TITLE OF INVENTION: 18S kinase, Subunits Thereof, and Methods of Using Same  
FILE REFERENCE: P-UD 3295  
CURRENT APPLICATION NUMBER: US/09/168,629  
CURRENT FILING DATE: 1998-10-08  
EARLIER APPLICATION NUMBER: 60/061,470  
EARLIER FILING DATE: 1997-10-09  
NUMBER OF SEQ ID NOS: 20

SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 2  
LENGTH: 745  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-168-629-2

Query Match  
Best Local Similarity 92.3%; Score 36; DB 4; Length 745;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEWSWL 6  
DB 738 LDMWSL 743

RESULT 11  
US-08-910-820-10  
Sequence 10, Application US/08910820  
Patent No. 6258579  
GENERAL INFORMATION:  
APPLICANT: Mercurio, Frank  
APPLICANT: Zhu, Hengyi  
APPLICANT: Barbosa, Miguel  
APPLICANT: Li, Jian  
TITLE OF INVENTION: STIMULUS-INDUCIBLE PROTEIN KINASE  
NUMBER OF SEQUENCES: 25  
TITLE OF INVENTION: COMPLEX AND METHODS OF USE THEREFOR  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SEED AND BERRY LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/910,820  
FILING DATE: 12-AUG-1997  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: MAKI, David J.  
REGISTRATION NUMBER: 31,392  
REFERENCE/DOCKET NUMBER: 860098.413C1  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 745 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
US-08-910-820-10

Query Match  
Best Local Similarity 92.3%; Score 36; DB 4; Length 745;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEWSWL 6  
DB 738 LDMWSL 743

RESULT 12  
US-08-810-131A-2  
Sequence 2, Application US/08810131A  
Patent No. 6268194

GENERAL INFORMATION:  
APPLICANT: Karlin, Michael  
APPLICANT: D'Donato, Joseph A.  
APPLICANT: Rothwarf, David M.  
APPLICANT: Hayakawa, Makio  
APPLICANT: Zandi, Ebrahim  
TITLE OF INVENTION: I-kappa-B kinase and Methods of Using  
NUMBER OF SEQUENCES: 9  
TITLE OF INVENTION: Same  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Campbell & Flores LLP  
STREET: 4370 La Jolla Village Drive, Suite 700  
CITY: San Diego  
STATE: California  
COUNTRY: United States  
ZIP: 92122  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/810,131A  
FILING DATE: 25-FEB-1997  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Campbell, Cathryn A.  
REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P-UD 2408  
TELEPHONE: (619) 535-9001  
TELEFAX: (619) 535-8949  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 745 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-810-131A-2

Query Match  
Best Local Similarity 92.3%; Score 36; DB 4; Length 745;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEWSWL 6  
DB 738 LDMWSL 743

RESULT 13  
US-08-887-518-4  
Sequence 4, Application US/08887518  
Patent No. 5843721  
GENERAL INFORMATION:  
APPLICANT: Roche, Mike  
APPLICANT: Wu, Lin  
TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
STREET: 268 BUSH STREET, SUITE 3200  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/887,518  
FILING DATE:

CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: OSMAN, RICHARD A  
REGISTRATION NUMBER: 36,627  
REFERENCE/DOCKET NUMBER: T97-008  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 343-4341  
TELEFAX: (415) 343-4342  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 756 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-887-518-4

Query Match 92.3%; Score 36; DB 2; Length 756;  
Best Local Similarity 83.3%; Pred. No. 4.4e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEWSWL 6  
|:||||  
DB 737 LDMSWL 742

RESULT 14  
US-09-023-321-4  
Sequence 4, Application US/09023321  
Patent No. 5844073  
GENERAL INFORMATION:  
APPLICANT: Roche, Mike  
APPLICANT: Wu, Lin  
TITLE OF INVENTION: NIK Proteins, Nucleic Acids and Methods  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
STREET: 268 BUSH STREET, SUITE 3200  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/023.321  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/887.518  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: OSMAN, RICHARD A  
REGISTRATION NUMBER: 36,627  
REFERENCE/DOCKET NUMBER: T97-008  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 343-4341  
TELEFAX: (415) 343-4342  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 756 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-023-321-4

Query Match 92.3%; Score 36; DB 2; Length 756;  
Best Local Similarity 83.3%; Pred. No. 4.4e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEWSWL 6  
|:||||  
DB 737 LDMSWL 742

RESULT 15  
US-08-890-853-2  
Sequence 2, Application US/08890853  
Patent No. 5851812  
GENERAL INFORMATION:  
APPLICANT: Goeddel, David V.  
APPLICANT: Woronicz, John  
TITLE OF INVENTION: IKK Proteins, Nucleic Acids and Methods  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
STREET: 268 BUSH STREET, SUITE 3200  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/890.853  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: OSMAN, RICHARD A  
REGISTRATION NUMBER: 36,627  
REFERENCE/DOCKET NUMBER: T97-006-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 343-4341  
TELEFAX: (415) 343-4342  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 756 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-890-853-2

Query Match 92.3%; Score 36; DB 2; Length 756;  
Best Local Similarity 83.3%; Pred. No. 4.4e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEWSWL 6  
|:||||  
DB 737 LDMSWL 742

Search completed: May 30, 2003, 14:41:26  
Job time : 7.03947 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 30, 2003, 14:32:12 ; Search time 19.6974 Seconds  
(without alignments)  
40.589 Million cell updates/sec

Title: US-09-643-260-8  
Perfect score: 39  
Sequence: 1 LEWSWL 6

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues  
Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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3: /SID2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:\*  
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23: /SID2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:\*  
24: /SID2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:\*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	39	100.0	6	23	ABB08730
2	39	100.0	6	23	AAW48513
3	39	100.0	756	23	ABB77305
4	36	92.3	6	23	ABB08725
5	36	92.3	6	23	AAW48530
6	36	92.3	6	23	AAW48535
7	36	92.3	7	23	AAW48534
8	36	92.3	8	23	AAW48527
9	36	92.3	8	23	AAW48535
10	36	92.3	9	20	AAW96182

11	36	92.3	9	23	AAW48526	Anti-Inflammatory
12	36	92.3	9	23	AAW48529	Anti-Inflammatory
13	36	92.3	9	23	AAW48532	Anti-Inflammatory
14	36	92.3	9	23	AAW48533	Anti-Inflammatory
15	36	92.3	10	23	ABB77313	IKKbeta NEMO bindi
16	36	92.3	10	23	AAW48528	Anti-Inflammatory
17	36	92.3	10	23	AAW48531	Anti-Inflammatory
18	36	92.3	11	23	ABB77311	Human NBD peptide
19	36	92.3	11	23	AAW48506	Human IKKbeta pept
20	36	92.3	11	23	AAW48525	Anti-Inflammatory
21	36	92.3	11	23	AAW48553	NBD peptide. Synt
22	36	92.3	13	23	AAW48640	Anti-Inflammatory
23	36	92.3	13	23	AAW48641	Anti-Inflammatory
24	36	92.3	13	23	AAW48642	Anti-Inflammatory
25	36	92.3	13	23	AAW48645	Anti-Inflammatory
26	36	92.3	17	23	AAW48638	Anti-Inflammatory
27	36	92.3	17	23	AAW48639	Anti-Inflammatory
28	36	92.3	17	23	AAW48643	Anti-Inflammatory
29	36	92.3	17	23	AAW48644	Anti-Inflammatory
30	36	92.3	18	23	AAW48628	Anti-Inflammatory
31	36	92.3	18	23	AAW48629	Anti-Inflammatory
32	36	92.3	18	23	AAW48632	Anti-Inflammatory
33	36	92.3	18	23	AAW48633	Anti-Inflammatory
34	36	92.3	22	23	AAW48630	Anti-Inflammatory
35	36	92.3	22	23	AAW48631	Anti-Inflammatory
36	36	92.3	22	23	AAW48634	Anti-Inflammatory
37	36	92.3	22	23	AAW48635	Anti-Inflammatory
38	36	92.3	22	23	AAW48636	Anti-Inflammatory
39	36	92.3	22	23	AAW48637	Anti-Inflammatory
40	36	92.3	28	23	ABB08740	IKKbeta NEMO bindi
41	36	92.3	28	23	AAW48533	NBD peptide SEQ ID
42	36	92.3	36	23	AAW48652	IKKbeta mutated pe
43	36	92.3	220	21	AAW48488	Human protein sequ
44	36	92.3	552	22	AAW48483	A GPP-I-kappa kin
45	36	92.3	745	19	AAW49096	Human I-kappa-B k1

## ALIGNMENTS

RESULT 1	ABB08730	standard; peptide: 6 AA.
ID	ABB08730:	
AC	ABB08730:	
XX	14-JUN-2002 (first entry)	
DE	Mutated IKKbeta NEMO binding domain peptide SEQ ID NO 8.	
XX	IKKbeta; IKKalpha; NEMO; NEMO binding domain; NBD; NF-kappaB; NF-kB;	
KW	kinase activation; leukocyte; inflammation; E-selectin; osteoclast;	
KW	autoimmune disease; transplant rejection; osteoporosis; cancer;	
KW	Alzheimer's disease; viral; infection; asthma; anaplasia; peptidosis;	
KW	rheumatoid arthritis; Crohn's disease; multiple sclerosis; HIV;	
KW	corticosteroid; immunosuppression; anti-inflammatory; immunosuppressive;	
KW	osteopathic; cytostatic; nocotropic; neuroprotective; anti-HIV; human;	
KW	antiarteriosclerotic; virucide; antiaslomatic; antiallergic;	
KW	dermatological; antibacterial; antiparasitic; antipneumatic;	
KW	antiarthritic; osteopathic; antitumor; mutant; mutain.	
XX		
OS	Homo sapiens.	
OS	Synthetic.	
FH	Key	Location/Qualifiers
FT	Misc-difference 2	/note- "Wildtype Asp substituted by Glu"
XX		
PN	MO200183547-A2.	
XX		
PD	08-NOV-2001.	
XX		
PF	02-MAY-2001; 2001MO-US40654.	

XX 02-MAY-2000; 2000US-201261P.  
 PR 22-AUG-2000; 2000US-0643260.  
 XX (UYVA ) UNIV YALE.  
 PA May MJ, Ghosh S;  
 PI WPI: 2002-179350/23.  
 DR  
 XX  
 PT Modulating NF-kappaB induction in a cell, useful for treating e.g.  
 PT inflammatory disorders, osteoporosis and cancer, comprising contacting a  
 PT cell with an anti-inflammatory compound comprising at least one NEMO  
 PT binding domain -  
 PS  
 XX  
 PS Claim 23; Page 44; 82pp; English.  
 CC The invention relates to modulating NF-kappaB (NF-kB) induction in a cell  
 CC comprising contacting a cell with an anti-inflammatory compound  
 CC (ABB08725-ABB08742) comprising at least one NEMO binding domain  
 CC (ABB77313). The compound has acts through selective inhibition of  
 CC cytokine-mediated NF-kB activation by blocking the interaction of NEMO,  
 CC with IKKbeta at the NEMO binding domain. Blockage of IKKbeta-NEMO  
 CC interaction results in inhibition of IKKbeta kinase activation and  
 CC subsequent decreased phosphorylation of Ikbppa. The compound may also  
 CC act (directly or indirectly) by blocking the recruitment of leukocytes  
 CC into sites of acute and chronic inflammation, by down-regulating the  
 CC expression of E-selectin on leukocytes or by blocking osteoclast  
 CC differentiation. The compound is useful in treating NF-kB mediated  
 CC conditions, where the condition is an inflammatory disorder, an  
 CC autoimmune disease, transplant rejection, osteoporosis, cancer,  
 CC Alzheimer's disease, atherosclerosis, a viral infection or ataxia  
 CC telangiectasia. The inflammatory disorder is asthma, allergies,  
 CC urticaria, anaphylaxis, cutaneous inflammation, sepsis, psoriasis,  
 CC rheumatoid arthritis, osteoarthritis, psoriatic arthritis, inflammatory  
 CC bowel disease, chronic obstructive pulmonary disease, vasculitis and  
 CC psoriasis. The inflammatory disorder may also be dermatitis, eczema,  
 CC bursitis, osteoarthritis, psoriatic arthritis, lupus and  
 CC spondylarthritis. Also for Crohn's disease, ulcerative colitis,  
 CC polyomyalgia, scleroderma, Wegner's granulomatosis, temporal arteritis,  
 CC cryoglobulinemia or multiple sclerosis. For chronic viral infections  
 CC caused by Epstein-Barr, cytomegalovirus or herpes simplex. Other viral  
 CC diseases include HIV and influenza. The compound may also be useful for  
 CC treating anaphylaxis, drug and food sensitivity, contact dermatitis,  
 CC sunburn or aging. The compound may be used to replace corticosteroids in  
 CC any application in which corticosteroids are used, including  
 CC immunosuppression in transplants and cancer therapy. Also for identifying  
 CC anti-inflammatory compounds and for diagnosis of an inflammatory disorder.  
 CC The compound may be administered alone or in combination with other known  
 CC anti-inflammatory agents. The present sequence is that of a mutated NEMO  
 CC binding domain of IKKbeta.  
 XX  
 SQ Sequence 6 AA;  
 QY 1 LEWSML 6  
 DB 1 LEWSML 6  
 100.0%; Score 39; DB 23; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

KW Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; neurotropic;  
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; vitruide;  
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;  
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;  
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;  
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
 KW autoimmune disorder; multiple sclerosis; transplant rejection;  
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200183554-A2.  
 PD  
 XX  
 PD 08-NOV-2001.  
 XX  
 PF 02-MAY-2001; 2001WO-US14346.  
 XX  
 PR 02-MAY-2000; 2000US-201261P.  
 XX 22-AUG-2000; 2000US-0643260.  
 XX (PRAE-) PRAECIS PHARM INC.  
 XX (UYVA ) UNIV YALE.  
 PA May MJ, Ghosh S, Flindeis MA, Phillips K;  
 PI WPI: 2002-121889/16.  
 DR  
 XX  
 PT Novel antiinflammatory compound comprising membrane translocation  
 PT domain fused to NEMO binding sequence, useful for blocking nuclear  
 PT factor kappaB activation, and for treating asthma, lung inflammation,  
 PT psoriasis -  
 PS  
 XX Example 6; Page 47; 88pp; English.  
 CC The invention relates to an antiinflammatory compound (especially  
 CC AAM48628-AAM48645), comprising a membrane translocation domain  
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15  
 CC amino acid residues, fused to a NEMO binding sequence  
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,  
 CC cytostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,  
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,  
 CC neurotropic, antiatherosclerotic, vitruide and antiallergic activity. The  
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB  
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at  
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase  
 CC activation and subsequent decreased phosphorylation of IkappaB. The  
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,  
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,  
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,  
 CC bursitis; autoimmune diseases such as lupus, polyomyalgia, scleroderma,  
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;  
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia  
 CC telangiectasia. The compounds are also useful for treating  
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,  
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and  
 CC arthritis.  
 XX  
 SQ Sequence 6 AA;  
 QY 1 LEWSML 6  
 DB 1 LEWSML 6  
 100.0%; Score 39; DB 23; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 2  
 AAM48513  
 ID AAM48513 standard; Peptide: 6 AA.  
 XX  
 AC AAM48513;  
 XX  
 DT 20-MAR-2002 (first entry)  
 XX  
 DE NBD mutant peptide SEQ ID NO 8.  
 XX

RESULT 3  
 ABB77305  
 ID ABB77305 standard; protein: 756 AA.  
 XX

AC ABB77305;  
 XX 14-JUN-2002 (first entry)  
 DT  
 XX  
 DE Human IKKbeta mutant D738E.  
 XX  
 XX IKKbeat; IKKalpha; NEMO; NEMO binding domain; NBD; NF-kappaB; NF-kB;  
 KW kinase activation; leukocyte; inflammation; E-selectin; osteoclast;  
 KW autoimmune disease; transplant rejection; osteoporosis; cancer;  
 KW Alzheimer's disease; viral; infection; asthma; anaphylaxis; psoriasis;  
 KW rheumatoid arthritis; Crohn's disease; multiple sclerosis; HIV;  
 KW corticosteroid; immunosuppression; antiinflammatory; immunosuppressive;  
 KW osteopathic; cytosolic; neutrotic; neuroprotective; anti-HIV; human;  
 KW antiarteriosclerotic; virucide; antiasthmatic; antiallergic;  
 KW dermatological; antibacterial; antipsoriatic; antirheumatic;  
 KW antiarthritic; osteopathic; antitumor; mutant; mutein.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 XX Key Location/Qualifiers  
 FH Misc-difference 738 /note- "Wildtype Asp substituted by Glu"  
 FT  
 FT  
 XX W0200183547-A2.  
 XX  
 XX 08-NOV-2001.  
 XX  
 XX 02-MAY-2001; 2001WO-US40654.  
 XX  
 XX 02-MAY-2000; 2000US-201261P.  
 XX 22-AUG-2000; 2000US-0643260.  
 XX  
 XX (UYIA ) UNIV YALE.  
 XX  
 XX May MJ, Ghosh S;  
 XX  
 XX WPI; 2002-179350/23.  
 XX  
 XX Modulating NF-kappaB induction in a cell, useful for treating e.g.  
 PT inflammatory disorders, osteoporosis and cancer, comprises contacting a  
 PT cell with an anti-inflammatory compound comprising at least one NEMO  
 PT binding domain -  
 PT  
 XX  
 XX Example 11; Page -: 82pp; English.  
 XX  
 XX The invention relates to modulating NF-kappaB (NF-kB) induction in a cell  
 CC comprising contacting a cell with an anti-inflammatory compound  
 CC (ABB08725-ABB08742) comprising at least one NEMO binding domain  
 CC (ABB77313). The compound has acts through selective inhibition of  
 CC cytokine-mediated NF-kB activation by blocking the interaction of NEMO  
 CC with IKKbeta at the NEMO binding domain. Blockage of IKKbeta-NEMO  
 CC interaction results in inhibition of IKKbeta kinase activation and  
 CC subsequent decreased phosphorylation of Ikbapb. The compound may also  
 CC act (directly or indirectly) by blocking the recruitment of leukocytes  
 CC into sites of acute and chronic inflammation, by down-regulating the  
 CC expression of E-selectin on leukocytes or by blocking osteoclast  
 CC differentiation. The compound is useful in treating NF-kB mediated  
 CC conditions, where the condition is an inflammatory disorder, an  
 CC autoimmune disease, transplant rejection, osteoporosis, cancer,  
 CC Alzheimer's disease, atherosclerosis, a viral infection or ataxia  
 CC telangiectasia. The inflammatory disorder is asthma, allergies,  
 CC urticaria, anaphylaxis, cutaneous inflammation, sepsis, psoriasis,  
 CC rheumatoid arthritis, osteoarthritis, psoriatic arthritis, inflammatory  
 CC bowel disease, chronic obstructive pulmonary disease, vasculitis and  
 CC bursitis. The inflammatory disorder may also be dermatitis, eczema,  
 CC psoriasis, osteoarthritis, psoriatic arthritis, lupus and  
 CC spondylarthritis. Also for Crohn's disease, ulcerative colitis,  
 CC polyarthritis, scleroderma, Wegner's granulomatosis, temporal arteritis,  
 CC cryoglobulinemia or multiple sclerosis. For chronic viral infections  
 CC caused by Epstein-Barr, cytomegalovirus or herpes simplex. Other viral  
 CC diseases include HIV and influenza. The compound may also be useful for  
 CC treating anaphylaxis, drug and food sensitivity, contact dermatitis,

CC sunburn or aging. The compound may be used to replace corticosteroids in  
 CC any application in which corticosteroids are used, including  
 CC immunosuppression in transplant and cancer therapy. Also for identifying  
 CC antiinflammatory compounds and for diagnosis of an inflammatory disorder.  
 CC The compound may be administered alone or in combination with other known  
 CC anti-inflammatory agents. The present sequence is that of an IKKbeta  
 CC mutant, useful in examples of the invention.  
 CC Note: The present sequence is not given in the specification but is  
 CC derived from Genbank Accession No. 014920 (ABB77294).  
 CC  
 XX  
 SO Sequence 756 AA;  
 QY 1 LEWSWL 6  
 DB 737 LEWSWL 742  
 Query Match 100.0%; Score 39; DB 23; Length 756;  
 Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 RESULT 4  
 ABB08725  
 ID ABB08725 standard; peptide: 6 AA.  
 AC  
 XX ABB08725;  
 XX  
 XX 14-JUN-2002 (first entry)  
 DE  
 DE IKKbeta NEMO binding domain peptide SEQ ID NO 2.  
 XX  
 XX IKKbeat; IKKalpha; NEMO; NEMO binding domain; NBD; NF-kappaB; NF-kB;  
 KW kinase activation; leukocyte; inflammation; E-selectin; osteoclast;  
 KW autoimmune disease; transplant rejection; osteoporosis; cancer;  
 KW Alzheimer's disease; viral; infection; asthma; anaphylaxis; psoriasis;  
 KW rheumatoid arthritis; Crohn's disease; multiple sclerosis; HIV;  
 KW corticosteroid; immunosuppression; antiinflammatory; immunosuppressive;  
 KW osteopathic; cytosolic; neutrotic; neuroprotective; anti-HIV; human;  
 KW antiarteriosclerotic; virucide; antiasthmatic; antiallergic;  
 KW dermatological; antibacterial; antipsoriatic; antirheumatic;  
 KW antiarthritic; osteopathic; antitumor.  
 XX  
 OS Homo sapiens.  
 OS  
 XX W0200183547-A2.  
 XX  
 XX 08-NOV-2001.  
 XX  
 XX 02-MAY-2001; 2001WO-US40654.  
 XX  
 XX 02-MAY-2000; 2000US-201261P.  
 XX 22-AUG-2000; 2000US-0643260.  
 XX  
 XX (UYIA ) UNIV YALE.  
 XX  
 XX May MJ, Ghosh S;  
 XX  
 XX WPI; 2002-179350/23.  
 XX  
 XX Modulating NF-kappaB induction in a cell, useful for treating e.g.  
 PT inflammatory disorders, osteoporosis and cancer, comprises contacting a  
 PT cell with an anti-inflammatory compound comprising at least one NEMO  
 PT binding domain -  
 PT  
 XX  
 XX Claim 23; Page 44; 82pp; English.  
 XX  
 XX The invention relates to modulating NF-kappaB (NF-kB) induction in a cell  
 CC comprising contacting a cell with an anti-inflammatory compound  
 CC (ABB08725-ABB08742) comprising at least one NEMO binding domain  
 CC (ABB77313). The compound has acts through selective inhibition of  
 CC cytokine-mediated NF-kB activation by blocking the interaction of NEMO  
 CC with IKKbeta at the NEMO binding domain. Blockage of IKKbeta-NEMO  
 CC interaction results in inhibition of IKKbeta kinase activation and

CC subsequent decreased phosphorylation of IkappaB. The compound may also  
CC act (directly or indirectly) by blocking the recruitment of leukocytes  
CC into sites of acute and chronic inflammation, by down-regulating the  
CC expression of E-selectin on leukocytes or by blocking osteoclast  
CC differentiation. The compound is useful in treating NF-kB mediated  
CC conditions, where the condition is an inflammatory disorder, an  
CC autoimmune disease, transplant rejection, osteoporosis, cancer,  
CC Alzheimer's disease, atherosclerosis, a viral infection or ataxia  
CC telangiectasia. The inflammatory disorder is asthma, allergies,  
CC urticaria, anaphylaxis, cutaneous inflammation, sepsis, psoriasis,  
CC rheumatoid arthritis, osteoarthritis, psoriatic arthritis, inflammatory  
CC bowel disease, chronic obstructive pulmonary disease, vasculitis and  
CC bursts. The inflammatory disorder may also be dermatitis, eczema,  
CC psoriasis, osteoarthritis, psoriatic arthritis, lupus and  
CC spondylarthritis. Also for Crohn's disease, ulcerative colitis,  
CC polymyalgia, scleroderma, Wegner's granulomatosis, temporal arteritis,  
CC cryoglobulinemia or multiple sclerosis. For chronic viral infections  
CC caused by Epstein-Barr, cytomegalovirus or herpes simplex. Other viral  
CC diseases include HIV and influenza. The compound may also be useful for  
CC treating anaphylaxis, drug and food sensitivity, contact dermatitis,  
CC sunburn or aging. The compound may be used to replace corticosteroids in  
CC any application in which corticosteroids are used, including  
CC immunosuppression in transplants and cancer therapy. Also for identifying  
CC antiinflammatory compounds and for diagnosis of an inflammatory disorder.  
CC The compound may be administered alone or in combination with other known  
CC anti-inflammatory agents. The present sequence is that of the NEMO  
CC binding domain of IkappaB.

**SQ Sequence 6 AA;**

Query Match	92.3%	Score 36;	DB 23;	Length 6;
Best Local Similarity	83.3%	Pred. No. 7.8e+05;		
Matches	5;	Conservative	1;	Mismatches 0;
				Indels 0;
				Gaps 0;

QY	1	LEWSWL	6
		1:1111	
Db	1	LDWSWL	6

RESULT 5  
AAM48530  
ID AAM48530 standard; Peptide; 6 AA.

AC AAM48530;

DT 20-MAR-2002 (first entry)

DE Anti-Inflammatory peptide SEQ ID NO 33.

KM Antihistaminatory; antihistaminic; cytosolatic; antipariatic; nootropic;  
KM Antipneumatic; antipneumatic; osteopathic; antibacterial; virucide;  
KM Immunopressiveive; dermatological; neuroprotective; antithrombotic;  
KM Antiallergic; membrane translocation domain; NEMO binding domain; eczema  
KM cytokine; NKkappaB; IkappaB kinase beta; IkappaB; cancer; psoriasis;  
KM Rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
KM Autoimmune disorder; multiple sclerosis; transplant rejection;  
KM Osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
KM Ataxia telangiectasia; allergy; anaphylaxis; arthritis.

OS Synthetic.

PN W0200183554-A2.

PD 08-NOV-2001.

PF 02-MAY-2001; 2001WO-US14346.

PR 02-MAY-2000; 2000US-201261P.

XX

PA (UYYA ) UNIV YALE.

XX.

XX

PI May MJ, Ghosh S, Flindels MA, Phillips K;

DR WPI: 2002-121889/16.

PT Novel antiinflammatory compound comprising membrane translocation  
PT domain fused to NEMO binding sequence, useful for blocking nuclear  
PT factor kappaB activation, and for treating asthma, lung inflammation,  
PT psoriasis -

PS Claim 6; Page 61; 88pp; English.

CC The invention relates to an antiinflammatory compound (especially  
CC AAM48628-AAM48645), comprising a membrane translocation domain  
CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15  
CC amino acid residues, fused to a MEMO binding sequence

Sequence 6 AA, SQ

Query Match	92.3%	Score 36;	DB 23;	Length 6;
Best Local Similarity	83.3%	Pred. No. 7.8e+05;		
Matches	5;	Conservative	0;	Indels 0;
		Mismatches	0;	Gaps 0;

QY	1 LEWSWL 6
	1:1111
Db	1 LDWSWL 6

RESULT 6  
AAM48655  
ID AAM48655 standard; Peptide; 6 AA

AC AAM48655;

DT 20-MAR-2002 (first entry)

NBD mutant peptide SEQ ID NO 2.

KM Antihlammatory; antiaethmatic; cytostatic; antiporiatic; nootropic;  
KM antineumatic; antiarthritis; osteopathic; antibacterial; virucide;  
KM immunosuppressive; dermatological; neuroprotective; antithrombotic;  
KM anti allergic; membrane translocation domain; NEMO binding domain; eczema  
KM cytokine; NKkappaB; IkappaN kinase beta; IKKbeta; cancer; psoriasis;  
KM rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
KM autoimmune disorder; multiple sclerosis; transplant rejection;  
KM osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
KM ataxia telangiectasia; allergy; anaphylaxis; arthritis.

OS Synthetic

PN W0200183554-A2

PD 08-NOV-2001.

PF 02-MAY-2001; 2001WO-US14346

XX

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PR 02-MAY-2000; 20000US-201261P.
PR 22-AUG-2000; 20000US-0643260.
XX
XX (PRAE-) PRAECIS PHARM INC.
XX (OXYA ) UNIV YALE.
XX
XX May MJ, Ghosh S, Findels MA, Phillips K;
XX
XX WPI: 2002-121889/16.
XX
XX Example 6: Page 47; 88pp; English.
XX
XX The invention relates to an antiinflammatory compound (especially
CC AAM48628-AAM48645), comprising a membrane translocation domain
CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15
CC amino acid residues, fused to a NEMO binding sequence
CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,
CC cytoprotective, immunosuppressive, dermatological, antirheumatic,
CC antibacterial, antipsoietic, antirheumatic, antirheumatic, osteopathic,
CC nootropic, antiatherosclerotic, virucide and anti-allergic activity. The
CC compounds act as selective inhibitors of cytokine-mediated NFkappaB
CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
CC the NEMO binding domain that results in inhibition of IKKbeta kinase
CC activation and subsequent decreased phosphorylation of IkappaB. The
CC compounds are useful for treating inflammatory disorders, e.g. asthma,
CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,
CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
CC bursts; autoimmune diseases such as lupus, polyarthritis, scleroderma,
CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia
CC telangiectasia. The compounds are also useful for treating
CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and
CC arthritis.
CC
XX
XX Sequence 6 AA:
XX
XX Query Match 92.3%; Score 36; DB 23; Length 6;
XX Best Local Similarity 83.3%; Pred. No. 7.8e+05;
XX Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 LEWSML 6
XX 1:|||||
XX 1 LDMSML 6
XX
XX RESULT 7
XX AAM48534
XX ID AAM48534 standard; Peptide; 7 AA.
XX
XX AAM48534:
XX
XX 20-MAR-2002 (first entry)
XX
XX Anti-inflammatory peptide SEQ ID NO 37.
XX
XX Antiinflammatory; antiasthmatic; cytoprotective; antipsoietic; nootropic;
XX antirheumatic; antirheumatic; osteopathic; antibacterial; virucide;
XX immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
XX antiallergic; membrane translocation domain; NEMO binding domain; eczema;
XX cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;
XX rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
XX autoimmune disorder; multiple sclerosis; transplant rejection;
XX osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
XX ataxia telangiectasia; allergy; anaphylaxis; arthritis.
XX
XX Synthetic.
XX

```

KW	autoimmune disorder; multiple sclerosis; transplant rejection;
KW	osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
KW	ataxia telangiectasia; allergy; anaphylaxis; arthritis.
OS	Synthetic.
PN	WO200183554-A2.
PD	08-NOV-2001.
PF	02-MAY-2001; 2001WO-US14346.
XX	
XX	02-MAY-2000; 2000US-201261P.
PR	22-AUG-2000; 2000US-0643260.
XX	
PA	(PRAE-) PRAECIS PHARM INC.
PA	(UYVA ) UNIV YALE.
XX	
PI	May MJ, Ghosh S, Findels MA, Phillips K;
XX	
XX	WPI: 2002-121889/16.
PT	Novel antiinflammatory compound comprising membrane translocation
PT	domain fused to NEMO binding sequence, useful for blocking nuclear
PT	factor kappaB activation, and for treating asthma, lung inflammation,
PT	psoriasis
PS	
XX	Claim 6: Page 61; 88pp; English.
XX	
CC	The invention relates to an antiinflammatory compound (especially
CC	AA48628-AA48645), comprising a membrane translocation domain
CC	(AA48620-AA48627, or AA48646-AA48651) which comprises from 6-15
CC	amino acid residues, fused to a NEMO binding sequence
CC	(AA48525-AA48619). The antiinflammatory compounds have antiasthmatic,
CC	cytostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,
CC	antibacterial, immunosuppressive, dermatological, neuroprotective,
CC	neurotropic, antiatherosclerotic, virucide and antiallergic activity. The
CC	compounds act as selective inhibitors of cytokine-mediated NFkappa B
CC	activation by blocking interaction of Ikbppa kinase beta (IKKbeta) at
CC	the NEMO binding domain that results in inhibition of IKKbeta kinase
CC	activation and subsequent decreased phosphorylation of Ikbppa. The
CC	compounds are useful for treating inflammatory disorders, e.g. asthma,
CC	lung inflammation or cancer, psoriasis, rheumatoid arthritis,
CC	osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
CC	buritis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
CC	granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
CC	Alzheimer's disease; atherosclerosis; viral infections; and ataxia
CC	telangiectasia. The compounds are also useful for treating
CC	pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
CC	drug or food sensitivity, eczema, dermatitis, sunburn, aging and
CC	arthritis.
XX	
SO	Sequence 8 AA:
XX	
Query Match	92.3%; Score 36; DB 23; Length 8;
Best Local Similarity	83.3%; Pred. No. 7.8e+05;
Matches 5; Conservative	1; Mismatches 0; Indels 0; Gaps 0;
OY	1 LEWSWL 6
DB	3 LDMSWL 8
XX	
RESULT 9	
ID	AA48535
XX	AA48535 standard; Peptide; 8 AA.
XX	
XX	AA48535;
XX	
DT	20-MAR-2002 (first entry)
XX	
DE	Anti-inflammatory peptide SEQ ID NO 38.
XX	

XX	Anti-inflammatory; antiarthritic; osteopathic; antipsoriatic; neurotropic; CC
KM	antirheumatic; antiarthritic; osteopathic; antipsoriatic; neurotropic; CC
KM	immunosuppressive; dermatological; neuroprotective; antiatherosclerotic; CC
KM	antiallergic; membrane translocation domain; NEMO binding domain; eczema; CC
KM	cytokine; Nkappa; Ikappa kinase beta; IKKbeta; cancer; psoriasis; CC
KW	rheumatoid arthritis; osteoarthritis; inflammatory bowel disease; CC
KM	autoimmune disorder; multiple sclerosis; transplant rejection; CC
KM	osteoporosis; Alzheimer's disease; atherosclerosis; viral infection; CC
KM	ataxia telangiectasia; allergy; anaphylaxis; arthritis. CC
XX	
OS	Synthetic. CC
XX	
PN	WO200183554-A2. CC
PD	
PD	08-NOV-2001. CC
XX	
PF	02-MAY-2001: 2001WO-US14346. CC
XX	
PR	02-MAY-2000: 2000US-201261P. CC
PR	22-AUG-2000: 2000US-0643260. CC
XX	
XX	(PRAE-) PRAECIS PHARM INC. CC
PA	(UYVA ) UNIT VALE. CC
XX	
PI	May MJ, Ghosh S, Findels MA, Phillips K; CC
XX	WPI: 2002-121889/16. CC
XX	
PT	Novel antiinflammatory compound comprising membrane translocation CC
PT	domain fused to NEMO binding sequence, useful for blocking nuclear CC
PT	factor kappaB activation, and for treating asthma, lung inflammation, CC
XX	psoriasis - CC
PS	Claim 6: Page 61; 88pp; English. CC
XX	
CC	The invention relates to an antiinflammatory compound (especially CC
CC	AA48625-AA48645), comprising a membrane translocation domain CC
CC	(AA48650-AA48662, or AA48646-AA48651) which comprises from 6-15 CC
CC	amino acid residues, fused to a NEMO binding sequence CC
CC	(AA48655-AA48661). The antiinflammatory compounds have antiasthmatic, CC
CC	cytostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic, CC
CC	antibacterial, immunosuppressive, dermatological, neuroprotective, CC
CC	neotropic, antiatherosclerotic, virucide and antiallergic activity. The CC
CC	compounds act as selective inhibitors of cytokine-mediated NkappaB CC
CC	activation by blocking interaction of Ikappa kinase beta (IKKbeta) at CC
CC	the NEMO binding domain that results in inhibition of Ikappa kinase CC
CC	activation and subsequent decreased phosphorylation of IkappaB. The CC
CC	compounds are useful for treating inflammatory disorders, e.g. asthma, CC
CC	lung inflammation or cancer, psoriasis, rheumatoid arthritis, CC
CC	osteoarthritis, inflammatory bowel disease, sepsis, vasculitis, CC
CC	buritis; autoimmune diseases such as lupus, polyaralgia, scleroderma, CC
CC	granulomatosis, multiple sclerosis; transplant rejection; osteoporosis, CC
CC	Alzheimer's disease; atherosclerosis; viral infections; and ataxia CC
CC	telangiectasia. The compounds are also useful for treating CC
CC	pro-inflammatory responses such as allergies, urticaria, anaphylaxis, CC
CC	drug or food sensitivity, eczema, dermatitis, sunburn, aging and CC
CC	arthritis. CC
XX	
SQ	Sequence 8 AA: CC
XX	
Query Match	92.3%; Score 36; DB 23; Length 8; CC
Best Local Similarity	83.3%; Pred. No. 7,8e+05; CC
Matches	5; Conservative 1; Mismatches 0; Indels 0; Gaps 0; CC
QY	1 LEWSWL 6 CC
	CC
DB	1 IDMSWL 6 CC
XX	
RESULT 10	
AA486182	
ID	AA486182 standard; peptide; 9 AA. CC
XX	

AAW96182:  
 27-APR-1999 (first entry)  
 IKK-alpha polypeptide with binding activity.  
 I-kappa-B kinase; IKK-alpha; gene expression; modulation; suppression; activation; tumour necrosis factor; TNF; interleukin-1; IL-1; TNF receptor associated factor; TRAF.  
 Homo sapiens.  
 W09901541-A1.  
 14-JAN-1999.  
 01-JUL-1998; 98MO-US13782.  
 10-JUL-1997; 97US-0890854.  
 01-JUL-1997; 97US-0887115.  
 (TULA-) TULARIK INC.  
 Cao Z, Regnier C, Rothe M.  
 WPI; 1999-106044/09.  
 Newly isolated human kinase IkappaB Kinase (IKK- $\alpha$ ) polypeptides - useful in screening for agents that modulate the interaction of an IKK polypeptide to a binding target and for modulating signal transduction involving IkappaB in a cell.  
 Disclosure; Page -: 32pp; English.  
 I-kappa-B kinase activity and I-kappa-B polypeptides (comprising a six residue domain of I-kappa-B containing one of Ser32 and Ser36, and a candidate agent) can be used to screen for agents that modulate the interaction of an IKK polypeptide to a binding target. The modulation of the kinase activity of IKK-alpha forms a method for modulating signal transduction involving I-kappa-B in a cell. The IKK-alpha polypeptides are useful for generating oligonucleotide primers and probes for use in the isolation of natural IKK-alpha-encoding nucleic acids. The nucleic acids are useful as -translatable transcripts, hybridization probes, polymerase chain reaction (PCR) probes and primers. Their diagnostic applications include IKK-alpha hybridization probes for identifying wild-type and mutant IKK-alpha alleles in clinical and laboratory samples. Therapeutic application includes the use of IKK- $\alpha$  nucleic acids for modulating cellular expression or intracellular concentration/availability of active IKK-alpha.  
 Catalytically inactive IKK-alpha mutants suppress NF-kappa-B activation induced by tissue necrosis factor (TNF), interleukin-1 (IL-1) stimulation, TNF receptor-associated factor (TRAF) and NF-kappa-B-inducing kinase (NIK) overexpression. Polypeptides of IKK-alpha showing exemplary binding activity are described in AAW96182. These peptides all comprise one of Cys30, Glu54, Leu604, Thr679, Ser684, Thr686 or Ser687 of the full length IKK-alpha described in AAW96182. Deletion mutants of the invention comprise at least one of these regions.  
 N.B. The present sequence is not given in the present specification but is derived from the sequence given in AAW96182 as specified.  
 Sequence 9 AA:  
 Query Match 92.3%; Score 36; DB 20; Length 9;  
 Best Local Similarity 83.3%; Pred. No. 7.8e+05;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RESULT 11  
 AAW48526  
 ID AAW48526 standard; Peptide; 9 AA.  
 AC AAW48526;  
 DT 20-MAR-2002 (first entry)  
 XX  
 DE Anti-inflammatory peptide SEQ ID NO 29.  
 XX  
 XX Antinflammatory; antialastmatic; cyostatic; antipsoriatic; nootropic; antirheumatic; antiarthritic; osteopathic; antibacterial; virucide; immunosuppressive; dermatological; neuroprotective; antiatherosclerotic; antiallergic; membrane translocation domain; NEMO binding domain; eczema; cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis; rheumatoid arthritis; osteoarthritis; inflammatory bowel disease; autoimmune disorder; multiple sclerosis; transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis; viral infection; ataxia telangiectasia; allergy; anaphylaxis; arthritis.  
 XX Synthetic.  
 XX  
 XX W0200183554-A2.  
 XX  
 XX PD 08-NOV-2001.  
 XX  
 XX PE 02-MAY-2001; 2001WO-US14346.  
 XX  
 XX PR 02-MAY-2000; 2000US-201261P.  
 XX PR 22-AUG-2000; 2000US-0643260.  
 XX  
 XX (PRAE-) PRAECIS PHARM INC.  
 XX (UYA-) UNIV YALE.  
 XX  
 XX PI May M, Ghosh S, Findeis M, Phillips K.  
 XX WPI; 2002-121889/16.  
 XX  
 XX PT Novel antinflammatory compound comprising membrane translocation factor kappaB activation, and for treating asthma, lung inflammation, psoriasis -  
 XX  
 XX PS Claim 6; Page 61; 88pp; English.  
 XX  
 XX The invention relates to an antinflammatory compound (especially AAW48628-AAW48645), comprising a membrane translocation domain (AAW48620-AAW48627 or AAW48646-AAW48651) which comprises from 6-15 amino acid residues, fused to a NEMO binding sequence (AAW48525-AAW48619). The antinflammatory compounds have antialastmatic, cyostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic, antibacterial, immunosuppressive, dermatological, neuroprotective, nootropic, antiatherosclerotic, virucide and antiallergic activity. The compounds act as selective inhibitors of cytokine-mediated NFkappaB activation by blocking interaction of IkappaB kinase beta (IKKbeta) at the NEMO binding domain that results in inhibition of IKKbeta kinase activation and subsequent decreased phosphorylation of IkappaB. The compounds are useful for treating inflammatory disorders, e.g. asthma, lung inflammation or cancer, psoriasis, rheumatoid arthritis, osteoarthritis, inflammatory bowel disease, sepsis, vasculitis, bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma, granulomatosis, multiple sclerosis; transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis; viral infections; and ataxia telangiectasia. The compounds are also useful for treating pro-inflammatory responses such as allergies, urticaria, anaphylaxis, drug or food sensitivity, eczema, dermatitis, sunburn, aging and arthritis.  
 XX  
 XX Sequence 9 AA:  
 Query Match 92.3%; Score 36; DB 23; Length 9;  
 Best Local Similarity 83.3%; Pred. No. 7.8e+05;

Matches 5: Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LEWSWL 6  
1:1111  
Db 1 LDMSWL 6

## RESULT 12

AAM48529  
ID AAM48529 standard; Peptide: 9 AA.

AC AAM48529;

DT 20-MAR-2002 (first entry)

DE Anti-inflammatory peptide SEQ ID NO 32.

XX Antiinflammatory; antiasthmatic; cyostatic; antipsoriatic; nootropic;  
XX antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;  
XX immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;  
XX antiallergic; membrane translocation domain; NEMO binding domain; eczema;  
XX cytokine; NFkappaB; Ikappab kinase beta; IKKbeta; cancer; psoriasis;  
XX rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
XX autoimmune disorder; multiple sclerosis; transplant rejection;  
XX osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
XX ataxia telangiectasia; allergy; anaphylaxis; arthritis.

OS Synthetic.

PN WO200183554-A2.

PD 08-NOV-2001.

PF 02-MAY-2001; 2001WO-US14346.

PR 02-MAY-2000; 2000US-201261P.

PR 22-AUG-2000; 2000US-0643260.

XX (PRAE-) PRAECTS PHARM INC.

PA (UYVA ) UNITV YALE.

PI May MJ, Ghosh S, Fandels MA, Phillips K;

DR WPI: 2002-121889/16.

XX Novel antiinflammatory compound comprising membrane translocation  
PT domain fused to NEMO binding sequence, useful for blocking nuclear  
PT factor kappaB activation, and for treating asthma, lung inflammation,  
PT psoriasis

PS Claim 6; Page 61; 88pp; English.

XX The invention relates to an antiinflammatory compound (especially  
CC AAM48628-AAM48645), comprising a membrane translocation domain  
CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15  
CC amino acid residues, fused to a NEMO binding sequence  
CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,  
CC cyostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,  
CC antibacterial, immunosuppressive, dermatological, neuroprotective,  
CC nootropic, antiatherosclerotic, virucide and antiallergic activity. The  
CC compounds act as selective inhibitors of cytokine-mediated NFkappaB  
CC activation by blocking interaction of Ikappab kinase beta (IKKbeta) at  
CC the NEMO binding domain that results in inhibition of IKKbeta kinase  
CC activation and subsequent decreased phosphorylation of Ikappab. The  
CC compounds are useful for treating inflammatory disorders, e.g. asthma,  
CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,  
CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,  
CC bursitis, autoimmune diseases such as lupus, polyarthritis, scleroderma,  
CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;  
CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia  
CC telangiectasia. The compounds are also useful for treating  
CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,  
CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and

CC arthritis.  
XX Sequence 9 AA;

Query Match 92.3%; Score 36; DB 23; Length 9;  
Best Local Similarity 83.3%; Pred. No. 7.8e+05;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LEWSWL 6  
1:1111  
Db 1 LDMSWL 6

## RESULT 13

AAM48532  
ID AAM48532 standard; Peptide: 9 AA.

AC AAM48532;

DT 20-MAR-2002 (first entry)

DE Anti-inflammatory peptide SEQ ID NO 35.

XX Antiinflammatory; antiasthmatic; cyostatic; antipsoriatic; nootropic;  
XX antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;  
XX immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;  
XX antiallergic; membrane translocation domain; NEMO binding domain; eczema;  
XX cytokine; NFkappaB; Ikappab kinase beta; IKKbeta; cancer; psoriasis;  
XX rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
XX autoimmune disorder; multiple sclerosis; transplant rejection;  
XX osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
XX ataxia telangiectasia; allergy; anaphylaxis; arthritis.

OS Synthetic.

PN WO200183554-A2.

PD 08-NOV-2001.

PF 02-MAY-2001; 2001WO-US14346.

PR 02-MAY-2000; 2000US-201261P.

PR 22-AUG-2000; 2000US-0643260.

XX (PRAE-) PRAECTS PHARM INC.

PA (UYVA ) UNITV YALE.

PI May MJ, Ghosh S, Fandels MA, Phillips K;

DR WPI: 2002-121889/16.

XX Novel antiinflammatory compound comprising membrane translocation  
PT domain fused to NEMO binding sequence, useful for blocking nuclear  
PT factor kappaB activation, and for treating asthma, lung inflammation,  
PT psoriasis

PS Claim 6; Page 61; 88pp; English.

XX The invention relates to an antiinflammatory compound (especially  
CC AAM48628-AAM48645), comprising a membrane translocation domain  
CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15  
CC amino acid residues, fused to a NEMO binding sequence  
CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,  
CC cyostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,  
CC antibacterial, immunosuppressive, dermatological, neuroprotective,  
CC nootropic, antiatherosclerotic, virucide and antiallergic activity. The  
CC compounds act as selective inhibitors of cytokine-mediated NFkappaB  
CC activation by blocking interaction of Ikappab kinase beta (IKKbeta) at  
CC the NEMO binding domain that results in inhibition of IKKbeta kinase  
CC activation and subsequent decreased phosphorylation of Ikappab. The  
CC compounds are useful for treating inflammatory disorders, e.g. asthma,  
CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,  
CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,

CC bursts; autoimmune diseases such as lupus, polymyalgia, scleroderma,  
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;  
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia  
 CC telangiectasia. The compounds are also useful for treating  
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,  
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and  
 CC arthritis.  
 CC  
 SQ Sequence 9 AA;  
 Query Match 92.3%; Score 36; DB 23; Length 9;  
 Best Local Similarity 83.3%; Pred. No. 7.8e+05;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 LEWSWL 6  
 Db 3 LDMSWL 8  
 RESULT 14  
 ID AAM48533 standard; Peptide; 9 AA.  
 AC AAM48533;  
 DT 20-MAR-2002 (first entry)  
 DE Anti-inflammatory peptide SEQ ID NO 36.  
 XX  
 DE Anti-inflammatory; antiasthmatic; cytosolic; antipsoriatic; nootropic;  
 KW antiinflammatory; antiarthritic; osteopathic; antibacterial; vituclide;  
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;  
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;  
 KW cytokine; NF-kappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;  
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
 KW autoimmune disorder; multiple sclerosis; transplant rejection;  
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.  
 KW  
 OS Synthetic.  
 XX  
 PN WO200183554-A2.  
 XX  
 PD 08-NOV-2001.  
 XX  
 PF 02-MAY-2001; 2001WO-US14346.  
 XX  
 PR 02-MAY-2000; 2000US-201261P.  
 PR 22-AUG-2000; 2000US-0643260.  
 XX  
 PA (PRAE-) PRAECIS PHARM INC.  
 PA (UYVA) UNIV YALE.  
 PI May MJ, Ghosh S, Fandels MA, Phillips K;  
 DR WPI: 2002-121889/16.  
 XX  
 PT Novel antiinflammatory compound comprising membrane translocation  
 PT domain fused to NEMO binding sequence, useful for blocking nuclear  
 PT factor kappaB activation, and for treating asthma, lung inflammation,  
 PT psoriasis  
 PT  
 PS Claim 6; Page 61; 88pp; English.  
 XX  
 CC The invention relates to an antiinflammatory compound (especially  
 CC AAM48628-AAM48645), comprising a membrane translocation domain  
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15  
 CC amino acid residues, fused to a NEMO binding sequence  
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,  
 CC cytosolic, antipsoriatic, antiinflammatory, antiarthritic, osteopathic,  
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,  
 CC nootropic, antiatherosclerotic, vituclide and antiallergic activity. The  
 CC compounds act as selective inhibitors of cytokine-mediated NF-kappaB

CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at  
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase  
 CC activation and subsequent decreased phosphorylation of IkappaB. The  
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,  
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,  
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,  
 CC bursts; autoimmune diseases such as lupus, polymyalgia, scleroderma,  
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;  
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia  
 CC telangiectasia. The compounds are also useful for treating  
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,  
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and  
 CC arthritis.  
 CC  
 SQ Sequence 9 AA;  
 Query Match 92.3%; Score 36; DB 23; Length 9;  
 Best Local Similarity 83.3%; Pred. No. 7.8e+05;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 LEWSWL 6  
 Db 2 LDMSWL 7  
 RESULT 15  
 ID ABB77313 standard; peptide; 10 AA.  
 AC ABB77313;  
 DT 14-JUN-2002 (first entry)  
 DE IKKbeta NEMO binding domain peptide SEQ ID NO 1.  
 XX  
 DE IKKbeta; IKKalpha; NEMO; NEMO binding domain; NBD; NF-kappaB; NF-kB;  
 KW kinase activation; leukocyte; inflammation; E-selectin; osteoclast;  
 KW autoimmune disease; transplant rejection; osteoporosis; cancer;  
 KW Alzheimer's disease; viral; infection; asthma; anaphylaxis; psoriasis;  
 KW rheumatoid arthritis; Crohn's disease; multiple sclerosis; HIV;  
 KW corticosteroid; immunosuppression; antiinflammatory; immunosuppressive;  
 KW osteopathic; cytosolic; nootropic; neuroprotective; anti-HIV; human;  
 KW antiarteriosclerotic; vituclide; antiasthmatic; antiallergic;  
 KW dermatological; antibacterial; antipsoriatic; antirheumatic;  
 KW antiarthritic; osteopathic; antitumor.  
 KW  
 OS Homo sapiens.  
 XX  
 PN WO200183547-A2.  
 XX  
 PD 08-NOV-2001.  
 XX  
 PF 02-MAY-2001; 2001WO-US40654.  
 XX  
 PR 02-MAY-2000; 2000US-201261P.  
 PR 22-AUG-2000; 2000US-0643260.  
 XX  
 PA (UYVA) UNIV YALE.  
 PI May MJ, Ghosh S;  
 DR WPI: 2002-179350/23.  
 XX  
 PT Modulating NF-kappaB induction in a cell, useful for treating e.g.  
 PT inflammatory disorders, osteoporosis and cancer, comprises contacting a  
 PT cell with an anti-inflammatory compound comprising at least one NEMO  
 PT binding domain  
 PT  
 PS Example 4; Page -; 82pp; English.  
 XX  
 CC The invention relates to modulating NF-kappaB (NF-kB) induction in a cell  
 CC comprises contacting a cell with an anti-inflammatory compound  
 CC (ABB08725-ABB08742) comprising at least one NEMO binding domain



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 30, 2003, 14:32:12 ; Search time 6.5921 Seconds

(Without alignments)  
87.500 Million cell updates/sec

Title: US-09-643-260-8

Perfect score: 39

Sequence: 1 LEKSWL 6

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 segs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : PIR\_73:\*\*

1: p1r1:\*\*

2: p1r2:\*\*

3: p1r3:\*\*

4: p1r4:\*\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	36	92.3	645	2 T11137	NADH2 dehydrogenas
2	36	92.3	745	1 I49101	conserved helix-lo
3	35	89.7	150	2 PNO444	Ig heavy chain V r
4	35	89.7	242	2 T27590	hypothetical prote
5	35	89.7	371	2 S20075	promastigote surfa
6	35	89.7	387	2 AD3426	mannose-6-phosphat
7	35	89.7	391	2 AG2318	hypothetical prote
8	35	89.7	400	2 B64733	protein transport
9	35	89.7	474	1 G2MS11	Ig gamma-2b chain
10	35	89.7	522	2 A84606	hypothetical prote
11	35	89.7	1367	2 H82874	conserved hypochet
12	35	89.7	1379	2 JC4954	vascular endotheli
13	35	89.7	2054	2 T32413	probable acetyl-Co
14	34	87.2	116	2 T03472	conserved hypochet
15	34	87.2	117	2 S03289	Ig heavy chain pre
16	34	87.2	133	2 PC1155	Ig heavy chain pre
17	34	87.2	355	2 F70983	probable serine pr
18	34	87.2	395	2 E90438	hypothetical prote
19	34	87.2	398	2 S76763	hypothetical prote
20	34	87.2	685	1 A48289	neurotrophic recep
21	34	87.2	919	2 T37062	probable transcript
22	34	87.2	1139	2 A10379	probable potassium
23	33	84.6	160	2 E71560	hypothetical prote
24	33	84.6	161	2 C81711	conserved hypochet
25	33	84.6	267	2 G90579	hypothetical prote
26	33	84.6	273	2 A81696	PTS mannosyl-specif
27	33	84.6	273	2 A81324	PTS mannosyl-specif
28	33	84.6	322	2 A13395	NADH2 dehydrogenas
29	33	84.6	358	2 F97654	mcb protein (AF29

30	33	84.6	358	2 AD2878	iron-chelator utli
31	33	84.6	480	2 T24087	hypothetical prote
32	33	84.6	700	2 T24092	hypothetical prote
33	33	84.6	723	2 T32136	hypothetical prote
34	33	84.6	783	2 F88808	protein R09E10.3 l
35	33	84.6	903	2 T20804	hypothetical prote
36	33	84.6	1753	2 T00350	hypothetical prote
37	32	82.1	72	2 AD2464	hypothetical prote
38	32	82.1	83	2 S30986	gene 41 protein -
39	32	82.1	94	2 F72804	gp41 protein - Myc
40	32	82.1	100	2 AG0447	probable phage-rel
41	32	82.1	122	2 S69909	Ig V-D-J region (M
42	32	82.1	132	2 S65785	mel-13a protein -
43	32	82.1	154	2 A72029	conserved hypochet
44	32	82.1	154	2 H85594	C556 hypothetical
45	32	82.1	203	2 T50421	hypothetical prote

## ALIGNMENTS

## RESULT 1

T11137

NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 - acorn worm mitochondrion

C:Species: mitochondrion Balanoglossus carnosus

C>Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 03-Jun-2002

C:Accession: T11137

R:Castresana, J.; Feldmeyer-Fuchs, G.; Yokobori, S.; Satoh, N.; Pardo, S.  
Genetics 150, 1115-1123, 1998

A:Title: The mitochondrial genome of the hemichordate Balanoglossus carnosus and the

A:Reference number: Z1750; MUID:99016090; PMID:9799263

A:Accession: T11137

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-645 <CDS>

A:Cross-references: EMBL:AF051097; NID:93065680; PTD:93065682; PIDN:AD11945.1

C:Genetics:

A:Genome: mitochondrion

C:Superfamily: NADH dehydrogenase (ubiquinone) chain 5

C:Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation

Query Match 92.3% Score 36; DB 2; Length 645;

Best Local Similarity 83.3% Pred. No. 2e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

DB 96 LEWTL 101

RESULT 2

149101

conserved helix-loop-helix ubiquitous kinase (EC 2.7.1.-) CHUK - mouse

C:Species: Mus musculus (house mouse)

C>Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999

C:Accession: I49101

R:Mock, B.A.; Connolly, M.A.; McBride, O.W.; Kozak, C.A.; Marcu, K.B.  
Genomics 27, 348-351, 1995

A:Title: CHUK, a conserved helix-loop-helix ubiquitous kinase, maps to human chromosome

A:Reference number: I49101; MUID:96044444; PMID:7558004

A:Accession: I49101

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-745 <RES>

A:Cross-references: EMBL:U12473; NID:g1079492; PIDN:AMC52589.1; PID:g1079493

C:Genetics:

A:Gene: CHUK

C:Superfamily: mouse conserved helix-loop-helix ubiquitous kinase; protein kinase hom

C:Keywords: ATP; phosphotransferase

F:13-283/Domain: protein kinase homology <KIN>

Query Match 92.3% Score 36; DB 1; Length 745;

Best Local Similarity 83.3% Pred. No. 2.3e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LEWSWL 6  
 |||||  
 DB 738 LDMSWL 743

RESULT 3  
 P00444  
 Ig heavy chain V region precursor - human (fragment)

C:Species: Homo sapiens (man)  
 C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 21-Jan-2000  
 C:Accession: P00444  
 R:Kaluzna, B.; Betzl, G.; Shao, H.; Diamantstein, T.; Weidle, U.H.  
 Gene 122, 321-328, 1992  
 A:Title: A general method for chimerization of monoclonal antibodies by inverse polymerase  
 A:Reference number: P00444; MUID:93138402; PMID:1339379

A:Accession: P00444  
 A:Molecule type: mRNA  
 A:Residues: 1-150 <KAL>  
 A:Cross-references: GB:I02346  
 C:Superfamily: Immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotrimer; immunoglobulin  
 F:1-19/Domain: signal sequence #status predicted <SIG>  
 F:20-150/Product: Ig heavy chain V region #status predicted <MAT>  
 F:20-117/Domain: variable region <VRG>  
 F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 89.7%; Score 35; DB 2; Length 150;  
 Best Local Similarity 66.7%; Pred. No. 66;  
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEWSWL 6  
 :|||:  
 DB 1 MEMSWI 6

#### RESULT 4

T27590  
 hypothetical protein ZC47.13 - Caenorhabditis elegans  
 C:Species: Caenorhabditis elegans  
 C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 20-Jun-2000  
 C:Accession: T27590  
 R:McMurray, A.

submitted to the EMBL Data Library, October 1996  
 A:Reference number: Z20391

A:Accession: T27590  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-242 <WLL>  
 A:Cross-references: EMBL:Z81141; PIDN:CAB03488.1; CESP:ZC47.13  
 A:Experimental source: clone ZC47  
 C:Genetics:  
 A:Gene: CESP:ZC47.13  
 A:Introns: 172/3

C:Superfamily: Caenorhabditis elegans hypothetical protein ZC47.9

Query Match 89.7%; Score 35; DB 2; Length 242;  
 Best Local Similarity 83.3%; Pred. No. 1.1e+02;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LEWSWL 6  
 |||||  
 DB 226 LEWSWL 231

#### RESULT 5

S20075  
 Promastigote surface antigen P2 (clone 2.5) precursor - Leishmania major (fragment)  
 C:Species: Leishmania major  
 C:Date: 13-Jan-1995 #sequence\_revision 06-Feb-1998 #text\_change 31-Jan-2000  
 C:Accession: S20075; C41710  
 R:Murray, P.J.; Spithill, T.W.

J. Biol. Chem. 266, 24477-24484, 1991  
 A:Title: Variants of a Leishmania surface antigen derived from a multigenic family.  
 A:Reference number: A41710; MUID:92105105; PMID:1761547  
 A:Accession: S20075

A:Molecule type: mRNA  
 A:Residues: 1-371 <MUR>  
 A:Cross-references: EMBL:X57134; MID:g9580; PID:g9581  
 C:Keywords: blocked carboxyl end; glycoprotein; lipoprotein; phosphatidylinositol 1in  
 F:1-343/Product: promastigote surface antigen P2 (fragment) #status predicted <PSA>  
 F:344-371/Domain: carboxyl-terminal propeptide #status predicted <CTP>  
 F:343/Modified site: GPI anchor ethanolamine amidated carboxyl end (Asp) (In mature f

Query Match 89.7%; Score 35; DB 2; Length 371;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EWSWL 6  
 |||||  
 DB 1 EWSWL 5

#### RESULT 6

AD3426  
 mannose-6-phosphate isomerase (EC 5.3.1.8) [Imported] - Brucella melitensis (strain 1  
 C:Species: Brucella melitensis  
 C:Date: 01-Feb-2002 #sequence\_revision 01-Feb-2002 #text\_change 01-Feb-2002  
 C:Accession: AD3426

R:DelVecchio, V.G.; Kapral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanov  
 Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002  
 A:Title: The genome sequence of the facultative intracellular pathogen Brucella melit  
 A:Reference number: AD3252; PMID:11756688  
 A:Accession: AD3426  
 A:Status: preliminary

A:Molecule type: DNA  
 A:Residues: 1-387 <KUR>  
 A:Cross-references: GB:AE008917; PIDN:AAL52575.1; PID:g17983392; GSPDB:GN00190

A:Experimental source: strain 16M  
 C:Genetics:  
 A:Gene: BME11394  
 A:Map position: 1  
 C:Keywords: intramolecular oxidoreductase; isomerase

Query Match 89.7%; Score 35; DB 2; Length 387;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EWSWL 6  
 |||||  
 DB 245 EWSWL 249

#### RESULT 7

AG2318  
 hypothetical protein all4102 [Imported] - Nostoc sp. (strain PCC 7120)

C:Species: Nostoc sp.  
 A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120  
 C:Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 30-Jun-2002

C:Accession: AG2318  
 R:Kaneko, T.; Nakamura, Y.; Molk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Irtigu  
 Nakazaki, N.; Shimo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata  
 DNA Res. 8, 205-213, 2001  
 A:Title: Complete genomic sequence of the filamentous nitrogen-fixing Cyanobacterium  
 A:Reference number: AB1807; MUID:21595285; PMID:11759840  
 A:Accession: AG2318  
 A:Status: preliminary

A:Molecule type: DNA  
 A:Residues: 1-391 <KUR>  
 A:Cross-references: GB:BA000019; PIDN:BA075801.1; PID:g17133237; GSPDB:GN00179  
 A:Experimental source: strain PCC 7120  
 C:Genetics:  
 A:Gene: all4102

Query Match 89.7%; Score 35; DB 2; Length 391;  
 Best Local Similarity 83.3%; Pred. No. 1.7e+02;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LEWSWL 6  
 |||||  
 Db 37 LEWDWL 42

## RESULT 8

B64733  
 protein transport protein hofc - Escherichia coli (strain K-12)

C:Species: Escherichia coli  
 C:Date: 12-Sep-1997 #sequence\_revision 17-Sep-1997 #text\_change 01-Mar-2002  
 C:Accession: B64733; S45184; S45183  
 R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; CC  
 A.; Rose, D.J.; Mau, B.; Shaq, Y.  
 Science 277, 1453-1462, 1997  
 A:Title: The complete genome sequence of Escherichia coli K-12.  
 A:Reference number: A64720; M01D:97426617; PMID:9278503  
 A:Accession: B64733  
 A:Status: nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-400 <BLAT>

A:Cross-references: GB:AEO00119; GB:U00096; NID:q1786283; PIDN:AACT3217.1; PID:q1786295;  
 A:Experimental source: strain K-12, substrain MG1655  
 R:Fujita, N.  
 submitted to the EMBL Data Library, January 1994  
 A:Reference number: S45181  
 A:Accession: S45184

A:Molecule type: DNA

A:Residues: MGRE, 28-147, 'PK', 150-173, 'NHGGCGNAFCVCRSLPSTPRH', <F03>  
 A:Cross-references: EMBL:D26562; NID:9473770; PIDN:BA05563.1; PID:9473774

A:Experimental source: strain K-12

A:Accession: S45183

A:Status: preliminary

A:Molecule type: DNA  
 A:Residues: 207-366, 'NRVADHNGNRYTAGGNSANPPFRCDCEMGITYACCTPALDGYLLKMRFSQCT', 'INV'  
 A:Cross-references: EMBL:D26562; NID:9473770; PIDN:BA05562.1; PID:9473773

A:Experimental source: strain K-12

C:Genetics:  
 A:Gene: hofc; hopC  
 C:Superfamily: secretion protein xcpS

C:Keywords: protein transport; transmembrane protein  
 F:167-183/Domain: transmembrane #status predicted <TM1>  
 F:119-235/Domain: transmembrane #status predicted <TM2>  
 F:369-385/Domain: transmembrane #status predicted <TM3>

Query Match 89.7%; Score 35; DB 2; Length 400;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EWSWL 6  
 |||||  
 Db 215 EWSWL 219

## RESULT 9

G2MS11

Ig gamma-2b chain - mouse  
 C:Species: Mus musculus (house mouse)

C:Date: 31-Mar-1980 #sequence\_revision 01-Dec-2000 #text\_change 01-Dec-2000  
 C:Accession: S25057; A02157; A26232; A26233; A53598  
 R:Fischer, R.; Voss, A.; Niersbach, M.; Munziker, W.; Hirsch, H.J.; Kreuzaler, F.  
 submitted to the EMBL Data Library, July 1992  
 A:Description: Production of a Tobacco mosaic virus (TMV) inactivating neotop specific P

A:Reference number: S25057  
 A:Accession: S25057

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-474 <FIS>  
 A:Cross-references: EMBL:X67210; NID:954826; PIDN:CAA47649.1; PID:954827  
 R:Yamawaki-Kataoka, Y.; Kataoka, T.; Takahashi, N.; Ohta, M.; Honjo, T.

Nature 283, 786-789, 1980  
 A:Title: Complete nucleotide sequence of immunoglobulin gamma2b chain gene cloned fro  
 A:Reference number: A02157; M01D:80120715; PMID:676534  
 A:Contents: a allele  
 A:Accession: A02157

A:Molecule type: DNA  
 A:Residues: 138-161, 'L', 163-169, 'FP', 193-474 <RAM>  
 A:Cross-references: GB:J00461  
 A:Note: the sequence was determined from the germ-line gene  
 R:Tucker, P.W.; Marcu, K.B.; Slightom, J.L.; Blattner, F.R.  
 Science 206, 1299-1303, 1979

A:Title: Structure of the constant and 3' untranslated regions of the murine gamma2b  
 A:Reference number: A26235; M01D:80081501; PMID:117548

A:Contents: MPC 11

A:Accession: A26235

A:Molecule type: mRNA

A:Residues: 138-172, 'P', 174-189, 'FP', 193-376, 'T', 378-474 <TU1>  
 A:Note: Lys-474 is probably removed posttranslationally  
 R:Tucker, P.W.; Marcu, K.B.; Newell, N.; Richards, J.; Blattner, F.R.  
 Science 206, 1303-1306, 1979

A:Title: Sequence of the cloned gene for the constant region of murine gamma2b immuno  
 A:Reference number: A26232; M01D:80081502; PMID:117549

A:Accession: A26232

A:Molecule type: DNA

A:Residues: 138-172, 'P', 174-189, 'FP', 193-376, 'T', 378-474 <TU2>  
 R:Ollo, R.; Rougeon, F.

A:Title: Mouse immunoglobulin allotypes: post-duplication divergence of gamma2a and g  
 A:Reference number: A26233; M01D:82173203; PMID:6003173

A:Contents: b allele

A:Accession: A26233

A:Molecule type: DNA

A:Residues: 138-161, 'L', 163-169, 'FP', 193-300, 'R', 302-331, 'A', 333-437, 'DI', 440-474 <OL  
 A:Cross-references: GB:J00461

R:Kim, H.; Yamaguchi, Y.; Masuda, K.; Yamamoto, K.; Irimura, T.; Takah

J. Biol. Chem. 269, 12345-12350, 1994

A:Title: O-glycosylation in hinge region of mouse immunoglobulin g2b.

A:Reference number: A53598; M01D:94216359; PMID:7512967

A:Accession: A53598

A:Status: preliminary

A:Molecule type: protein

A:Residues: 234-251 <KIM>

C:Comment: The a allele sequence is shown.

C:Genetics:

A:Insertions: 138/1; 236/1; 258/1; 368/1

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (

hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into

C:Superfamily: immunoglobulin C region; immunoglobulin homology

C:Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunogl

F:157-222/Domain: immunoglobulin homology <TM1>  
 F:236-257/Region: hinge  
 F:281-350/Domain: immunoglobulin homology <TM2>  
 F:387-454/Domain: immunoglobulin homology <TM3>  
 F:152/Disulfide bonds: interchain (to light chain) #status predicted  
 F:164-220, 288-348, 394-452/Disulfide bonds: #status predicted  
 F:247, 250, 253, 256/Disulfide bonds: interchain (to heavy chain) #status predicted  
 F:324/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 89.7%; Score 35; DB 1; Length 474;  
 Best Local Similarity 66.7%; Pred. No. 2.1e+02;  
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEWSWL 6  
 |||||  
 Db 1 MEMSWI 6

## RESULT 10

A84606

hypothetical protein At2g21860 [Imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)  
 C:Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 02-Feb-2001  
 C:Accession: A84606

R.Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Bentto, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umeyam, T.; Tallon, L. euss, D.; Niernan, W.C.; White, O.; Elsen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999

A:Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.  
A:Reference number: AB4420; MUID:20083487; PMID:10617197  
A:Accession: AB4606  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-522 <STG>  
A:Cross-references: GB:AE002093; NID:g4417279; PIDN:AA020404.1; GSPDB:GN00139  
A:Gene: At2g21860  
A:Map position: 2

Query Match 89.7%; Score 35; DB 2; Length 522;  
Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LEWSW 5  
DB 341 LEWSW 345

RESULT 11  
H82874  
conserved hypothetical ATP/GTP-binding protein U0571 [Imported] - Ureaplasma urealyticum  
C:Species: Ureaplasma urealyticum  
C>Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 20-Aug-2000  
C:Accession: H82874  
R:Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H. submitted to GenBank, February 2000  
A:Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a min  
A:Reference number: AB2870  
A:Accession: H82874  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1367 <GUA>  
A:Cross-references: GB:AE002155; GB:AF222894; NID:96899572; PIDN:AAF30985.1; GSPDB:GN001  
A:Experimental source: serovar 3; biovar 1  
C:Genetics:  
A:Gene: U0571  
A:Genetic code: SGC3

Query Match 89.7%; Score 35; DB 2; Length 1367;  
Best Local Similarity 100.0%; Pred. No. 5.9e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 EMSWL 6  
DB 786 EMSWL 790

RESULT 12  
JC4954  
vascular endothelial growth factor receptor 2 precursor - Japanese quail  
N:Alternate names: Quail endothelial kinase 2; Quak 2  
C:Species: Coturnix coturnix japonica (Japanese quail)  
C>Date: 31-Dec-1996 #sequence\_revision 31-Dec-1996 #text\_change 24-Sep-1999  
C:Accession: JC4954  
R:Elchmann, A.; Marcelle, C.; Breant, C.; Le Douarin, N.M. Gene 174, 3-8, 1996  
A:Title: Molecular cloning of Quak 1 and 2, two quail vascular endothelial growth factor  
A:Reference number: JC4953; MUID:97017121; PMID:8863722  
A:Accession: JC4954  
A:Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-1379 <ETC>  
A:Cross-references: EMBL:X83287; NID:9619665; PIDN:CA58267.1; PID:e283815; PID:g1707416  
C:Comment: This protein is an endothelial-specific receptor and binds vascular endothelial  
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolo  
C:Keywords: ATP; embryo; growth factor receptor; transmembrane protein  
F:1-20/Domain: signal sequence #status predicted <SIG>

F:789-810/Domain: transmembrane #status predicted <TM>  
F:856-1188/Domain: protein kinase homology <KIN>  
F:864-872/Region: protein kinase ATP-binding motif

Query Match 89.7%; Score 35; DB 2; Length 1379;  
Best Local Similarity 100.0%; Pred. No. 5.9e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LEWSW 5  
DB 57 LEWSW 61

RESULT 13  
T32413  
probable acetyl-CoA carboxylase (EC 6.4.1.2) W09B6.1 [similarity] - Caenorhabditis el  
C:Species: Caenorhabditis elegans  
C>Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 18-Aug-2000  
C:Accession: T32413  
R:Goela, D.; Maggii, L.; Andrews, S. submitted to the EMBL Data Library, September 1997  
A:Description: The sequence of C. elegans cosmid W09B6.  
A:Reference number: Z21162  
A:Accession: T32413  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-2054 <GOE>  
A:Cross-references: EMBL:AF025469; PIDN:AA071048.1; GSPDB:GN00020; CESP:W09B6.1  
A:Experimental source: strain Bristol N2; clone W09B6  
C:Genetics:  
A:Gene: CESP:W09B6.1  
A:Map position: 2  
A:Insertions: 18/3; 97/1; 734/2; 793/3; 1975/2; 2037/2  
C:Superfamily: human acetyl-CoA carboxylase; biotin carboxylase homology; lipoyl/biot  
C:Keywords: ligase

Query Match 89.7%; Score 35; DB 2; Length 2054;  
Best Local Similarity 100.0%; Pred. No. 8.8e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LEWSW 5  
DB 773 LEWSW 777

RESULT 14  
T03472  
conserved hypothetical protein - Rhodobacter capsulatus  
C:Species: Rhodobacter capsulatus  
C>Date: 24-Mar-1999 #sequence\_revision 24-Mar-1999 #text\_change 08-Oct-1999  
C:Accession: T03472  
R:Vlcek, C.; Paces, V.; Maltsev, N.; Paces, J.; Haselkorn, R.; Fonstein, M. Proc. Natl. Acad. Sci. U.S.A. 94, 9384-9388, 1997  
A:Title: Sequence of a 189-kb segment of the chromosome of Rhodobacter capsulatus SBI  
A:Reference number: Z14955; MUID:97404404; PMID:9255491  
A:Accession: T03472  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-116 <VLC>  
A:Cross-references: EMBL:AF010496; NID:g3128256; PIDN:AA016125.1; PID:g3128273  
C:Genetics:  
A:Map position: 1

Query Match 87.2%; Score 34; DB 2; Length 116;  
Best Local Similarity 83.3%; Pred. No. 73;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 LEWSWL 6  
DB 63 LEWSWL 68

RESULT 15

S03289  
 Ig heavy chain precursor V region (VARL00) - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 31-Dec-1990 #sequence\_revision 31-Dec-1990 #text\_change 23-Jul-1999  
 C:Accession: S03289  
 R:Blankenstein, T.; Bonhomme, F.; Krawinkel, U.  
 Immunogenetics 26, 237-248, 1987  
 A:Title: Evolution of pseudogenes in the immunoglobulin V(H)-gene family of the mouse.  
 A:Reference number: S03289; MUID:88006305; PMID:2820872  
 A:Accession: S03289  
 A:Status: translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-117 <BLA>  
 A:Cross-references: EMBL:X06866; NID:g52454; PIDN:CAA29991.1; PID:g758157  
 C:Genetics:  
 A:Introns: 16/1  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 87.2%; Score 34; DB 2; Length 117;  
 Best Local Similarity 66.7%; Pred. No. 74;  
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LEWSWL 6  
 :||||:  
 Db 1 MEMSWV 6

Search completed: May 30, 2003, 14:52:49  
 Job time : 10.5921 secs



GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: May 30, 2003, 14:41:40 ; Search time 3.11842 Seconds  
(Without alignments)  
79.803 Million cell updates/sec

Title: US-09-643-260-8  
Perfect score: 39  
Sequence: 1 LEKSWL 6

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues  
Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	36	92.3	745 1 IKKA_HUMAN	O15111 h inhibitor
2	36	92.3	745 1 IKKA_MOUSE	O60680 m inhibitor
3	36	92.3	756 1 IKKB_HUMAN	O14920 homo sapien
4	36	92.3	757 1 IKKB_MOUSE	O88351 mus musculu
5	36	92.3	757 1 IKKB_MOUSE	O9qy78 rattus norv
6	35	89.7	400 1 HOFC_ECOLI	P36646 escherichia
7	34	87.2	334 1 GTR8_BOVIN	P58354 bos taurus
8	34	87.2	477 1 GTR8_HUMAN	O9ny64 homo sapien
9	34	87.2	477 1 GTR8_MOUSE	O9j143 mus musculu
10	34	87.2	478 1 GTR8_MOUSE	O9j141 rattus norv
11	33	84.6	512 1 VG29_BPMU	O9t1w5 bacterioph
12	33	84.6	777 1 TDRI_HUMAN	O9bxt4 homo sapien
13	33	84.6	928 1 TDRI_MOUSE	O14999 mus musculu
14	33	84.6	1698 1 Y076_HUMAN	O05252 mycobacteri
15	32	82.1	83 1 VG41_BPMU5	O05252 mycobacteri
16	32	82.1	94 1 VG41_BPMU2	O64231 buchnera ap
17	32	82.1	296 1 CYOA_BOCAI	P57544 aceticbacter
18	32	82.1	307 1 COX2_ACAC	P50653 pseudomonas
19	32	82.1	314 1 CYOA_PSEPU	O9wrt1 saccharomyc
20	32	82.1	362 1 DCUP_YEAST	B32347 crepilis alpi
21	32	82.1	375 1 D12_CREAL	O81931 crepilis alpi
22	32	82.1	367 1 MANA_RHIME	P29954 thizobium m
23	32	82.1	561 1 RK_BOVIN	P28337 bos taurus
24	32	82.1	563 1 RK_HUMAN	O15835 homo sapien
25	32	82.1	564 1 RK_MOUSE	O9wv14 mus musculu
26	32	82.1	564 1 RK_MOUSE	O63651 rattus norv
27	32	82.1	576 1 GRK6_HUMAN	B43250 homo sapien
28	32	82.1	576 1 GRK6_MOUSE	O70293 mus musculu
29	32	82.1	576 1 GRK6_MOUSE	P97711 rattus norv
30	32	82.1	578 1 GRK4_HUMAN	P32288 homo sapien
31	32	82.1	590 1 GRK5_BOVIN	P43249 bos taurus
32	32	82.1	590 1 GRK5_HUMAN	P34947 homo sapien
33	32	82.1	590 1 GRK5_MOUSE	O62833 rattus norv

34	32	82.1	642 1 YOR1_CAEEL	O09537 caenorhabdi
35	32	82.1	714 1 GPR2_DROME	P32866 drosophila
36	32	82.1	775 1 ECEL_MOUSE	O9jml0 mus musculu
37	32	82.1	775 1 ECEL_MOUSE	O9jhl3 rattus norv
38	32	82.1	826 1 CRAA_BACUH	O9s597 bacillus th
39	32	82.1	842 1 AMPN_LACDL	P37886 lactobacilli
40	32	82.1	983 1 EPA3_CHICK	P29318 gallus galli
41	32	82.1	983 1 EPA3_HUMAN	P29319 mus musculu
42	32	82.1	983 1 EPA3_MOUSE	O08680 rattus norv
43	32	82.1	984 1 EPA3_MOUSE	P10474 c endogluc
44	32	82.1	1039 1 GUNB_CALSA	O10283 schizosacch
45	32	82.1	1053 1 HMDH_SCHPO	

## ALIGNMENTS

RESULT 1  
IKKA\_HUMAN STANDARD: PRT: 745 AA.  
ID IKKA\_HUMAN  
AC O15111; O14666; Q13132; Q92467;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Inhibitor of nuclear factor kappa-B kinase alpha subunit (EC 2.7.1.-)  
DE (I kappa-B kinase alpha) (IKBA) (IKK-A) (Ikbpa kinase  
DE (I kappa-B kinase 1) (IKK1) (Conserved helix-loop-helix ubiquitous  
DE kinase) (Nuclear factor NF-kappaB inhibitor kinase alpha) (NFKBIA).  
GN IKKA OR CHUK. (Human).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_Taxid:9606;  
RN [1]  
RP TISSUE-FROM N.A., AND MUTAGENESIS OF LYS-44.  
RC MEDLINE-97386461; PubMed-9244310.  
RA Regnier C.H., Song H.Y., Gao X., Goeddel D.V., Cao Z., Rothe M.;  
RT "Identification and characterization of an IkappaB kinase.";  
RL Cell 90:373-383(1997).  
RN [2]  
RP TISSUE-FROM N.A., AND PARTIAL SEQUENCE.  
RC MEDLINE-97394468; PubMed-9252186;  
RA DiDonato J.A., Hayakawa M., Rothwarf D.M., Zandi E., Karin M.;  
RT "A cytokine-responsive IkappaB kinase that activates the transcription  
RT factor NF-kappaB.";  
RL Nature 386:548-554(1997).  
RN [3]  
RP TISSUE-FROM N.A., PARTIAL SEQUENCE, AND MUTAGENESIS OF LYS-44 AND  
RP SER-176.  
RC TISSUE-Cervical carcinoma;  
RX MEDLINE-98008813; PubMed-9346484;  
RA Mercutio F., Zhu H., Murray B.W., Shevchenko A., Bennett B.L.,  
RA Li J.W., Young D.B., Barbosa M., Mann M., Manning A., Rao A.;  
RT "IKK-1 and IKK-2: cytokine-activated IkappaB kinases essential for  
RT NF-kappaB activation.";  
RL Science 278:860-866(1997).  
RN [4]  
RP TISSUE-Heart; N.A.  
RC MEDLINE-99032998; PubMed-9813230;  
RA Hu M.C.-T., Wang Y.-P.;  
RT "IkappaB kinase-alpha and -beta genes are coexpressed in adult and  
RT embryonic tissues but localized to different human chromosomes.";  
RL Gene 222:31-40(1998).  
RN [5]  
RP TISSUE-OF 32-745 FROM N.A.  
RC TISSUE-Cervical carcinoma;  
RX MEDLINE-96258427; PubMed-8777433;  
RA Connolly M.A., Marcu K.B.;  
RT "CHUK, a new member of the helix-loop-helix and leucine zipper  
RT families of interacting proteins, contains a serine-threonine kinase  
RT catalytic domain.";

Cell. Mol. Biol. Res. 41:537-549(1995).

[6] PHOSPHORYLATION BY MAPK14/NIK, AND MUTAGENESIS OF S-176; T-179 AND S-180.

RX MEDLINE-98188283; PubMed-9520446;

RA Ling L., Cao Z., Goeddel D.V.;

RT "NF-kappaB-inducing kinase activates IKK-alpha by phosphorylation of Ser-176.";

RL Proc. Natl. Acad. Sci. U.S.A. 95:3792-3797(1998).

RN [7]

RP PHOSPHORYLATION BY AKT, AND MUTAGENESIS OF THR-23.

RX MEDLINE-99413720; PubMed-10485710;

RA Ozes O.N., Mayo L.D., Gustin J.A., Pfeiffer S.R., Pfeiffer L.M.,

RA Donner D.B.;

RT "NF-kappaB activation by tumour necrosis factor requires the Akt serine-threonine kinase.";

RL Nature 401:82-85(1999).

RN [8]

RP IKK-BINDING.

RX MEDLINE-99212141; PubMed-10195894;

RA Delhase M., Hayakawa M., Chen Y., Karin M.;

RT "Positive and negative regulation of IkappaB kinase activity through IKKbeta subunit phosphorylation.";

RL Science 284:309-313(1999).

RN [9]

RP IKK PHOSPHORYLATION.

RX MEDLINE-99038238; PubMed-9819420;

RA Nemoto S., Didonato J.A., Lin A.;

RT "Coordinate regulation of IkappaB kinases by mitogen-activated protein kinase kinase kinase 1 and NF-kappaB-inducing kinase.";

RL Mol. Cell. Biol. 18:7336-7343(1998).

RN [10]

RP REVIEW.

RX MEDLINE-20178139; PubMed-10712233;

RA Jobin C., Sartor R.B.;

RT "The I kappa B/NF-kappa B system: a key determinant of mucosal inflammation and protection.";

RL Am. J. Physiol. 278:C451-C462(2000).

CC -1- FUNCTION: PHOSPHORYLATES INHIBITORS OF NF-KAPPA-B THUS LEADING TO THE DISSOCIATION OF THE INHIBITOR/NF-KAPPA-B COMPLEX AND ULTIMATELY THE DEGRADATION OF THE INHIBITOR.

CC -1- ENZYME REGULATION: ACTIVATED WHEN PHOSPHORYLATED AND INACTIVATED WHEN DEPHOSPHORYLATED.

CC -1- SUBUNIT: PREFERENTIALLY FOUND AS A HETERODIMER WITH IKK-BETA BUT ALSO AS AN HOMODIMER. DIRECTLY INTERACTS WITH IKK-GAMMA/IKK-ALPHA AND HERODIMERS FORM THE ACTIVE COMPLEX. THE TRIPARTITE COMPLEX CAN ALSO BIND TO MAPK14/NIK, MEK1, IKAP AND IKK-ALPHA-P65-P50 COMPLEX. A WEAK INTERACTION WITH TRAF2 CANNOT BE EXCLUDED.

CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.

CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED.

CC -1- PHN: PHOSPHORYLATED BY MAPK14/NIK, AKT AND TO A LESSER EXTENT BY MEK1. AND DEPHOSPHORYLATED BY PP2A. AUTOPHOSPHORYLATED.

CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES. IKAPAB KINASE SUBFAMILY.

CC -----

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CC -----

CC EMBL; AF012890; AAC51662.1; -

DR EMBL; AF009225; AAC51671.1; -

DR EMBL; AF080157; AAO08966.1; -

DR EMBL; U22512; AAC50713.1; -

DR HSSP; 063450; 1A06.

DR Genew; HGNC:1974; CHUK.

DR MIM; 600664; -

DR InterPro; IPR000719; Euk\_Pkinase.

DR InterPro; IPR002290; Ser\_thr\_Pkinase.

DR Pfam; PF00069; pkinase; 1.

DR ProDom; P0000001; Euk\_Pkinase; 1.

DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.

DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.

DR PROSITE; PS00011; PROTEIN\_KINASE\_DOM; 1.

KW Transferrase; Serine/threonine-protein kinase; ATP-binding; phosphorylation.

KM Phosphorylation.

FT DOMAIN 15 302

FT DOMAIN 455 476

FT DOMAIN 738 743

FT NP\_BIND 21 29

FT BINDING 44 44

FT ACT\_SITE 144 144

FT MOD\_RES 23 23

FT MOD\_RES 176 176

FT MUTAGEN 23 23

FT MUTAGEN 44 44

FT MUTAGEN 44 44

FT MUTAGEN 176 176

FT MUTAGEN 176 176

FT MUTAGEN 176 176

FT MUTAGEN 179 179

FT MUTAGEN 180 180

FT CONFLICT 543 543

FT CONFLICT 604 604

FT CONFLICT 679 680

FT CONFLICT 684 684

FT CONFLICT 686 687

SO SEQUENCE 745 AA; 84653 MW; 7A90B59BC98A56C2 CRC64;

QY 1 LEWSWL 6

DB 738 LDMSWL 743

Query Match 92.3%; Score 36; DB 1; Length 745;

Best Local Similarity 83.3%; Pred. No. 1.3e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RESULT 2

IKKA\_MOUSE STANDARD; PRI; 745 AA.

AC 060680; 09D2X3;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Inhibitor of nuclear factor kappa-B kinase alpha subunit (EC 2.7.1.-)

DE (I kappa-B kinase alpha) (IKK-A) (IkappaB kinase)

DE (I-kappa-B kinase 1) (IKK1) (conserved helix-loop-helix ubiquitous kinase) (Nuclear factor NFkappaB inhibitor kinase alpha) (NFKBIA).

GN IKKA OR CHUK.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A. (ISOFORM 1).

RC STRAIN-BALB/c;

RX MEDLINE-9604444; PubMed-7558004;

RA Mock B.A., Connolly M.A., McBride O.W., Kozak C.A., Marcu K.B.;

RT "CHUK, a conserved helix-loop-helix ubiquitous kinase, maps to human chromosome 10 and mouse chromosome 19.";

RL Genomics 27:348-351(1995).

RN [2]

RP SEQUENCE FROM N.A. (ISOFORM 1).

RC STRAIN-BALB/c;

RX MEDLINE-96258427; PubMed-8777433;

RA Connolly M.A., Marcu K.B.;

RT "CHUK, a new member of the helix-loop-helix and leucine zipper families of interacting proteins, contains a serine-threonine kinase catalytic domain.";

RL Cell. Mol. Biol. Res. 41:537-549(1996).

RN [3]

RP SEQUENCE FROM N.A. (ISOFORM 3).  
 RX STRAIN-C57BL/6J; TISSUE-Colon;  
 RA MEDLINE-21085660; PubMed-11217051;  
 RA Kawal J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,  
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
 RA Fleischmann W., Gaasterland T., Glass I., Kling B., Kochia H.,  
 RA Knehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,  
 RA Schirml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Mashio T.,  
 RA Sakai K., Okido T., Furuno M., Aono H., Balderelli R., Barsh G.,  
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
 RA Gustinich S., Hill D., Hofmann M., Hume D.A., Kamuya M., Lee N.H.,  
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
 RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,  
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,  
 RA Hayashizaki Y.;  
 RA "Functional annotation of a full-length mouse cDNA collection.";  
 RA Nature 409:685-690(2001).  
 RN [4]  
 RN ALTERNATIVE SPLICING.  
 RX MEDLINE-20198447; PubMed-10733566;  
 RA McKenzie F.R., Connelly M.A., Balzarano D., Mueller J.R.,  
 RA Gelezianas R., Marcu K.B.;  
 RA "Functional isoforms of Ikappab kinase alpha (IKKalpha) lacking  
 RT leucine zipper and helix-loop-helix domains reveal that IKKalpha and  
 RT IKKbeta have different activation requirements.";  
 RL Mol. Cell. Biol. 20:2635-2649(2000).  
 RN [5]  
 RN PHOSPHORYLATION BY MAP3K14/NIK.  
 RX MEDLINE-98188238; PubMed-9520401;  
 RA Nakano H., Shando M., Sakon S., Nishinaka S., Mihara M., Yagita H.,  
 RA Okumura K.;  
 RA "Differential regulation of Ikappab kinase alpha and beta by two  
 RT upstream kinases, NF-kappaB-inducing kinase and mitogen-activated  
 RT protein kinase/ERK kinase-1.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 95:3537-3542(1998).  
 RN [6]  
 RN IKK- $\alpha$  BINDING.  
 RX MEDLINE-99212141; PubMed-10195894;  
 RA Delnase M., Hayakawa M., Chen Y., Karin M.;  
 RA "Positive and negative regulation of Ikappab kinase activity through  
 RT IKKbeta subunit phosphorylation.";  
 RL Science 284:309-313(1999).  
 RN [7]  
 RN IKK PHOSPHORYLATION.  
 RX MEDLINE-99038238; PubMed-9819420;  
 RA Nemoto S., DiDonato J.A., Lin A.;  
 RA "Coordinate regulation of Ikappab kinases by mitogen-activated protein  
 RT kinase kinase kinase 1 and NF-kappaB-inducing kinase.";  
 RL Mol. Cell. Biol. 18:7336-7343(1998).  
 RN [8]  
 RN REVIEW.  
 RX MEDLINE-20178139; PubMed-10712233;  
 RA Jobin C., Sartor R.B.;  
 RA "The I kappa B/NF-kappa B system: a key determinant of  
 RT mucosal inflammation and protection";  
 RL Am. J. Physiol. 278:C451-C462(2000).  
 CC -1- FUNCTION: PHOSPHORYLATES INHIBITORS OF NF-KAPPA-B THUS LEADING TO  
 CC THE DISSOCIATION OF THE INHIBITOR/NF-KAPPA-B COMPLEX AND  
 CC ULTIMATELY THE DEGRADATION OF THE INHIBITOR.  
 CC -1- ENZYME REGULATION: ACTIVATED WHEN PHOSPHORYLATED AND INACTIVATED  
 CC WHEN DEPHOSPHORYLATED.  
 CC -1- SUBUNIT: PREPARENTIALLY FOUND AS A HETERODIMER WITH IKK-BETA BUT  
 CC ALSO AS A HOMODIMER. DIRECTLY INTERACTS WITH IKK-GAMMA/NEMO.  
 CC HETERODIMERS FORM THE ACTIVE COMPLEX. THE TRIPARTITE COMPLEX CAN  
 CC ALSO BIND TO MAP3K14/NIK, MEK1, IKAP AND IKK- $\alpha$ -PE5-P50  
 CC COMPLEX. A WEAK INTERACTION WITH TRAF2 CANNOT BE EXCLUDED.  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.

CC -1- ALTERNATIVE PRODUCTS: 3 ISOFORMS; 1 (SHOWN HERE), 2/DELTA LH AND  
 CC 3/DELTA H; ARE PRODUCED BY ALTERNATIVE SPLICING.  
 CC -1- TISSUE SPECIFICITY: UBICUITOUS ONLY FOR ISOFORM 1, ISOFORMS 2 AND  
 CC 3 ARE EXPRESSED PREDOMINANTLY IN BRAIN AND T-LYMPHOCYTES.  
 CC -1- DEVELOPMENTAL STAGE: MAXIMALLY EXPRESSED AT E7 DAY FOLLOWED BY  
 CC E11, E15 AND E17 DAYS. IN THE LIMB DEVELOPMENT, ITS EXPRESSION  
 CC PREDOMINATES IN THE LIMB BUDS AT E12.5 DAY.  
 CC -1- PTM: PHOSPHORYLATED BY MAP3K14/NIK, AKT AND TO A LESSER EXTENT BY  
 CC MEK1, AND DEPHOSPHORYLATED BY PP2A. AUTOPHOSPHORYLATED.  
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 CC IKKAPAB KINASE SUBFAMILY.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; U12473; AAC52589.1; -;  
 DR EMBL; AK018671; BAB31335.1; -;  
 DR HSSP; 063450; 1A06.  
 DR MGD; MGI:99484; Chuk.  
 DR InterPro; IPR000719; Euk\_pkinase.  
 DR InterPro; IPR002290; Ser\_thr\_pkinase.  
 DR Pfam; PF00069; pkinase; 1.  
 DR ProDom; PD000001; Euk\_pkinase; 1.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
 DR PROSITE; PS00118; PROTEIN\_KINASE\_DOM; 1.  
 DR TRANSFERASE; Serine/threonine-protein kinase; ATP-binding;  
 KW Phosphorylation; Alternative splicing.  
 KW DOMAIN 15 300  
 FT DOMAIN 455 476  
 FT DOMAIN 738 743  
 FT NP\_BIND 21 29  
 FT BINDING 44 44  
 FT ACT\_SITE 144 144  
 FT MOD\_RES 23 23  
 FT MOD\_RES 176 176  
 FT MOD\_RES 452 471  
 FT VARSPPLIC 472 745  
 FT VARSPPLIC 577 584  
 FT VARSPPLIC 585 745  
 FT CONFLICT 236 236  
 FT CONFLICT 400 400  
 SQ SEQUENCE 745 AA; 3FEF5582AF92233 CRC64;  
 Query Match 92.3%; Score 36; DB 1; Length 745;  
 Best Local Similarity 83.3%; Pred. NO. 1.3e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 RESULT 3  
 ID IKKB\_HUMAN STANDARD; PRT; 756 AA.  
 AC 014920; 075327;  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Inhibitor of nuclear factor kappa B kinase beta subunit (EC 2.7.1.-)  
 DE (I-kappa-B-kinase beta) (IKKB) (IKK-B) (I-kappa-B kinase  
 DE 2) (IKK2) (Nuclear factor NF-kappa-B inhibitor kinase beta) (NFKB1KB).  
 GN IKKB OR IKKBK.  
 OS Homo sapiens (human).

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 CC NCBI\_TaxID=9606;  
 CC [1]  
 CC SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-44; SER-177 AND SER-181.  
 CC MEDLINE=98008813; PubMed=9346484;  
 CC RA Mercurio F., Zhu H., Murray B.W., Shevchenko A., Bennett B.L.,  
 CC RA Li J.W., Young D.B., Barbosa M., Mann M., Manning A., Rao A.;  
 CC RA "IRK-1 and IRK-2: cytoskeleton-activated ikkappa kinases essential for  
 CC NF-kappa activation.";  
 CC Science 278:860-866(1997).  
 CC [2]  
 CC SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-44.  
 CC MEDLINE=98008814; PubMed=9346485;  
 CC RA Woronicz J.D., Gao X., Cao Z., Rothe M., Goeddel D.V.;  
 CC RA "IkappaB kinase-beta: NF-kappaB activation and complex formation with  
 CC IkappaB kinase-alpha and NIK.";  
 CC Science 278:866-869(1997).  
 CC [3]  
 CC SEQUENCE FROM N.A.  
 CC TISSUE=Heart;  
 CC MEDLINE=99032998; PubMed=9813330;  
 CC RA Hu M.C.-T., Wang Y.-P.;  
 CC RA "IkappaB kinase-alpha and -beta genes are coexpressed in adult and  
 CC embryonic tissues but localized to different human chromosomes.";  
 CC Gene 222:31-40(1998).  
 CC [4]  
 CC SEQUENCE FROM N.A., AND GENE MAPPING.  
 CC MEDLINE=98438415; PubMed=9763654;  
 CC RA Shindo M., Nakano H., Sakon S., Yagita H., Mihara M., Okumura K.;  
 CC RA "Assignment of IkappaB kinase beta (IKKB) to human chromosome Dand  
 CC 8p2->p11 by in situ hybridization.";  
 CC Cytogenet. Cell Genet. 82:32-33(1998).  
 CC [5]  
 CC SEQUENCE OF 1-256 FROM N.A.  
 CC TISSUE=Lung;  
 CC Strausberg R.;  
 CC Submitted (Apr-2001) to the EMBL/GenBank/DBJ databases.  
 CC [6]  
 CC IKK PHOSPHORYLATION.  
 CC MEDLINE=99038238; PubMed=9819420;  
 CC RA Nemoto S., Didonato J.A., Lin A.;  
 CC RA "Coordinate regulation of IkappaB kinases by mitogen-activated protein  
 CC kinase kinase kinase 1 and NF-kappaB-inducing kinase.";  
 CC Mol. Cell. Biol. 18:7336-7343(1998).  
 CC [7]  
 CC REVIEW.  
 CC MEDLINE=20178139; PubMed=10712233;  
 CC RA Jobin C., Sartor R.B.;  
 CC RA "The I kappa B/NF-kappa B system: a key determinant of  
 CC mucosal inflammation and protection.";  
 CC Am. J. Physiol. 278:C451-C462(2000).  
 CC [8]  
 CC FUNCTION: PHOSPHORYLATES INHIBITORS OF NF-KAPPA-B THUS LEADING TO  
 CC THE DISSOCIATION OF THE INHIBITOR/NF-KAPPA-B COMPLEX AND  
 CC ULTIMATELY THE DEGRADATION OF THE INHIBITOR.  
 CC [9]  
 CC SUBUNIT: PREFERENTIALLY POUND AS A HETERODIMER WITH IKK-ALPHA BUT  
 CC ALSO AS A HOMODIMER. DIRECTLY INTERACTS WITH IKK-GAMMA/IKK-  
 CC HETERODIMERS FORM THE ACTIVE COMPLEX. THE TRIPARTITE COMPLEX CAN  
 CC ALSO BIND TO MEK1, MAP3K14/NIK, IKAP AND IKK-ALPHA-P65-P50  
 CC COMPLEX. PHOSPHORYLATED IKK-ALPHA IS FURTHER RELEASED FROM THE  
 CC COMPLEX.  
 CC [10]  
 CC SUBCELLULAR LOCATION: Cytoplasmic.  
 CC [11]  
 CC TISSUE SPECIFICITY: HIGHLY EXPRESSED IN HEART, PLACENTA, SKELETAL  
 CC MUSCLE, KIDNEY, PANCREAS, SPLEEN, THYMUS, PROSTATE, TESTIS AND  
 CC PERIPHERAL BLOOD.  
 CC [12]  
 CC PTM: PHOSPHORYLATED BY MEK1 AND PROBABLY ALSO BY MAP3K14/NIK.  
 CC WEAKLY AUTOHOSPHORYLATED.  
 CC [13]  
 CC SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 CC IKAPAB KINASE SUBFAMILY.  
 CC [14]  
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 CC -----  
 CC DR EMBL: AF029684; AAC51860.1;  
 CC DR EMBL: AF080158; AAD08997.1;  
 CC DR EMBL: AF031416; AAC64675.1;  
 CC DR EMBL: BC006231; AAH06231.1;  
 CC DR HSSP: 063450; 1A06.  
 CC DR Gene: HGNC:5960; IKKB.  
 CC DR MIM: 603258;  
 CC DR InterPro: IPR000719; Euk\_pkinase.  
 CC DR InterPro: IPR002290; Ser\_thr\_pkinase.  
 CC DR InterPro: IPR001245; Tyr\_pkinase.  
 CC DR Pfam: PF00069; pkinase; 1.  
 CC DR Pfam: PF00240; ubiquitin; 1.  
 CC DR PRINTS: PR00109; TYRKINASE.  
 CC DR PRODOM: PD000001; Euk\_pkinase; 1.  
 CC DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP; FALSE\_NEG.  
 CC DR PROSITE: PS00108; PROTEIN\_KINASE\_ST; 1.  
 CC DR PROSITE: PS50011; PROTEIN\_KINASE\_DOM; 1.  
 CC DR Transferrase: Serine/threonine-protein kinase; ATP-binding;  
 CC KW phosphorylation.  
 CC FT DOMAIN 15 300  
 CC FT DOMAIN 458 479  
 CC FT DOMAIN 737 742  
 CC FT NP\_BIND 21 29  
 CC FT BINDING 44 44  
 CC FT ACT\_SITE 145 145  
 CC FT MOD\_RES 23 23  
 CC FT MOD\_RES 177 177  
 CC FT MOD\_RES 181 181  
 CC FT MUTAGEN 44 44  
 CC FT MUTAGEN 177 177  
 CC FT MUTAGEN 181 181  
 CC FT MUTAGEN 231 255  
 CC FT CONFLICT 425 425  
 CC FT SEQUENCE 756 AA; 86563 MW; F9CAD671AE9E14E CRC64;  
 CC SQ  
 CC Query Match 92.3%; Score 36; DB 1; Length 756;  
 CC Best Local Similarity 83.3%; Pred. NO. 1.3e+02;  
 CC Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 CC  
 CC QY 1 LEMSWL 6  
 CC Db 737 LDMSWL 742  
 CC  
 CC RESULT 4  
 CC IKKB\_MOUSE STANDARD; PRT; 757 AA.  
 CC AC 088351; Q9RLJ6;  
 CC DT 16-OCT-2001 (Rel. 40, Created)  
 CC DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 CC DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 CC DE Inhibitor of nuclear factor kappa B kinase beta subunit (EC 2.7.1.1.-)  
 CC DE (I-kappa-B-kinase beta) (IKKB) (IKK-B) (I-kappa-B kinase  
 CC DE 2) (IKK2) (Nuclear factor NF-kappa-B inhibitor kinase beta) (NFKBIB).  
 CC GN IKKB OR IKKB.  
 CC OS Mus musculus (Mouse).  
 CC CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 CC CC NCBI\_TaxID=10090;  
 CC CC [1]  
 CC SEQUENCE FROM N.A., AND PHOSPHORYLATION BY MEK1.  
 CC RC STRAIN=C57BL/6; TISSUE=Spleen;  
 CC MEDLINE=98188238; PubMed=9520401;  
 CC RX

RA Nakano H., Shindo M., Sakon S., Nishinaka S., Mihara M., Yagita H.,  
 RA Okumura K.;  
 RT "Differential regulation of Ikkappa kinase alpha and beta by two  
 RT upstream kinases, NF-kappaB-inducing kinase and mitogen-activated  
 RT protein kinase/ERK kinase kinase-1.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 95:3537-3542(1998).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Hu M.C.-T., Wang Y.-P., Mikhail A., Qiu W.R.;  
 RT "Murine Ikb kinase-B, a developmentally regulated protein kinase that  
 RT constitutively phosphorylates serine residues of Ikb.";  
 RL Submitted (M06-1998) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP DEVELOPMENTAL STAGE.  
 RX MEDLINE=99455228; PubMed=10523828;  
 RA Hu M.C.-T., Wang Y.-P., Qiu W.R., Mikhail A., Meyer C.F., Tan T.-H.;  
 RT "Hematopoietic progenitor kinase-1 (HPK1) stress response signaling  
 RT pathway activates Ikkappa kinases (IKK-alpha/beta) and IKK-beta is a  
 RT developmentally regulated protein kinase.";  
 RL Oncogene 18:5514-5524(1999).  
 RN [4]  
 RP IKK PHOSPHORYLATION.  
 RX MEDLINE=99038238; PubMed=9819420;  
 RA Nemoto S., Didonato J.A., Lin A.;  
 RT "Coordinate regulation of Ikkappa kinases by mitogen-activated protein  
 RT kinase kinase kinase 1 and NF-kappaB-inducing kinase.";  
 RL Mol. Cell. Biol. 18:7336-7343(1998).  
 RN [5]  
 RP REVIEW.  
 RX MEDLINE=20178139; PubMed=10712233;  
 RA Jobin C., Sartor R.B.;  
 RT "The Ikkappa/NF-kappaB system: a key determinant of mucosal  
 RT inflammation and protection.";  
 RL Am. J. Physiol. 278:C451-C462(2000).  
 CC -1- FUNCTION: PHOSPHORYLATES INHIBITORS OF NF-KAPPA-B THUS LEADING TO  
 CC THE DISSOCIATION OF THE INHIBITOR/NF-KAPPA-B COMPLEX AND  
 CC ULTIMATELY THE DEGRADATION OF THE INHIBITOR.  
 CC -1- SUBUNIT: PREFERENTIALLY FOUND AS A HETERODIMER WITH IKK-ALPHA BUT  
 CC ALSO AS A HOMODIMER. DIRECTLY INTERACTS WITH IKK-GAMMA/NEMO.  
 CC HETERODIMERS FORM THE ACTIVE COMPLEX. THE TRIPARTITE COMPLEX CAN  
 CC ALSO BIND TO MEK1, MAPK14/NIK, IKAP AND IKK-ALPHA-P65-P50  
 CC COMPLEX. PHOSPHORYLATED IKK-ALPHA IS FURTHER RELEASED FROM THE  
 CC COMPLEX.  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN LIVER, KIDNEY AND SPLEEN.  
 CC -1- DEVELOPMENTAL STAGE: WHILE IT IS EXPRESSED OBVIOUSLY THROUGHOUT  
 CC THE MOUSE EMBRYO, AT E9.5 DAY ITS EXPRESSION BEGINS TO BE  
 CC LOCALIZED TO THE BRAIN, NEURAL GANGLIA, NEURAL TUBE, AND IN LIVER  
 CC AT E12.5 DAY. AT E15.5 DAY, THE EXPRESSION IS FURTHER RESTRICTED  
 CC TO SPECIFIC TISSUES OF THE EMBRYO.  
 CC -1- PTM: PHOSPHORYLATED BY MEK1 AND PROBABLY ALSO BY MAPK14/NIK.  
 CC WEAKLY AUTOPHOSPHORYLATED.  
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 CC IKAPPA KINASE SUBFAMILY.  
 CC -----  
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 CC -----  
 CC EMBL: AF026524; AAC23557.1; -  
 DR EMBL: AF088910; AAD52095.1; -  
 DR HSSP: 063450; 1A06.  
 DR MGD: MGI:1338071; Ikbkb.  
 DR InterPro: IPR000719; Euk\_pkinase.  
 DR InterPro: IPR002290; Ser\_thr\_pkinase.  
 DR Pfam: PF00069; pkinase; 1.  
 DR PRODOM: PD000001; Euk\_pkinase; 1.  
 DR PROSITE: PS00107; PROTEIN\_KINASE\_APP; FALSE\_NEG.  
 DR PROSITE: PS00108; PROTEIN\_KINASE\_ST; 1.

DR PROSITE; PS00011; PROTEIN\_KINASE\_DOM; 1.  
 KW Transferase; Serine/threonine-protein kinase; ATP-binding;  
 RM Phosphorylation.  
 FT DOMAIN 15 300  
 FT BINDING 458 479  
 FT DOMAIN 737 742  
 FT NP\_BIND 21 29  
 FT BINDING 44 44  
 FT ACT\_SITE 145 145  
 FT MOD\_RES 23 23  
 FT MOD\_RES 177 177  
 FT MOD\_RES 181 181  
 FT MOD\_RES 56 56  
 FT CONFLICT 343 343  
 FT CONFLICT 356 356  
 FT CONFLICT 390 390  
 FT CONFLICT 406 406  
 FT CONFLICT 573 573  
 FT CONFLICT 736 757  
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 Query Match 92.38; Score 36; DB 1; Length 757;  
 Best Local Similarity 83.38; Pred. No. 1.4e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LEWSML 6  
 Db 737 LDWSML 742  
 ID 1  
 AC 09QY78 STANDARD; PRT; 757 AA.  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Inhibitor of nuclear factor kappa B kinase beta subunit (EC 2.7.1.-)  
 DE (I-kappa-B-kinase beta) (IKKB) (IKK-beta) (IKK-B) (I-kappa-B kinase  
 DE 2) (IKK2) (Nuclear factor NF-kappa-B inhibitor kinase beta) (NFKB1NB).  
 GN IKKB OR IKKBX.  
 OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.  
 OX NCBI\_Taxid=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Zhang Y., Sun S., Ravid K.;  
 RT "IKK beta in megakaryocyte differentiation.";  
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP IKK PHOSPHORYLATION.  
 RX MEDLINE=99038238; PubMed=9819420;  
 RA Nemoto S., Didonato J.A., Lin A.;  
 RT "Coordinate regulation of Ikkappa kinases by mitogen-activated protein  
 RT kinase kinase kinase 1 and NF-kappaB-inducing kinase.";  
 RL Mol. Cell. Biol. 18:7336-7343(1998).  
 RN [3]  
 RP REVIEW.  
 RX MEDLINE=20178139; PubMed=10712233;  
 RA Jobin C., Sartor R.B.;  
 RT "The I kappa B/NF-kappa B system: a key determinant of  
 RT mucosal inflammation and protection.";  
 RL Am. J. Physiol. 278:C451-C462(2000).  
 CC -1- FUNCTION: PHOSPHORYLATES INHIBITORS OF NF-KAPPA-B THUS LEADING TO  
 CC THE DISSOCIATION OF THE INHIBITOR/NF-KAPPA-B COMPLEX AND  
 CC ULTIMATELY THE DEGRADATION OF THE INHIBITOR.  
 CC -1- SUBUNIT: PREFERENTIALLY FOUND AS A HETERODIMER WITH IKK-ALPHA BUT  
 CC ALSO AS A HOMODIMER. DIRECTLY INTERACTS WITH IKK-GAMMA/NEMO.  
 CC HETERODIMERS FORM THE ACTIVE COMPLEX. THE TRIPARTITE COMPLEX CAN  
 CC ALSO BIND TO MEK1, MAPK14/NIK, IKAP AND IKK-ALPHA-P65-P50  
 CC COMPLEX. PHOSPHORYLATED IKK-ALPHA IS FURTHER RELEASED FROM THE

CC COMPLEX.  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -1- PTM: PHOSPHORYLATED BY MENK1 AND PROBABLY ALSO BY MAP3K14/NIK.  
 CC WEAKLY AUTOPHOSPHORYLATED.  
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 CC IKAPKB KINASE SUBFAMILY.  
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 CC -----  
 DR EMBL: AF115282; AAF21978.1; -  
 DR HSSP: 063450; 1A06.  
 DR InterPro: IPR000719; Euk\_pkinase.  
 DR InterPro: IPR002290; Ser\_thr\_pkinase.  
 DR InterPro: IPR001245; Tyr\_pkinase.  
 DR Pfam: PF00069; pkinase; 1.  
 DR PRINTS: PR00109; TYRKINASE.  
 DR PRODOM: PD000001; Euk\_pkinase; 1.  
 DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP; FALSE\_NEG.  
 DR PROSITE: PS50011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE: PS00108; PROTEIN\_KINASE\_ST; 1.  
 DR Trnsterase; Serine/threonine-protein kinase; ATP-binding;  
 DR Phosphorylation.  
 FT DOMAIN 15 300 PROTEIN KINASE.  
 FT DOMAIN 458 479 LEUCINE-ZIPPER (POTENTIAL).  
 FT DOMAIN 737 742 NEMO-BINDING.  
 FT NP\_BIND 21 29 ATP (BY SIMILARITY).  
 FT BINDING 44 44 ATP (BY SIMILARITY).  
 FT ACT\_SITE 145 145 BY SIMILARITY.  
 FT MOD\_RES 23 23 PHOSPHORYLATION (BY SIMILARITY).  
 FT MOD\_RES 177 177 PHOSPHORYLATION (BY SIMILARITY).  
 FT MOD\_RES 181 181 PHOSPHORYLATION (BY SIMILARITY).  
 SQ SEQUENCE 757 AA; 86866 MW; 3AFPE6A7DF91F9C CRC64;  
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 DB 737 LDWSWL 742  
 Query Match 92.3%; Score 36; DB 1; Length 757;  
 Best Local Similarity 83.3%; Pred. No. 1.4e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RX MEDLINE-94261430; PubMed-8202364;  
 RA Fujita N., Mori H., Yura T., Ishihama A.;  
 RT "Systematic sequencing of the *Escherichia coli* genome: analysis of  
 RT the 2.4-4.1 min (110,917-193,643 bp) region.";  
 RL Nucleic Acids Res. 22:1637-1639(1994).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-K12 / MG1655;  
 RX MEDLINE-97426617; PubMed-9278503;  
 RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,  
 RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,  
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,  
 RA Mau B., Shao Y.;  
 RT "The complete genome sequence of *Escherichia coli* K-12.";  
 RL Science 277:1453-1474(1997).  
 RN [4]  
 RP SEQUENCE OF 165-400 FROM N.A.  
 RC STRAIN-K12;  
 RX MEDLINE-89061679; PubMed-2904262;  
 RA Andrews S.C., Guest J.R.;  
 RT "Nucleotide sequence of the gene encoding the GMP reductase of  
 RT *Escherichia coli* K12.";  
 RL Biochem. J. 255:35-43(1988).  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane  
 CC (Probable).  
 CC -1- SIMILARITY: BELONGS TO THE PULF/OUTF/EXEF/XPSF/XCPS FAMILY.  
 CC -1- CAUTION: REF.2 AND REF.4 SEQUENCES DIFFER IN THE N- AND C-TERMINAL  
 CC AS WELL AS IN THE CENTRAL PART DUE TO FRAMESHIFTS.  
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 CC -----  
 DR EMBL: L28105; AAC36925.1; -  
 DR EMBL: D26562; -; NOT\_ANNOTATED\_CDS.  
 DR EMBL: AE000119; AAC73217.1; -  
 DR EMBL: X07917; -; NOT\_ANNOTATED\_CDS.  
 DR Ecogene: BG11798; hoFC.  
 DR InterPro: IPR001992; Bact\_sect\_systII.  
 DR Pfam: PF00482; GSP11\_F; 1.  
 DR PROSITE: PS00874; T2SP\_F; 1.  
 DR Trnsterase; Transmembrane; Inner membrane; Complete proteome.  
 FT TRANSMEM 165 185 POTENTIAL.  
 FT TRANSMEM 209 229 POTENTIAL.  
 FT TRANSMEM 370 390 POTENTIAL.  
 FT CONFLICT 1 39 MASKED [RMHGIITGDGNAQDGMALNNESTLLMALIQQM  
 FT SEQUENCE 400 AA; 44450 MW; 9D37332B87AE07D5 CRC64;  
 OY 2 EWSWL 6  
 DB 215 EWSWL 219  
 Query Match 89.7%; Score 35; DB 1; Length 400;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 6  
 ID HOFC\_ECOLI STANDARD; PRT; 400 AA.  
 AC P36646; P75648;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Protein transport protein hoFC.  
 GN HOFC OR HOFC OR B0106.  
 OS *Escherichia coli*.  
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
 OC *Escherichia*.  
 OX NCBI\_TaxID=562;  
 RX [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-K12;  
 RX MEDLINE-95047556; PubMed-7959070;  
 RA Whitchurch C.B., Mattick J.S.;  
 RT "*Escherichia coli* contains a set of genes homologous to those  
 RT involved in protein secretion, DNA uptake and the assembly of type-4  
 RT fimbriae in other bacteria.";  
 RL Gene 150:9-15(1994).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-K12 / W3110;

RESULT 7  
 ID GTR8\_BOVIN STANDARD; PRT; 334 AA.  
 AC P58354;  
 DT 15-JUN-2002 (Rel. 41, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Solute carrier family 2, facilitated glucose transporter, member 8  
 DE (Glucose transporter type 8) (Glucose transporter type XI) (Fragment).  
 GN SLC2A8 OR GLUT8 OR GLUTX1.  
 OS *Bos taurus* (Bovine).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-21482567; PubMed-11599048;  
 RA Augustin R., Focar P., Navarrete-Santos A., Wrenzycki C., Gandolfi F.,  
 RA Niemann H., Fischer B.;  
 RT "Glucose transporter expression is developmentally regulated in in  
 RT vitro derived bovine preimplantation embryos.";  
 RL Mol. Reprod. Dev. 60:370-376(2001)  
 CC -1- FUNCTION: Insulin-regulated facilitative glucose transporter.  
 CC Binds cytochalasin B in a glucose-inhibitable manner. Seems to be  
 CC a dual-specific sugar transporter as it is inhibitable by  
 CC fructose (by similarity).  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Principally  
 CC intracellular. May move between intracellular vesicles and the  
 CC plasma membrane. The dileucine internalization motif is critical  
 CC for intracellular sequestration (by similarity).  
 CC SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY. GLUCOSE  
 CC TRANSPORTERS SUBFAMILY.  
 CC -----  
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 CC -----  
 DR EMBL: AF21324; AKK69606.1; -  
 DR InterPro: IPR003662; sub\_transporter.  
 DR Pfam: PF00083; sugar\_tr; 1.  
 DR PROSITE: PS00216; SUGAR\_TRANSPORT\_1; 1.  
 DR PROSITE: PS00217; SUGAR\_TRANSPORT\_2; PARTIAL.  
 KW Transport; Sugar transport; Transmembrane; Multigene family.  
 FT NON\_TER 1 1  
 FT DOMAIN 1 14  
 FT TRANSMEM 15 35  
 FT DOMAIN 36 38  
 FT TRANSMEM 39 59  
 FT DOMAIN 60 113  
 FT TRANSMEM 114 134  
 FT DOMAIN 135 149  
 FT TRANSMEM 150 170  
 FT DOMAIN 171 176  
 FT TRANSMEM 177 197  
 FT DOMAIN 198 224  
 FT TRANSMEM 225 245  
 FT DOMAIN 246 261  
 FT TRANSMEM 262 282  
 FT DOMAIN 283 295  
 FT TRANSMEM 296 316  
 FT DOMAIN 317 334  
 FT SEQUENCE 334 AA; 36699 MW; 0EE9B670ADAB71DD CRC64;  
 Query Match 87.2%; Score 34; DB 1; Length 334;  
 Best Local Similarity 83.3%; Pred. No. 1.3e+02;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

DE Solute carrier family 2, facilitated glucose transporter, member 8  
 DE (Glucose transporter type 8) (Glucose transporter type X1).  
 GN SLC2A8 OR GLUT8 OR GLUTX1.  
 OS Homo sapiens (human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RP TISSUE=Testis;  
 RX MEDLINE-20283667; PubMed-10821868;  
 RA Doerge H., Schuermann A., Bahrenberg G., Brauers A., Joost H.-G.;  
 RT "GLUT8, a novel member of the sugar transport facilitator family with  
 RT glucose transport activity.";  
 RL J. Biol. Chem. 275:16275-16280(2000).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-20138191; PubMed-10671487;  
 RA Ibberson M.R., Uldry M.A., Thorens B.;  
 RT "GLUTX1, a novel mammalian glucose transporter expressed in the  
 RT central nervous system and insulin-sensitive tissues.";  
 RL J. Biol. Chem. 275:4607-4612(2000).  
 CC -1- FUNCTION: Insulin-regulated facilitative glucose transporter.  
 CC Binds cytochalasin B in a glucose-inhibitable manner. Seems to be  
 CC a dual-specific sugar transporter as it is inhibitable by  
 CC fructose (by similarity).  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Principally  
 CC intracellular. May move between intracellular vesicles and the  
 CC plasma membrane. The dileucine internalization motif is critical  
 CC for intracellular sequestration (by similarity).  
 CC -1- TISSUE SPECIFICITY: Highly expressed in testis, but not in  
 CC testicular carcinoma. Lower amounts present in most other tissues.  
 CC -1- INDUCTION: In testis, downregulated by estrogen.  
 CC SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY. GLUCOSE  
 CC TRANSPORTERS SUBFAMILY.  
 CC -----  
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 CC -----  
 DR EMBL: Y17801; CAB89809.1; -  
 DR EMBL: AJ245937; CAB75702.1; -  
 DR Genew; HGNC:13812; SLC2A8.  
 DR MIM: 605245; -  
 DR InterPro: IPR003663; CHO\_transport.  
 DR InterPro: IPR003662; sub\_transporter.  
 DR Pfam: PF00083; sugar\_tr; 1.  
 DR PRINTS: PR00171; SUGARTRANSPORT.  
 DR TIGRPSMs: TIGR00879; SP; 1.  
 DR PROSITE: PS00216; SUGAR\_TRANSPORT\_1; 2.  
 DR PROSITE: PS00217; SUGAR\_TRANSPORT\_2; 1.  
 KW Transport; Sugar transport; Transmembrane; Glycoprotein;  
 KW Multigene family.  
 FT DOMAIN 1 25  
 FT TRANSMEM 26 46  
 FT DOMAIN 47 70  
 FT TRANSMEM 71 91  
 FT TRANSMEM 92 96  
 FT TRANSMEM 97 117  
 FT TRANSMEM 118 127  
 FT TRANSMEM 128 148  
 FT TRANSMEM 149 156  
 FT TRANSMEM 157 177  
 FT TRANSMEM 178 182  
 FT TRANSMEM 183 203  
 FT TRANSMEM 204 256  
 FT TRANSMEM 257 277  
 FT TRANSMEM 278 292  
 FT TRANSMEM 293 313  
 FT SEQUENCE 313 AA; 36699 MW; 0EE9B670ADAB71DD CRC64;  
 Query Match 87.2%; Score 34; DB 1; Length 334;  
 Best Local Similarity 83.3%; Pred. No. 1.3e+02;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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FT DOMAIN 314 319 CYTOPLASMIC (POTENTIAL).
FT TRANSNM 320 340 9 (POTENTIAL).
FT DOMAIN 341 367 EXTRACELLULAR (POTENTIAL).
FT TRANSNM 368 388 10 (POTENTIAL).
FT DOMAIN 389 404 CYTOPLASMIC (POTENTIAL).
FT TRANSNM 405 425 11 (POTENTIAL).
FT DOMAIN 426 438 EXTRACELLULAR (POTENTIAL).
FT TRANSNM 439 459 12 (POTENTIAL).
FT DOMAIN 460 477 CYTOPLASMIC (POTENTIAL).
FT SITE 12 DILEUCINE INTERNALIZATION MOTIF (BY
SITE 13 SIMILARITY).
FT CARBOHD 349 349 N-LINKED (GLCNAC. . .) (BY SIMILARITY).
FT CONFLICT 377 377 S -> N (IN REF. 2).
FT CONFLICT 456 457 FS -> LF (IN REF. 2).
FT CONFLICT 462 462 T -> I (IN REF. 2).
SQ SEQUENCE 477 AA; 50792 MW; 0B480F94B40AE76 CRC64;

Query Match 87.2%; Score 34; DB 1; Length 477;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LEWSML 6
Db 179 LEWRML 184

RESULT 9
GTR8_MOUSE STANDARD: PRF: 477 AA.
ID GTR8_MOUSE
AC 09JFE3; 09JF4; 09JF20;
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Solute carrier family 2, facilitated glucose transporter, member 8
DE (Glucose transporter type 8) (Glucose transporter type XI).
GN SLC2A8 OR GLUT8 OR GLUTX1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20138191; PubMed=10671487;
RA Ibberson M.R., Didry M.A., Thorens B.;
RT "GLUTX1, a novel mammalian glucose transporter expressed in the
RT central nervous system and insulin-sensitive tissues.";
RL J. Biol. Chem. 275:4607-4612(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX TISSUE-Testis;
RX MEDLINE=20283667; PubMed=10821868;
RA Doege H., Schuetzmann A., Bahrenberg C., Brauers A., Joost H.-G.;
RT "GLUT8, a novel member of the sugar transport facilitator family with
RT glucose transport activity.";
RL J. Biol. Chem. 275:16275-16280(2000).
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN=129; TISSUE=Embryonic carcinoma;
RX MEDLINE=20319023; PubMed=10860996;
RA Carayannopoulos M.O., Chi M.M.-Y., Cui Y., Plingsterhaus J.M.,
RA McInight R.A., Mueckler M., Devaskar S.U., Moley K.H.;
RT "GLUT8 is a glucose transporter responsible for insulin-stimulated
RT glucose uptake in the blastocyst.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:7313-7318(2000).
RN [4]
RP SEQUENCE FROM N.A.
RX STRAIN=129/Ola; TISSUE=Spleen;
RX MEDLINE=21547794; PubMed=11689004;
RA Scheepers A., Doege H., Joost H.-G., Schuetzmann A.;
RT "Mouse GLUT8: genomic organization and regulation of expression in
RT 3T3-L1 adipocytes by glucose.";
RL Biochem. Biophys. Res. Commun. 288:969-974(2001).
CC -1- FUNCTION: Insulin-regulated facilitative glucose transporter.

```

```

CC CC Binds cytochlaasin B in a glucose-inhibitable manner. Seems to be
CC CC a dual-specific sugar transporter as it is inhibitable by
CC CC fructose.
CC CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Principally
CC CC intracellular. May move between intracellular vesicles and the
CC CC plasma membrane. The dileucine internalization motif is critical
CC CC for intracellular sequestration (By similarity). Insulin induces a
CC CC change in the intracellular localization and gives rise to
CC CC insertion in the plasma membrane.
CC CC -1- TISSUE SPECIFICITY: Highest level of expression in placenta and
CC CC testis. Highly expressed in adult and pubertal testis, but not
CC CC prepubertal testis. Lower levels of expression in brain, liver,
CC CC heart, kidney, fat and skeletal muscle.
CC CC -1- DEVELOPMENTAL STAGE: High expression in blastocysts.
CC CC -1- INDUCTION: Inhibited under glucose deprivation.
CC CC -1- SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY. GLUCOSE
CC CC TRANSPORTERS SUBFAMILY.
CC CC -----
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CC CC -----
DR EMBL; AJ245936; CAB75719.1; -
DR EMBL; Y17802; CAB89815.1; -
DR EMBL; AF232061; AAF78366.1; -
DR EMBL; AJ413951; CAC88690.1; -
DR MGD; MGI:1860103; SLC2A8.
DR InterPro; IPR003663; CHO_transport.
DR InterPro; IPR003662; sub_transporter.
DR Pfam; PF00083; sugar_tr.1.
DR PRINTS; PR00171; SUGRTNSPORT.
DR TIGRFAMs; TIGR00879; SP.1.
DR PROSITE; PS00216; SUGAR_TRANSPORT_1; 1.
DR PROSITE; PS00217; SUGAR_TRANSPORT_2; 1.
DR KMW Multigene family.
FT FT DOMAIN 1 25
FT FT TRANSNM 26 46
FT FT DOMAIN 47 70
FT FT TRANSNM 71 91
FT FT DOMAIN 92 96
FT FT TRANSNM 97 117
FT FT DOMAIN 118 127
FT FT TRANSNM 128 148
FT FT DOMAIN 149 156
FT FT TRANSNM 157 177
FT FT DOMAIN 178 182
FT FT TRANSNM 183 203
FT FT DOMAIN 204 257
FT FT TRANSNM 258 278
FT FT DOMAIN 279 293
FT FT TRANSNM 294 314
FT FT DOMAIN 315 320
FT FT TRANSNM 321 341
FT FT DOMAIN 342 367
FT FT TRANSNM 368 388
FT FT DOMAIN 389 404
FT FT TRANSNM 405 425
FT FT DOMAIN 426 438
FT FT TRANSNM 439 459
FT FT DOMAIN 460 477
FT FT SITE 12 13
FT FT CARBOHD 350 350
FT FT CONFLICT 39 39
FT FT CONFLICT 94 94
FT FT CONFLICT 429 429
SQ SEQUENCE 477 AA; 51523 MW; A3753FB34E52F5A CRC64;

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 CC -----  
 DR EMBL: AF083977; AAF01107.1; -  
 DR SEQUENCE 512 AA; 56888 MW; 35E1B99373DCFC36 CRC64;

Query Match 84.6%; Score 33; DB 1; Length 512;  
 Best Local Similarity 66.7%; Pred. No. 2.6e+02;  
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 LEWSML 6  
 DB 139 LEWSML 144

## RESULT 12

TDRL\_HUMAN STANDARD: PRT: 777 AA.

AC Q9BX74; Q9H7B3; (Rel. 41, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Tudor domain containing protein 1.  
 GN TDRD1.

OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_Taxid=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RC TISSUE-Testis;  
 RX MEDLINE-21175748; PubMed-11279525;

RA Wang P.J., McCarrey J.R., Yang F., Page D.C.;  
 RL "An abundance of X-linked genes expressed in spermatogonia.";  
 Nat. Genet. 27:422-426(2001).

RT [2]  
 RP SEQUENCE OF 67-777 FROM N.A.

RA Kanakami T., Noguchi S., Itoh T., Shigeta K., Senba T., Matsumura K.,  
 RA Nakajima Y., Mizuno T., Morinaga M., Tanigami A., Fujiwara T., Ono T.,  
 RA Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y., Ota T., Suzuki Y.,  
 RA Obayashi M., Nishi T., Shibahara T., Tanaka T., Nakamura Y.,  
 RA Isoqal T., Sugano S.;

RT "NEDO human cDNA sequencing project.";  
 RL Submitted (AUG-2000) to the EMBL/Genbank/DBJ databases.

CC -1- TISSUE SPECIFICITY: Testis and ovary specific.  
 CC -1- SIMILARITY: CONTAINS 3 TUDOR DOMAINS.

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 CC -----

DR EMBL: AF285506; AAK31985.1; -  
 DR EMBL: AK024735; BAB14962.1; -  
 DR Genew; HGNC:11712; TDRD1.

DR MIM; 605796; -  
 DR InterPro; IPR001097; Maternal\_tudor.

DR InterPro; IPR002999; Tudor.

DR Pfam; PF00567; TUDOR; 6.  
 DR SMART; SM00333; TUDOR; 3.  
 DR PROSITE; PS50304; TUDOR; 3.

DR Repeat.  
 KW Repeat.

FT DOMAIN 138 197 TUDOR 1.  
 FT DOMAIN 359 418 TUDOR 2.  
 FT DOMAIN 587 645 TUDOR 3.

FT CONFLICT 737 737 T -> M (IN REF. 2).  
 FT CONFLICT 775 777 VKS -> KKKK (IN REF. 2).

SO SEQUENCE 777 AA; 86762 MW; A733E803D76A8EC CRC64;

Query Match 84.6%; Score 33; DB 1; Length 777;  
 Best Local Similarity 66.7%; Pred. No. 3.8e+02;  
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 LEWSML 6  
 DB 300 LEWTRV 305

## RESULT 13

TDRL\_MOUSE STANDARD: PRT: 928 AA.

AC Q99WV1; (Rel. 41, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Tudor domain containing protein 1.  
 GN TDRD1.

OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_Taxid=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RC TISSUE-Testis; and Ovary;  
 RX MEDLINE-21175748; PubMed-11279525;

RA Wang P.J., McCarrey J.R., Yang F., Page D.C.;  
 RL "An abundance of X-linked genes expressed in spermatogonia.";  
 Nat. Genet. 27:422-426(2001).

RT -1- TISSUE SPECIFICITY: Testis and ovary specific.  
 CC -1- SIMILARITY: CONTAINS 4 TUDOR DOMAINS.

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 CC -----

DR EMBL: AF285591; AAK31970.1; -  
 DR MGD; MGI:1933218; Tdrd1.

DR InterPro; IPR001097; Maternal\_tudor.

DR InterPro; IPR002999; Tudor.

DR Pfam; PF00567; TUDOR; 4.  
 DR SMART; SM00333; TUDOR; 4.  
 DR PROSITE; PS50304; TUDOR; 4.

DR Repeat.

FT DOMAIN 63 123 TUDOR 1.  
 FT DOMAIN 292 351 TUDOR 2.  
 FT DOMAIN 512 571 TUDOR 3.  
 FT DOMAIN 738 796 TUDOR 4.

SO SEQUENCE 928 AA; 103050 MW; 9CCFDBA3AF671AF CRC64;

Query Match 84.6%; Score 33; DB 1; Length 928;  
 Best Local Similarity 66.7%; Pred. No. 4.5e+02;  
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 LEWSML 6  
 DB 453 LEWTRV 458

## RESULT 14

TDRL\_HUMAN STANDARD: PRT: 1698 AA.

AC Q14999; (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Hypothetical protein KIAA0076 (HA0936).

GN KIAA0076.  
 OS Homo sapiens (Human).

OY 2 EWSWL 6  
 Db 56 EWSWL 60  
 Search completed: May 30, 2003, 15:48:53  
 Job time : 4.11842 secs

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-Bone marrow;  
 RX MEDLINE=96051398; PubMed=7584044;  
 RA Nomura N., Nagase T., Miyajima N., Sazuka T., Tanaka A., Sato S.,  
 RA Seki N., Kawarabayashi Y., Ishikawa K.-I., Tabata S.;  
 RT Prediction of the coding sequences of unidentified human genes. II.  
 RT The coding sequences of 40 new genes (KIA0041-KIA0080) deduced by  
 RT analysis of cDNA clones from human cell line KG-1.";  
 RL DNA Res. 1:223-229(1994).  
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 CC -----  
 DR EMBL: D38548; BAA07551.1; -  
 DR SMART: SM00182; CULIN; 1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 1698 AA; 19118 MW; 57B1CC478E3EEDA CRC64;  
 OY 1 LEWSWL 6  
 Db 1446 LQMTWL 1451  
 Query Match 84.6%; Score 33; DB 1; Length 1698;  
 Best local Similarity 66.7%; Pred. No. 7.8e+02;  
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 RESULT 15  
 VG41\_BPM15  
 ID VG41\_BPM15 STANDARD; PRT; 83 AA.  
 AC 005252;  
 DT 01-FEB-1994 (Rel. 28, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 01-FEB-1994 (Rel. 28, Last annotation update)  
 DE Gene 41 protein (GP41).  
 GN 41.  
 OS Mycobacteriophage L5.  
 OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;  
 OC L5-like viruses.  
 OX NCBI\_TaxID=31757;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=93211282; PubMed=8459766;  
 RA Hatfull G.F., Sarkis G.J.;  
 RT "DNA sequence, structure and gene expression of mycobacteriophage L5:  
 RT a phage system for mycobacterial genetics.";  
 RL Mol. Microbiol. 7:395-405(1993).  
 CC -----  
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 CC -----  
 DR EMBL: Z18946; CAA79417.1; -  
 DR PIR: S30986; S30986.  
 SQ SEQUENCE 83 AA; 9803 MW; 99619949074898B6 CRC64;  
 Query Match 82.1%; Score 32; DB 1; Length 83;  
 Best local Similarity 80.0%; Pred. No. 68;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;



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OM protein - protein search, using sw model

Run on: May 30, 2003, 14:32:11 ; Search time 14.7632 Seconds

(without alignments)  
83.741 Million cell updates/sec

Title: US-09-643-260-8

Perfect score: 39

Sequence: 1 LEWSWL 6

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08

Maximum Match 1008

Listing first 45 summaries

Database :

SPREMBL.21.\*  
1: sp\_archaea.\*  
2: sp\_bacteria.\*  
3: sp\_fungi.\*  
4: sp\_human.\*  
5: sp\_invertebrate.\*  
6: sp\_mammal.\*  
7: sp\_mhc.\*  
8: sp\_organelle.\*  
9: sp\_phage.\*  
10: sp\_plant.\*  
11: sp\_rodent.\*  
12: sp\_virus.\*  
13: sp Vertebrate.\*  
14: sp\_unclassified.\*  
15: sp\_rvirus.\*  
16: sp\_bacteriap.\*  
17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	36	92.3	544	10	Q9FEEL
2	36	92.3	645	8	Q63620
3	36	92.3	740	6	Q95KV1
4	36	92.3	756	6	Q95KV0
5	36	92.3	1201	5	Q9V045
6	35	89.7	48	16	Q8VK82
7	35	89.7	173	17	Q9HNP7
8	35	89.7	196	13	Q9YH31
9	35	89.7	276	2	Q47020
10	35	89.7	311	5	Q94380
11	35	89.7	371	5	Q25333
12	35	89.7	387	16	Q8YFW8
13	35	89.7	391	16	Q8YFW8
14	35	89.7	469	10	Q8XN31
15	35	89.7	481	11	Q8VCV5
16	35	89.7	512	5	Q9GY84

17	35	89.7	512	5	Q9GY14	Q9GY14 leishmania
18	35	89.7	522	10	Q9S513	Q9S513 arabidopsis
19	35	89.7	547	5	Q9GY86	Q9GY86 leishmania
20	35	89.7	560	5	Q9N752	Q9N752 leishmania
21	35	89.7	604	4	Q9V475	Q9V475 homo sapien
22	35	89.7	645	2	Q69315	Q69315 thermus sp.
23	35	89.7	683	4	Q96D07	Q96D07 homo sapien
24	35	89.7	760	5	Q9GYA8	Q9GYA8 leishmania
25	35	89.7	823	5	Q8S000	Q8S000 encephalito
26	35	89.7	1345	16	Q9L060	Q9L060 streptomyc
27	35	89.7	1367	16	Q9PPR8	Q9PPR8 ureaplasma
28	35	89.7	1379	13	P79701	P79701 colurnix co
29	35	89.7	1591	3	Q9HFW1	Q9HFW1 ashuya goss
30	35	89.7	2054	5	Q9G213	Q9G213 caenorhabdi
31	34	87.2	116	2	Q68039	Q68039 rhodobacter
32	34	87.2	135	2	Q05744	Q05744 mycobacteri
33	34	87.2	248	4	Q8WZ05	Q8WZ05 mus sapien
34	34	87.2	295	5	Q9VTL8	Q9VTL8 drosophila
35	34	87.2	321	5	Q94515	Q94515 drosophila
36	34	87.2	335	16	Q07175	Q07175 mycobacteri
37	34	87.2	395	17	Q97V10	Q97V10 sulfolobus
38	34	87.2	398	16	P74568	P74568 synechocyst
39	34	87.2	473	11	Q9D814	Q9D814 mus musculu
40	34	87.2	473	11	Q99125	Q99125 mus musculu
41	34	87.2	477	4	Q8W029	Q8W029 mus sapien
42	34	87.2	533	17	Q96VX5	Q96VX5 sulfolobus
43	34	87.2	685	5	Q24488	Q24488 drosophila
44	34	87.2	919	16	Q9S124	Q9S124 streptomyc
45	34	87.2	1139	16	Q8ZC91	Q8ZC91 yersinia pe

#### ALIGNMENTS

RESULT 1	ID	Q9FEEL	PRELIMINARY:	PRT:	544 AA.
AC	Q9FEEL				
DT	01-MAR-2001	(TREMBLrel. 16, Created)			
DT	01-MAR-2001	(TREMBLrel. 16, Last sequence update)			
DT	01-MAR-2002	(TREMBLrel. 20, Last annotation update)			
DE	Putative cytochrome P450.				
GN	P06880.9 OR P006C01.24.				
OS	Oryza sativa (Rice).				
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
OC	Spermatophyta; Magnoliopsida; Liliopsida; Poales; Poaceae;				
OC	Ehrhartoideae; Oryzaceae; Oryza.				
OX	NCBI_TaxID=4530;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=CV. NIPPONBARE;				
RA	Sasaki T., Matsumoto T., Yamamoto K.;				
RT	"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC				
RT	clone:P06880.4."				
RL	Submitted (Aug-2000) to the EMBL/GenBank/DBJ databases.				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=CV. NIPPONBARE;				
RA	Sasaki T., Matsumoto T., Yamamoto K.;				
RT	"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC				
RT	clone:P006C01."				
RL	Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.				
CC	-1- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.				
DR	EMBL: AP002839; BAB19103.1; -				
DR	EMBL: AP002744; BAB19082.1; -				
DR	InterPro: IPR001128; Cytochrome_P450.				
DR	Pfam: PF00067; P450.1.				
DR	PRINTS: PR00385; P450.				
DR	PROSITE: PS00086; CYTOCHROME_P450; UNKNOWN_1.				
KW	Heme; Monooxygenase; Oxidoreductase.				
SO	SEQUENCE 544 AA; 60867 MW; 273EAF5968D1A024 CRC64;				
	Query Match	92.38;	Score 36;	DB 10;	Length 544;

Best Local Similarity 83.3%; Pred. No. 3.9e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LEWSWL 6  
|||||  
Db 48 LEWSWL 53

## RESULT 2

063620 PRELIMINARY; PRT; 645 AA.

AC 063620:  
DT 01-AUG-1998 (TREMBlrel. 07, Created)  
DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)  
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)  
DE NADH dehydrogenase subunit 5.  
OS Balanoglossus carnosus.  
OG Mitochondrion.  
OC Eukaryota; Metazoa; Hemichordata; Enteropneusta; Pylchoderidae;  
OC Balanoglossus.  
OX NCBI\_TaxID=35080;  
RN [1]  
RP MEDLINE=99016090; PubMed=9799263;  
RX Castresana J., Feldmaier-Fuchs G., Yokobori S., Satoh N., Paabo S.;  
RT "The mitochondrial genome of the hemichordate Balanoglossus carnosus  
and the evolution of deuterostome mitochondria.";  
RL Genetics 150:1115-1123(1998).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98188267; PubMed=9520430;  
RA Castresana J., Feldmaier-Fuchs G., Paabo S.;  
RT "Codon reassigment and amino acid composition in hemichordate  
mitochondria.";  
RL Proc. Natl. Acad. Sci. U.S.A. 95:3703-3707(1998).  
RN [3]  
RP SEQUENCE FROM N.A.  
RA Castresana J., Feldmaier-Fuchs G., Paabo S.;  
RL Submitted (FEB-1998) to the EMBL/Genbank/DBJ databases.  
CC -1- CATALYTIC ACTIVITY: NADH + UBIQUINONE - NAD(+) + UBIQUINOL.  
DR EMBL; AF051097; AAD11945.1; -  
DR InterPro: IPR003916; NADH\_oxred5.  
DR InterPro: IPR001750; Oxidored\_q1.  
DR InterPro: IPR001516; Oxidored\_q1\_N.  
DR Pfam; PF00361; Oxidored\_q1; 1.  
DR Pfam; PF00662; Oxidored\_q1\_N; 1.  
DR PRINTS; PR01434; NADHDMGNASES.  
KW Mitochondrion; NAD; Oxidoreductase; Ubiquinone.  
SQ SEQUENCE 645 AA; 69455 MW; C8A498941B61F392 CRC64;

Query Match 92.3%; Score 36; DB 8; Length 645;  
Best Local Similarity 83.3%; Pred. No. 4.6e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LEWSWL 6  
|||||  
Db 96 LEWSWL 101

## RESULT 3

095KVL PRELIMINARY; PRT; 740 AA.

AC 095KVL:  
DT 01-DEC-2001 (TREMBlrel. 19, Created)  
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)  
DE IKB kinase-alpha.  
GN BIKKALPHA.  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Cranialia; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovidae; Bovinae; Bos.  
OX NCBI\_TaxID=9913;

RN [1]  
RP SEQUENCE FROM N.A.  
RA Rottenberg S., Dobbelaere D.A.E., Heussler V.T.;  
RT "Identification and characterisation of the bovine IKB kinases (IKKS)  
alpha, beta and gamma.";  
RL Submitted (SEP-2001) to the EMBL/Genbank/DBJ databases.  
DR EMBL; AJ414535; CAC93686.1; -  
DR InterPro: IPR000719; Euk\_pkinase.  
DR InterPro: IPR002290; Ser\_thr\_pkinase.  
DR InterPro: IPR001245; Tyr\_pkinase.  
DR Pfam; PF00069; pkinase; 1.  
DR ProDom; PD000001; Euk\_pkinase; 1.  
DR SMART; SM00219; Tyrc; 1.  
DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; UNKNOWN\_1.  
DR PROSITE; PS00011; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; UNKNOWN\_1.  
KW ATP-binding; Kinase; Transferase.  
SQ SEQUENCE 740 AA; 84343 MW; 01903BE11F44D176 CRC64;

Query Match 92.3%; Score 36; DB 6; Length 740;  
Best Local Similarity 83.3%; Pred. No. 5.3e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LEWSWL 6  
|||||  
Db 733 LEWSWL 738

## RESULT 4

095KVO PRELIMINARY; PRT; 756 AA.

AC 095KVO:  
DT 01-DEC-2001 (TREMBlrel. 19, Created)  
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)  
DE IKB kinase-beta.  
GN BIKKBEA.  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Cranialia; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovidae; Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Rottenberg S., Dobbelaere D.A.E., Heussler V.T.;  
RT "Identification and characterisation of the bovine IKB kinases (IKKS)  
alpha, beta and gamma.";  
RL Submitted (SEP-2001) to the EMBL/Genbank/DBJ databases.  
DR EMBL; AJ414536; CAC93687.1; -  
DR InterPro: IPR000719; Euk\_pkinase.  
DR InterPro: IPR002290; Ser\_thr\_pkinase.  
DR InterPro: IPR001245; Tyr\_pkinase.  
DR Pfam; PF00069; pkinase; 1.  
DR ProDom; PD000001; Euk\_pkinase; 1.  
DR SMART; SM00219; Tyrc; 1.  
DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; UNKNOWN\_1.  
DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; UNKNOWN\_1.  
KW ATP-binding; Kinase; Transferase.  
SQ SEQUENCE 756 AA; 86647 MW; A072D15614A176E5 CRC64;

Query Match 92.3%; Score 36; DB 6; Length 756;  
Best Local Similarity 83.3%; Pred. No. 5.4e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LEWSWL 6  
|||||  
Db 737 LEWSWL 742

## RESULT 5

09YQ45 PRELIMINARY; PRT; 1201 AA.

AC 09YQ45:

DT 01-MAY-2000 (TReMBLrel. 13, Created)  
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)  
 DE 01-DEC-2001 (TReMBLrel. 19, Last annotation update)  
 DE CG15622 protein.  
 GN CG15622.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 NCBI\_Taxid=7227;  
 [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BERKELEY;  
 RX MEDLINE=20196006; PubMed=10731132;  
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.H.C., Blazer R.G., Champe M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
 RA Abiril J.F., Adayani A., An H.-J., Andrews-Planckoch C., Baldwin D.,  
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S.,  
 RA Borokova D., Botchan M.R., Bouck J., Brockstein P., Bottler P.,  
 RA Burtis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
 RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasse K.,  
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris N.,  
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
 RA Jallali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kuip D., Lai Z.,  
 RA Lasmo P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Mishina N.V., Modyr C., Morris J., Mostrel A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,  
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Sanders R.D.C., Scheeler F., Shen T.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spiralling A.C., Stapleton M., Strong R., Sun E.,  
 RA Switskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of *Drosophila melanogaster*.";  
 RL Science 287:2185-2195(2000).  
 DR EMBL: AE003585; AAF51336.1; -  
 DR Flybase: FBgn0031366; CG15622.  
 DR InterPro: IPR004245; DUF229.  
 DR Pfam: PF02995; DUF229; 1.  
 SQ SEQUENCE 1201 AA; 138974 MW; CA25AD8DF8B42EE CRC64;

Query Match 92.3%; Score 36; DB 5; Length 1201;  
 Best Local Similarity 83.3%; Pred. No. 8.7e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 EWSML 6  
 DB 57 EWSML 62

RESULT 6  
 ID Q8VRB2 PRELIMINARY; PRT; 48 AA.  
 AC Q8VRB2;  
 DT 01-MAR-2002 (TReMBLrel. 20, Created)  
 DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)

DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)  
 DE Hypothetical protein MT0946.  
 GN MT0946.  
 OS Mycobacterium tuberculosis.  
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteriales;  
 OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.  
 NCBI\_Taxid=1773;  
 [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CDC 1551 / OSHKOSH;  
 RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,  
 RA Peterson J., DeBoy R., Dodson R., Gwim M.L., Hatt D., Hickey E.,  
 RA Kolonay J.F., Nelson W.C., Umayam L.A., Esmolaeva M.D., Salzberg S.T.,  
 RA Delcher A., Uitterback T., Weidman J., Khouri H., Gill J., Mikula A.,  
 RA Bishai W.;  
 RT "Whole genome comparison of *Mycobacterium tuberculosis* clinical and  
 RT laboratory strains";  
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AE006980; AAK45193.1; -  
 DR TIGR: MT0946; -  
 KW Hypothetical protein.  
 SQ SEQUENCE 48 AA; 5265 MW; C0BFA9D6AA2EF8DF CRC64;

Query Match 89.7%; Score 35; DB 16; Length 48;  
 Best Local Similarity 100.0%; Pred. No. 47;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 EWSML 6  
 DB 14 EWSML 18

RESULT 7  
 ID Q9HNP7 PRELIMINARY; PRT; 173 AA.  
 AC Q9HNP7;  
 DT 01-MAR-2001 (TReMBLrel. 16, Created)  
 DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)  
 DE Vng6292C.  
 GN Vng6292C.  
 OS Halobacterium sp. (strain NRC-1).  
 OC Archaea; Euryarchaeota; Halobacteria; Halobacteriales;  
 OC Halobacteriaceae; Halobacterium.  
 NCBI\_Taxid=64091;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20504463; PubMed=11016950;  
 RA Ng W.V., Kennedy S.P., Mahalingam G.G., Bergquist B., Pan M.,  
 RA Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Shrogha J.,  
 RA Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,  
 RA Leitauer B., Keller K., Cruz R., Danson M.J., Hough D.W.,  
 RA Maddocks D.G., Jablonski P.E., Krebs M.P., Angelvine C.M., Dale H.,  
 RA Iseubarger T.A., Peck R.F., Pohlenschoder M., Spudis J.L., Jung K.-H.,  
 RA Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,  
 RA Ehardt H., Lowe T.M., Liang P., Riley M., Hood L., Dassarma S.;  
 RT "Genome sequence of *Halobacterium* species NRC-1";  
 RL Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).  
 DR EMBL: AE005159; MAG20929.1; -  
 DR InterPro: IPR001584; Rve.  
 DR Pfam: PF00665; Irv1; 1.  
 KW Plasmid; Complete proteome.  
 SQ SEQUENCE 173 AA; 20267 MW; E8E02EDC76ED4371 CRC64;

Query Match 89.7%; Score 35; DB 17; Length 173;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 EWSML 6  
 DB 42 EWSML 46

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RESULT 8
OYH31 ID OYH31 PRELIMINARY: PRT: 196 AA.
AC OYH31:
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Putative fibroblast growth factor-4.
OS Notophthalmus viridescens (Eastern newt) (Triturus viridescens).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Caudata; Salamandroides; Salamandridae;
OC Notophthalmus.
OX NCBI_TaxID=8316;
RN [1]
RP SEQUENCE FROM N.A.
RA Wei Y.;
RT "Putative Newt Fibroblast Growth Factor-4."
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: U76598; AAC98812.1; -.
DR HSSP: P09038; 1BFF.
DR InterPro: IPR001064; Crystal1in.
DR InterPro: IPR002209; HB/F_growthfact.
DR InterPro: IPR002348; IL1_HBGF.
DR Pfam: PF00167; EGF_1.
DR PRINTS: PR00262; IL1HBGF.
DR ProDom: PD000831; HB/F_growthfact; 1.
DR SMART: SM00442; EGF_1.
DR PROSITE: PS00225; CRYSTALLIN_BETAGAMMA; UNKNOWN_1.
DR PROSITE: PS00247; HBGF_EGF_1.
DR SEQUENCE 196 AA; 22033 MW; AC4688CD989CCEAF CR64;

Query Match 89.7%; Score 35; DB 13; Length 196;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LEMSW 5
DB 37 LEMSW 41

RESULT 9
O47020 ID O47020 PRELIMINARY: PRT: 276 AA.
AC O47020:
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE 'orf'.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-K-12;
RC MEDLINE-82059454; PubMed-6272196;
RX An G., Bendisk D.S., Mamelek L.A., Friesen J.D.;
RT "Organization and nucleotide sequence of a new ribosomal operon in
RT Escherichia coli containing the genes for ribosomal proteins S2 and
RT elongation factors Ts."
RL Nucleic Acids Res. 9:4163-4172(1981).
RN [2]
RP SEQUENCE FROM N.A.
RA STRAIN-K-12;
RC MEDLINE-83209630; PubMed-6343085;
RX Stephens P.E., Darlison M.G., Lewis H.M., Guest J.R.;
RT "The pyruvate dehydrogenase complex of Escherichia coli K12.
RT Nucleotide sequence encoding the pyruvate dehydrogenase component."
RL Eur. J. Biochem. 133:155-162(1983).
RN [3]
RP SEQUENCE FROM N.A.
RA STRAIN-K-12;
RX MEDLINE-83234434; PubMed-6345153;
RA Stephens P.E., Darlison M.G., Lewis H.M., Guest J.R.;
RT "The pyruvate dehydrogenase complex of Escherichia coli K12.
RT Nucleotide sequence encoding the dihydrolipoamide acetyltransferase
RT component."
RL Eur. J. Biochem. 133:481-489(1983).
RN [4]
RP SEQUENCE FROM N.A.
RA STRAIN-K-12;
RC MEDLINE-84004369; PubMed-6352260;
RX Stephens P.E., Lewis H.M., Darlison M.G., Guest J.R.;
RT "Nucleotide sequence of the liponamide dehydrogenase gene of
RT Escherichia coli K12."
RL Eur. J. Biochem. 135:519-527(1983).
RN [5]
RP SEQUENCE FROM N.A.
RA STRAIN-K-12;
RC MEDLINE-85054973; PubMed-6094577;
RA Richard C., Richard F., Martin C., Haziza C., Patte J.C.;
RT "Regulation of expression and nucleotide sequence of the Escherichia
RT coli dapd gene."
RL J. Biol. Chem. 259:14824-14828(1984).
RN [6]
RP SEQUENCE FROM N.A.
RA STRAIN-K-12;
RC MEDLINE-85127060; PubMed-3882429;
RX Broome-Smith J.K., Edelman A., Youself S., Spratt B.G.;
RT "The nucleotide sequences of the ponA and ponB genes encoding
RT penicillin-binding proteins 1A and 1B of Escherichia coli K12."
RL Eur. J. Biochem. 147:437-446(1985).
RN [7]
RP SEQUENCE FROM N.A.
RA STRAIN-K-12;
RC MEDLINE-86085668; PubMed-3079747;
RX Coulton J.W., Mason P., Cameron D.R., Carmel G., Jean R., Rode H.N.;
RT "Protein fusions of beta-galactosidase to ferrichrome-iron receptor of
RT Escherichia coli K-12."
RL J. Bacteriol. 165:181-192(1986).
RN [8]
RP SEQUENCE FROM N.A.
RA STRAIN-K-12;
RC MEDLINE-86278132; PubMed-3015933;
RX Breton R., Sanfacon H., Papayannopoulos I., Blemann K., Lapointe J.;
RT "Glutaryl-L-lysine synthetase of Escherichia coli. Isolation and primary
RT structure of the glx gene and homology with other aminoacyl-tRNA
RT synthetases."
RL J. Biol. Chem. 261:10610-10617(1986).
RN [9]
RP SEQUENCE FROM N.A.
RA STRAIN-K-12;
RC MEDLINE-87014116; PubMed-3020380;
RX Koester W., Braun V.;
RT "Iron hydroxamate transport of Escherichia coli: Nucleotide sequence
RT of the fnb gene and identification of the protein."
RL Mol. Gen. Genet. 204:435-442(1986).
RN [10]
RP SEQUENCE FROM N.A.
RA STRAIN-K-12;
RC MEDLINE-87083395; PubMed-3025182;
RX Chye M.L., Pittard J.;
RT "Transcription control of the aroP gene in Escherichia coli K-12:
RT Analysis of operator mutants."
RL J. Bacteriol. 169:386-393(1987).
RN [11]
RP SEQUENCE FROM N.A.
RA STRAIN-K-12;
RC MEDLINE-87109068; PubMed-3027045;
RX Ben Bassat A., Bauer K., Chang S.Y., Myambo K., Boosman A., Chang S.;
RT "Processing of the initiation methionine from proteins: Properties of
RT the Escherichia coli methionine aminopeptidase and its gene
RT structure."
RL J. Bacteriol. 169:751-757(1987).
RN [12]

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RP SEQUENCE FROM N.A.  
 RC STRAIN-K-12;  
 RX MEDLINE-87279948; PubMed-3301821;  
 RA Coulton J.W., Mason P., Allatt D.D.;  
 RT \*fhuc and fhud genes for Iron(III)-ferrichrome transport into  
 RT *Escherichia coli* K-12.";  
 RL J. Bacteriol. 169:3844-3849(1987).  
 RN [13]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-K-12;  
 RX MEDLINE-88058963; PubMed-3316212;  
 RA Tabor C.W., Tabor H.;  
 RT "The speesped operon of *Escherichia coli*: Formation and processing of  
 RT a proenzyme form of S-adenosylmethionine decarboxylase.";  
 RL J. Biol. Chem. 262:16037-16040(1987).  
 RN [14]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-K-12;  
 RX MEDLINE-88152237; PubMed-2450046;  
 RA Gebhard W., Schreilmueller T., Hochstrasser K.;  
 RT "Complementary DNA and derived amino acid sequence of the precursor of  
 RT one of the three protein components of the inter-alpha-trypsin  
 RT inhibitor complex.";  
 RL FEBS Lett. 229:63-67(1988).  
 RN [15]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-K-12;  
 RX MEDLINE-89061679; PubMed-2904262;  
 RA Andrews S.C., Guest J.R.;  
 RT "Nucleotide sequence of the gene encoding the GMP reductase of  
 RT *Escherichia coli* K12.";  
 RL Biochem. J. 255:35-43(1988).  
 RN [16]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-K-12;  
 RX MEDLINE-88227880; PubMed-3372485;  
 RA Mellano M.A., Cooksey D.A.;  
 RT "Nucleotide sequence and organization of copper resistance genes from  
 RT *Pseudomonas syringae* pv. tomato.";  
 RL J. Bacteriol. 170:2879-2883(1988).  
 RN [17]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-K-12;  
 RX MEDLINE-89155419; PubMed-2537812;  
 RA Liu J., Parkinson J.S.;  
 RT "Genetics and sequence analysis of the pcnB locus, an *Escherichia coli*  
 RT gene involved in plasmid copy number control.";  
 RL J. Bacteriol. 171:1254-1261(1988).  
 RN [18]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-K-12;  
 RX MEDLINE-8908347; PubMed-3049588;  
 RA Sung Y., Fuchs J.A.;  
 RT "Characterization of the cya operon in *Escherichia coli* K12.";  
 RL J. Biol. Chem. 263:14769-14775(1988).  
 RN [19]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-K-12;  
 RX MEDLINE-89057448; PubMed-3057437;  
 RA Lipinska B., Sharma S., Georgopoulos C.;  
 RT "Sequence analysis and regulation of the htrA gene of *Escherichia*  
 RT *coli*: A sigma-32-independent mechanism of heat-inducible  
 RT transcription.";  
 RL Nucleic Acids Res. 16:10053-10067(1988).  
 RN [20]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-K-12;  
 RX MEDLINE-90128278; PubMed-2693214;  
 RA Roncero M.I., Jensen L.P., Stroman P., van Heeswijk R.;  
 RT "Characterization of a leuA gene and an ARS element from *Mucor*  
 RT *circinellus*.";  
 RL Gene 84:335-343(1989).  
 RN [21]

RP SEQUENCE FROM N.A.  
 RC STRAIN-K-12;  
 RX MEDLINE-89327165; PubMed-2666401;  
 RA Xie O.W., Tabor C.W., Tabor H.;  
 RT "Spermatine biosynthesis in *Escherichia coli* the promoter and the  
 RT termination regions of the speed operon.";  
 RL J. Bacteriol. 171:4457-4465(1989).  
 RN [22]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-K-12;  
 RX MEDLINE-90113890; PubMed-2691840;  
 RA Lindquist S., Gallant M., Lindberg F., Normark S.;  
 RT "Signalling proteins in enterobacterial ampC beta-lactamase  
 RT regulation.";  
 RL Mol. Microbiol. 3:1091-1102(1989).  
 RN [23]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-K-12;  
 RX MEDLINE-90202727; PubMed-2180916;  
 RA Kang P.J., Craig E.A.;  
 RT "Identification and characterization of a new *Escherichia coli* gene  
 RT that is a dosage-dependent suppressor of a dnaK deletion mutation.";  
 RL J. Bacteriol. 172:2055-2064(1990).  
 RN [24]

Query Match 89.7%; Score 35; DB 2; Length 276;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EWSWL 6  
 DB 9 EWSWL 13

RESULT 10  
 ID 094380 PRELIMINARY; PRT; 311 AA.  
 AC 094380;  
 DT 01-FEB-1997 (TrEMBLrel. 02, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
 DE ZC47.13 protein.  
 GN ZC47.13.  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;  
 OC Rhabditidae; Peloderinae; Caenorhabditis.  
 OX NCBI\_TaxID=6239;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA McMurray A.A.;  
 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-99069613; PubMed-9851916;  
 RA none;  
 RT "Genome sequence of the nematode *C. elegans*: A platform for  
 RT investigating biology.";  
 RT Science 282:2012-2018(1998).  
 DR EMBL: Z61141; CAB03488.2;  
 DR InterPro: IPR002900; DUF38.  
 DR InterPro: IPR001810; F-box.  
 DR Pfam: PF01827; DUF38; 1.  
 DR Pfam: PF00646; F-box; 1.  
 SQ SEQUENCE 311 AA; 36603 MW; 928464208868C48B CRC64;

Query Match 89.7%; Score 35; DB 5; Length 311;  
 Best Local Similarity 83.3%; Pred. No. 3.1e+02;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 EWSWL 6  
 DB 295 LEWEMWL 300

## RESULT 11

Q25333 PRELIMINARY; PRT; 371 AA.  
 ID Q25333  
 AC Q25333  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE Surface antigen P2 (Fragment).  
 OS Leishmania major.  
 CC Eukaryota; Eukaryotes; Kinetoplastida; Trypanosomatidae; Leishmania.  
 OX NCBI\_TaxID=5664;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-V121;  
 RX MEDLINE=92105105; PubMed=1761547;  
 RA Murray P.J., Splithill T.W.;  
 RT "Variants of a Leishmania Surface Antigen Derived from a Multigenic Family";  
 RL J. Biol. Chem. 266:24477-24484(1991).  
 DR EMBL; X57134; CAA40413.1; -;  
 DR InterPro; IPR001611; IRR.  
 DR InterPro; IPR003592; IRR\_out.  
 DR Pfam; PF00560; IRR; 2.  
 DR SMART; SM00370; IRR; 1.  
 FT NON\_TER  
 SQ SEQUENCE 371 AA; 39765 MW; 82D0A0BE163E247D CRC64;

## Query Match

Best Local Similarity 89.7%; Score 35; DB 5; Length 371;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

## OY 2 EWSWL 6

DB 1 EWSWL 5

## RESULT 12

Q8YFW8 PRELIMINARY; PRT; 387 AA.  
 ID Q8YFW8  
 AC Q8YFW8  
 DT 01-MAR-2002 (TREMBLrel. 20, Created)  
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)  
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)  
 DE Mannose-6-phosphate isomerase (EC 5.3.1.8).  
 GN BME11394.  
 OS Brucella melitensis.  
 CC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;  
 OC Brucellaceae; Brucella.  
 OX NCBI\_TaxID=29459;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-16W / ATCC 23456 / BIOTYPE 1;  
 RX MEDLINE=20020109; PubMed=11756688;  
 RA DelVecchio V.G., Kapatal V., Redkar R.J., Patra G., Muijer C., Los T., Ivanova N., Anderson I., Bhattacharya A., Lykakis A., Resznik G., Selkov E., Elizer P.H., Hagius S., O'Callaghan D., Teleson J.-J., Haselkorn R., Kyriades N., Overbeek R.;  
 RT "The genome sequence of the facultative intracellular pathogen Brucella melitensis";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).  
 DR EMBL; AE009577; AAL52575.1; -;  
 KW Isoenzyme; Complete proteome.  
 SQ SEQUENCE 387 AA; 44267 MW; 4E1F33C64461663F CRC64;

## Query Match

Best Local Similarity 89.7%; Score 35; DB 16; Length 387;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

## OY 2 EWSWL 6

DB 245 EWSWL 249

## RESULT 13

Q8YPT8 PRELIMINARY; PRT; 391 AA.  
 ID Q8YPT8  
 AC Q8YPT8  
 DT 01-MAR-2002 (TREMBLrel. 20, Created)  
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)  
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)  
 DE Hypothetical protein A114102.  
 GN A114102.  
 OS Anabaena sp. (strain PCC 7120).  
 CC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.  
 OX NCBI\_TaxID=103690;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21595285; PubMed=11759840;  
 RA Kaneko T., Nakamura Y., Wolk C.P., Kurita T., Sasamoto S., Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A., Nakazaki N., Shimo S., Sugimoto M., Takazawa M., Yamada M., Yasuda M., Tabata S.;  
 RT "Complete genomic sequence of the filamentous nitrogen-fixing cyanobacterium Anabaena sp. strain PCC 7120";  
 RL DNA Res. 8:205-213(2001).  
 DR EMBL; AP003595; BAB75801.1; -;  
 KW Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 391 AA; 45814 MW; 9B44EAD40CACFC29 CRC64;

## Query Match

Best Local Similarity 89.7%; Score 35; DB 16; Length 391;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

## OY 1 EWSWL 6

DB 37 LEWDWL 42

## RESULT 14

Q8RXB1 PRELIMINARY; PRT; 469 AA.  
 ID Q8RXB1  
 AC Q8RXB1  
 DT 01-JUN-2002 (TREMBLrel. 21, Created)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE Delta 5 fatty acid desaturase D5.  
 GN D5.  
 OS Phaeodactylum tricornutum.  
 CC Eukaryota; stramenopiles; Bacillariophyta; Bacillariophyceae;  
 OC Bacillariophyceae; Naviculales; Phaeodactylaceae; Phaeodactylum.  
 OX NCBI\_TaxID=2850;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-UTEX 646;  
 RA Domergue F., Lerchl J., Zaehringer U., Heinz E.;  
 RT "Cloning and functional characterization of Phaeodactylum tricornutum front-end desaturases involved in elcosapentaenoic acid biosynthesis";  
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY082392; AAL92562.1; -;  
 SQ SEQUENCE 469 AA; 53857 MW; 144534845317151 CRC64;

## Query Match

Best Local Similarity 89.7%; Score 35; DB 10; Length 469;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

## OY 1 LEWSW 5

DB 321 LEWSW 325

## RESULT 15

Q8VCV5

ID 08VCV5 PRELIMINARY; PRT; 481 AA.  
 AC 08VCV5;  
 DT 01-MAR-2002 (TREMblrel. 20, Created)  
 DT 01-MAR-2002 (TREMblrel. 20, last sequence update)  
 DT 01-JUN-2002 (TREMblrel. 21, last annotation update)  
 DE Hypothetical 52.3 kda protein.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxId=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=MAMMARY TUMOR;  
 RA Strausberg R.;  
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC018455; AAH18455.1; -  
 DR InterPro: IPR003599; Ig.  
 DR InterPro: IPR003597; Ig\_C1.  
 DR InterPro: IPR003006; Ig\_C1.  
 DR InterPro: IPR003596; Ig\_V.  
 DR Pfam: PF00047; Ig; 4.  
 DR SMART: SM00409; Ig; 3.  
 DR SMART: SM00407; IgC1; 3.  
 DR SMART: SM00406; IGV; 1.  
 DR PROSITE: PS00290; IG\_MHC; UNKNOWN\_2.  
 KW Hypothetical protein.  
 SQ SEQUENCE 481 AA; 52326 MW; 52B44C5826807143 CRC64;

Query Match 89.7%; Score 35; DB 11; Length 481;  
 Best Local Similarity 66.7%; Pred. No. 4.9e+02;  
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 LEMSWL 6  
 :||||:  
 Db 1 MEMSWI 6

Search completed: May 30, 2003, 14:38:54  
 Job time : 18.7632 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 30, 2003, 14:32:12 ; Search time 19.6974 Seconds

(without alignments)  
40.589 Million cell updates/sec

Title: US-09-643-260-7

Perfect score: 38

Sequence: 1 LAMSWL 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapept 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 08

Maximum Match 100%

Listing first 45 summaries

Database :  
1: /SID2/gcgdata/geneseq-emb1/AA1980.DAT:\*  
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12: /SID2/gcgdata/geneseq-emb1/AA1991.DAT:\*  
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23: /SID2/gcgdata/geneseq-emb1/AA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	38	100.0	6	23	ABB08729
2	38	100.0	6	23	AAA48512
3	38	100.0	756	23	ABB77303
4	35	92.1	196	22	AAU62777
5	35	92.1	321	22	ABB64219
6	35	92.1	329	22	ABB71850
7	35	92.1	1055	21	AAAY44787
8	34	89.5	13	21	AAAY78379
9	34	89.5	56	20	AAW88644
10	34	89.5	56	22	ABB50411

11	34	89.5	64	22	ABB39983	Peptide #7489 enco
12	34	89.5	64	22	ABB24510	Protein #6509 enco
13	34	89.5	64	22	AAU60730	Human brain expres
14	34	89.5	64	22	AAU73401	Human bone marrow
15	34	89.5	64	22	AAU33604	Peptide #7641 enco
16	34	89.5	93	23	ABB43260	Human peptide enco
17	34	89.5	123	22	AAU03124	Human polypeptide
18	34	89.5	138	20	AAU08298	Human polypeptide
19	34	89.5	140	20	AAU42442	Novel amino acid s
20	34	89.5	140	20	AAU42443	Extended novel ami
21	34	89.5	164	22	ABB28076	Novel human diagno
22	34	89.5	170	21	AAU87324	Human signal pepti
23	34	89.5	199	22	ABG07731	Novel human diagno
24	34	89.5	320	21	AAU54132	Amino acid sequenc
25	34	89.5	331	21	AAU54127	Amino acid sequenc
26	34	89.5	369	21	AAU54129	Amino acid sequenc
27	34	89.5	432	22	AAU48985	Protonibacterium
28	34	89.5	468	21	AAU44486	Bacillus agaradher
29	34	89.5	468	21	AAU54125	Amino acid sequenc
30	34	89.5	476	21	AAU54123	A mannanase-linker
31	34	89.5	487	22	ABB60890	Drosophila melanog
32	34	89.5	490	21	AAU54122	Amino acid sequenc
33	34	89.5	493	21	AAU54124	Bacillus agaradher
34	34	89.5	493	21	AAU54124	Amino acid sequenc
35	34	89.5	544	23	AAU21061	Human drug metabol
36	34	89.5	544	23	AAU91320	Human P450TEC prot
37	34	89.5	720	22	ABB66438	Drosophila melanog
38	33	86.8	6	23	ABB08730	Mutated IKKbeta NE
39	33	86.8	6	23	AAA48513	NBD mutant peptide
40	33	86.8	36	21	AAU40185	Human secreted pro
41	33	86.8	51	22	AAU14914	Novel bone marrow
42	33	86.8	56	23	ABP05260	Human ORFX protein
43	33	86.8	57	22	AAU55232	Protonibacterium
44	33	86.8	142	21	AAU64726	Human 5' EST relat
45	33	86.8	147	21	AAU41978	Human ORFX ORF1742

#### ALIGNMENTS

RESULT 1	ABB08729	standard; peptide: 6 AA.
ID	ABB08729	
XX	ABB08729	
AC	ABB08729	
XX	ABB08729	
DT	14-JUN-2002	(first entry)
XX	14-JUN-2002	
DE	Mutated IKKbeta NEMO binding domain peptide SEQ ID NO 7.	
XX		
XX	IKKbeat; IKKalpha; NEMO; NEMO binding domain; NBD; NF-kappaB; NF-KB;	
KW	kinase activation; leukocyte; inflammation; E-selectin; osteoclast;	
KW	autoimmune disease; transplant rejection; osteoporosis; cancer;	
KW	Alzheimer's disease; viral; infection; asthma; anaphylaxis; psoriasis;	
KW	rheumatoid arthritis; Crohn's disease; multiple sclerosis; HIV;	
KW	corticosteroid; immunosuppression; anti-inflammatory; immunosuppressive;	
KW	osteopathic; cytostatic; nootropic; neuroprotective; anti-HIV; human;	
KW	antiartherosclerotic; virucide; antiaslathmatic; antiallergic;	
KW	dermatological; antibacterial; antiporiatic; antirheumatic;	
KW	antiarthritic; osteopathic; antitumor; mutant; muten.	
XX		
OS	Homo sapiens.	
OS	Synthetic.	
FT	Key	Location/Qualifiers
FT	Misc-difference 2	/note- "Wildtype Asp substituted by Ala"
XX		
XX	WO200183547-A2.	
XX		
XX	08-NOV-2001.	
XX		
XX	02-MAY-2001; 2001WO-US40654.	

XX 02-MAY-2000; 2000US-201261P.  
 PR 22-AUG-2000; 2000US-0643260.  
 XX (UYVA ) UNIV YALE.  
 XX May MJ, Ghosh S;  
 XX WPI; 2002-179350/23.  
 DR  
 XX Modulating NF-kappaB induction in a cell, useful for treating e.g.  
 PT inflammatory disorders, osteoporosis and cancer, comprises contacting a  
 PT cell with an anti-inflammatory compound comprising at least one NEMO  
 PI binding domain -  
 XX  
 XX Claim 23; Page 44; 82pp; English.  
 PS  
 XX  
 XX The invention relates to modulating NF-kappaB (NF-kB) induction in a cell  
 CC comprises contacting a cell with an anti-inflammatory compound  
 CC (ABB08725-ABB08742) comprising at least one NEMO binding domain  
 CC (ABB77313). The compound has acts through selective inhibition of  
 CC cytokine-mediated NF-kB activation by blocking the interaction of NEMO  
 CC with IKBeta at the NEMO binding domain. Blockage of IKBeta-NEMO  
 CC interaction results in inhibition of IKBeta kinase activation and  
 CC subsequent decreased phosphorylation of Ikbppab. The compound may also  
 CC act (directly or indirectly) by blocking the recruitment of leukocytes  
 CC into sites of acute and chronic inflammation, by down-regulating the  
 CC expression of E-selectin on leukocytes or by blocking osteoclast  
 CC differentiation. The compound is useful in treating NF-kB mediated  
 CC conditions, where the condition is an inflammatory disorder, an  
 CC autoimmune disease, transplant rejection, osteoporosis, cancer, an  
 CC Alzheimer's disease, atherosclerosis, a viral infection or ataxia  
 CC telangiectasia. The inflammatory disorder is asthma, allergies,  
 CC urticaria, anaphylaxis, cutaneous inflammation, sepsis, psoriasis,  
 CC rheumatoid arthritis, osteoarthritis, psoriatic arthritis, inflammatory  
 CC bowel disease, chronic obstructive pulmonary disease, vasculitis and  
 CC bursitis. The inflammatory disorder may also be dermatitis, eczema,  
 CC psoriasis, osteoarthritis, psoriatic arthritis, lupus and  
 CC sporadic arthritis. Also for Crohn's disease, ulcerative colitis,  
 CC polyomyelitis, scleroderma, Wegner's granulomatosis, temporal arteritis,  
 CC cryoglobulinemia or multiple sclerosis. For chronic viral infections  
 CC caused by Epstein-Barr, cytomegalovirus or herpes simplex. Other viral  
 CC diseases include HIV and influenza. The compound may also be useful for  
 CC treating anaphylaxis, drug and food sensitivity, contact dermatitis,  
 CC sunburn or aging. The compound may be used to replace corticosteroids in  
 CC any application in which corticosteroids are used, including  
 CC immunosuppression in transplants and cancer therapy. Also for identifying  
 CC anti-inflammatory compounds and for diagnosis of an inflammatory disorder.  
 CC The compound may be administered alone or in combination with other known  
 CC anti-inflammatory agents. The present sequence is that of a mutated NEMO  
 CC binding domain of IKBeta.  
 CC  
 XX  
 SQ Sequence 6 AA;  
 QY  
 DB 1 LAMSWL 6  
 1 LAMSWL 6  
 Query Match 100.0%; Score 38; DB 23; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 2  
 AAM48512  
 ID AAM48512 standard; Peptide; 6 AA.  
 XX  
 AC AAM48512;  
 XX  
 DT 20-MAR-2002 (first entry)  
 XX  
 DE NBD mutant peptide seq ID NO 7.  
 XX

KW Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;  
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; vitruclide;  
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;  
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;  
 KW cytokine; NFkappaB; Ikbppab kinase beta; IKBeta; cancer; psoriasis;  
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
 KW autoimmune disorder; multiple sclerosis; transplant rejection;  
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.  
 XX  
 OS Synthetic.  
 XX  
 XX WO200183554-A2.  
 XX  
 XX 08-NOV-2001.  
 XX  
 XX 02-MAY-2001; 2001WO-US14346.  
 XX  
 XX 02-MAY-2000; 2000US-201261P.  
 PR 22-AUG-2000; 2000US-0643260.  
 XX  
 XX (PRAE-) PRAECIS PHARM INC.  
 XX (UYVA ) UNIV YALE.  
 XX  
 XX May MJ, Ghosh S, Findels MA, Phillips K;  
 XX WPI; 2002-121889/16.  
 DR  
 XX  
 XX Novel antiinflammatory compound comprising membrane translocation  
 PT domain fused to NEMO binding sequence, useful for blocking nuclear  
 PT factor kappaB activation, and for treating asthma, lung inflammation,  
 PT psoriasis  
 PT  
 XX  
 XX Example 6; Page 47; 88pp; English.  
 PS  
 XX  
 XX The invention relates to an antiinflammatory compound (especially  
 CC (AAM48628-AAM48645), comprising a membrane translocation domain  
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15  
 CC amino acid residues, fused to a NEMO binding sequence  
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,  
 CC cytostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,  
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,  
 CC nootropic, antiatherosclerotic, vitruclide and antiallergic activity. The  
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB  
 CC activation by blocking interaction of Ikbppab kinase beta (IKKbeta) at  
 CC the NEMO binding domain that results in inhibition of Ikbppab kinase  
 CC activation and subsequent decreased phosphorylation of Ikbppab. The  
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,  
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,  
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,  
 CC bursitis; autoimmune diseases such as lupus, polyomyelitis, scleroderma,  
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;  
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia  
 CC telangiectasia. The compounds are also useful for treating  
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,  
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and  
 CC arthritis.  
 CC  
 XX  
 SQ Sequence 6 AA;  
 QY  
 DB 1 LAMSWL 6  
 1 LAMSWL 6  
 Query Match 100.0%; Score 38; DB 23; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 3  
 ABB77303  
 ID ABB77303 standard; protein; 756 AA.  
 XX

AC ABB77303;  
 XX  
 DT 14-JUN-2002 (first entry)  
 XX  
 DE Human IKKbeta mutant D738A.  
 XX  
 KW IKKbeat; IKKalpha; NEMO; NEMO binding domain; NBD; NF-kappaB; NF-kB;  
 KW kinase activation; leukocyte; inflammation; E-selectin; osteoclast;  
 KW autoimmune disease; transplant rejection; osteoporosis; cancer;  
 KW Alzheimer's disease; viral; infection; asthma; anaphylaxis; psoriasis;  
 KW rheumatoid arthritis; Crohn's disease; multiple sclerosis; HIV;  
 KW corticosteroid; immunosuppression; antiinflammatory; immunosuppressive;  
 KW osteopathic; cytostatic; nocotropic; neuroprotective; anti-HIV; human;  
 KW antiarteriosclerotic; virucide; antiasthmatic; antiallergic;  
 KW dermatological; antibacterial; antipsoriatic; antirheumatic;  
 KW antiarthritic; osteopathic; antitumor; mutant; muten.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 738 /note="Wildtype Asp substituted by Ala"  
 FT  
 XX  
 PN WO200183547-A2.  
 XX  
 PD 08-NOV-2001.  
 XX  
 PF 02-MAY-2001; 2001WO-US40654.  
 XX  
 PR 02-MAY-2000; 2000US-201261P.  
 PR 22-AUG-2000; 2000US-0643260.  
 XX  
 PA (UYVA ) UNIV YALE.  
 XX  
 PI May MJ, Ghosh S;  
 XX  
 DR WPI; 2002-179350/23.  
 XX  
 PT Modulating NF-kappaB induction in a cell, useful for treating e.g.  
 PT inflammatory disorders, osteoporosis and cancer, comprises contacting a  
 PT cell with an anti-inflammatory compound comprising at least one NEMO  
 PT binding domain -  
 XX  
 PS Example 11; Page -: 82pp; English.  
 PS  
 CC The invention relates to modulating NF-kappaB (NF-kB) induction in a cell  
 CC comprising contacting a cell with an anti-inflammatory compound  
 CC (ABB08725-ABB08742) comprising at least one NEMO binding domain  
 CC (ABB77313). The compound has acts through selective inhibition of  
 CC cytokine-mediated NF-kB activation by blocking the interaction of NEMO  
 CC with IKKbeta at the NEMO binding domain. Blockage of IKKbeta-NEMO  
 CC interaction results in inhibition of IKKbeta kinase activation and  
 CC subsequent decreased phosphorylation of IkappaB. The compound may also  
 CC act (directly or indirectly) by blocking the recruitment of leukocytes  
 CC into sites of acute and chronic inflammation, by down-regulating the  
 CC expression of E-selectin on leukocytes or by blocking osteoclast  
 CC differentiation. The compound is useful in treating NF-kB mediated  
 CC conditions, where the condition is an inflammatory disorder, an  
 CC autoimmune disease, transplant rejection, osteoporosis, cancer,  
 CC Alzheimer's disease, atherosclerosis, a viral infection or ataxia  
 CC telangiectasia. The inflammatory disorder is asthma, allergies,  
 CC urticaria, anaphylaxis, cutaneous inflammation, sepsis, psoriasis,  
 CC rheumatoid arthritis, osteoarthritis, psoriatic arthritis, inflammatory  
 CC bowel disease, chronic obstructive pulmonary disease, vasculitis and  
 CC buritis. The inflammatory disorder may also be dermatitis, eczema,  
 CC psoriasis, osteoarthritis, psoriatic arthritis, lupus and  
 CC sporadic arthritis. Also for Crohn's disease, ulcerative colitis,  
 CC polymyalgia, scleroderma, Wegner's granulomatosis, temporal arteritis,  
 CC cryoglobulinemia or multiple sclerosis. For chronic viral infections  
 CC caused by Epstein-Barr, cytomegalovirus or herpes simplex. Other viral  
 CC diseases include HIV and influenza. The compound may also be useful for  
 CC treating anaphylaxis, drug and food sensitivity, contact dermatitis,

CC sunburn or aging. The compound may be used to replace corticosteroids in  
 CC any application in which corticosteroids are used, including  
 CC immunosuppression in transplants and cancer therapy. Also for identifying  
 CC antiinflammatory compounds and for diagnosis of an inflammatory disorder.  
 CC The compound may be administered alone or in combination with other known  
 CC anti-inflammatory agents. The present sequence is that of an IKKbeta  
 CC mutant, useful in examples of the invention.  
 CC Note: The present sequence is not given in the specification but is  
 CC derived from GenBank Accession No. 014920 (ABB77294).  
 XX  
 SQ Sequence 756 AA;  
 XX  
 QY 1 LANSWL 6  
 DB 737 LANSWL 742  
 XX  
 Query Match 100.0%; Score 38; DB 23; Length 756;  
 Best Local Similarity 100.0%; Pred. No. 5.7e+02;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 RESULT 4  
 AAU62777  
 ID AAU62777 standard; Protein; 196 AA.  
 XX  
 AC AAU62777;  
 XX  
 DT 27-FEB-2002 (first entry)  
 XX  
 DE Propionibacterium acnes immunogenic protein #23673.  
 XX  
 KW SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;  
 KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;  
 KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;  
 KW dermatological; osteopathic; neuroprotectant.  
 XX  
 OS Propionibacterium acnes.  
 XX  
 PN WO200181581-A2.  
 XX  
 PD 01-NOV-2001.  
 XX  
 PF 20-APR-2001; 2001WO-US12865.  
 XX  
 PR 21-APR-2000; 2000US-199047P.  
 PR 02-JUN-2000; 2000US-208841P.  
 PR 07-JUL-2000; 2000US-216747P.  
 XX  
 PA (CORI-) CORIXA CORP.  
 XX  
 PI Skelky YAM, Persing DH, Mitcham JL, Wang SS, Bhatia A;  
 PI L'walsonneuve J, Zhang Y, Jen S, Carter D;  
 XX  
 DR WPI; 2001-616774/71.  
 DR N-PSDB; AAS59629.  
 XX  
 PT Propionibacterium acnes polypeptides and nucleic acids useful for  
 PT vaccinating against and diagnosing infections, especially useful for  
 PT treating acne vulgaris -  
 XX  
 PS Example 1; SEQ ID No 23972; 1069pp; English.  
 PS  
 XX Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic  
 CC polypeptides. The proteins and their associated DNA sequences are used in  
 CC the treatment, prevention and diagnosis of medical conditions caused by  
 CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne,  
 CC pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.  
 CC P. acnes is also involved in infections of bone, joints and the central  
 CC nervous system, however it is particularly involved in the inflammatory  
 CC lesions associated with acne vulgaris. A method for detecting the  
 CC presence or absence of P. acnes in a patient comprises contacting a  
 CC sample with a binding agent that binds to the proteins of the invention  
 CC and determining the amount of bound protein in the sample. The

polypeptides may be used as antigens in the production of antibodies specific for *P. acnes* proteins. These antibodies can be used to downregulate expression and activity of *P. acnes* polypeptides and therefore treat *P. acnes* infections. The antibodies may also be used as diagnostic agents for determining *P. acnes* presence, for example, by enzyme linked immunosorbent assay (ELISA).  
Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.

Sequence - 196 AA;

Query Match 92.1%; Score 35; DB 22; Length 196;

Best Local Similarity 83.3%; Pred. No. 3.8e+02; Mismatches 0; Indels 0; Gaps 0;

DB 102 VAMSWL 107

RESULT 5  
ABB64219 standard; Protein; 321 AA.

XX ABB64219;

DT 26-MAR-2002 (first entry)

DE Drosophila melanogaster polypeptide SEQ ID NO 19449.

KW Drosophila: developmental biology; cell signalling; insecticide; pharmaceutical.

OS Drosophila melanogaster.

FN W0200171042-A2.

PD 27-SEP-2001.

PF 23-MAR-2001; 2001WO-US09231.

PR 23-MAR-2000; 2000US-191637P.

PR 11-JUL-2000; 2000US-0614150.

PA (PEKE ) PE CORP NY.

PI Venter JC, Adams M, Li PWD, Myers EW;

DR WPI: 2001-656860/75.

DR N-PSDB; ABL08322.

XX New isolated nucleic acid detection reagent for detecting 1000 or more genes from *Drosophila* and for elucidating cell signalling and cell-cell interactions -

PS Disclosure; SEQ ID NO 19449; 21pp + Sequence Listing; English;

XX The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from *Drosophila*. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (AB116176-AB130511), expressed DNA sequences (AB101840-AB116175) and the encoded proteins (AB116176-AB130511).  
XX The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 321 AA;

Query Match 92.1%; Score 35; DB 22; Length 321;

Best Local Similarity 83.3%; Pred. No. 6.4e+02; Mismatches 0; Indels 0; Gaps 0;

DB 64 LSMW 69

RESULT 6  
ABB71850 standard; Protein; 329 AA.

XX ABB71850;

DT 26-MAR-2002 (first entry)

DE Drosophila melanogaster polypeptide SEQ ID NO 42342.

KW Drosophila: developmental biology; cell signalling; insecticide; pharmaceutical.

OS Drosophila melanogaster.

FN W0200171042-A2.

PD 27-SEP-2001.

PF 23-MAR-2001; 2001WO-US09231.

PR 23-MAR-2000; 2000US-191637P.

PR 11-JUL-2000; 2000US-0614150.

PA (PEKE ) PE CORP NY.

PI Venter JC, Adams M, Li PWD, Myers EW;

DR WPI: 2001-656860/75.

DR N-PSDB; ABL15953.

XX New isolated nucleic acid detection reagent for detecting 1000 or more genes from *Drosophila* and for elucidating cell signalling and cell-cell interactions -

PS Disclosure; SEQ ID NO 42342; 21pp + Sequence Listing; English.

XX The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from *Drosophila*. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (AB116176-AB130511), expressed DNA sequences (AB101840-AB116175) and the encoded proteins (AB116176-AB130511).  
XX The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 329 AA;

Query Match 92.1%; Score 35; DB 22; Length 329; Best Local Similarity 83.3%; Pred. No. 6.5e+02; Mismatches 0; Indels 0; Gaps 0;

DB 17 LAWTWL 22

RESULT 7  
AA44787 standard; Protein; 1055 AA.

XX AA44787;



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PR 06-JUN-1997; 97US-0048877.
PR 06-JUN-1997; 97US-0048881.
PR 06-JUN-1997; 97US-0048884.
PR 06-JUN-1997; 97US-0048893.
PR 06-JUN-1997; 97US-0048896.
PR 06-JUN-1997; 97US-0048899.
PR 06-JUN-1997; 97US-0048915.
PR 06-JUN-1997; 97US-0048949.
PR 06-JUN-1997; 97US-0048964.
PR 06-JUN-1997; 97US-0048972.
PR 06-JUN-1997; 97US-0049020.
PR 05-SEP-1997; 97US-0057628.
PR 05-SEP-1997; 97US-0057635.
PR 05-SEP-1997; 97US-0057644.
PR 05-SEP-1997; 97US-0057650.
PR 05-SEP-1997; 97US-0057661.
PR 05-SEP-1997; 97US-0057667.
PR 05-SEP-1997; 97US-0057761.
PR 05-SEP-1997; 97US-0057764.
PR 05-SEP-1997; 97US-0057770.
PR 05-SEP-1997; 97US-0057775.
PR 05-SEP-1997; 97US-0057778.
PR 06-JUN-1997; 97US-0048875.
PR 06-JUN-1997; 97US-0048878.
PR 06-JUN-1997; 97US-0048882.
PR 06-JUN-1997; 97US-0048885.
PR 06-JUN-1997; 97US-0048894.
PR 06-JUN-1997; 97US-0048897.
PR 06-JUN-1997; 97US-0048900.
PR 06-JUN-1997; 97US-0048916.
PR 06-JUN-1997; 97US-0048962.
PR 06-JUN-1997; 97US-0048970.
PR 06-JUN-1997; 97US-0048974.
PR 05-SEP-1997; 97US-0049373.
PR 05-SEP-1997; 97US-0057584.
PR 05-SEP-1997; 97US-0057629.
PR 05-SEP-1997; 97US-0057642.
PR 05-SEP-1997; 97US-0057645.
PR 05-SEP-1997; 97US-0057648.
PR 05-SEP-1997; 97US-0057651.
PR 05-SEP-1997; 97US-0057662.
PR 05-SEP-1997; 97US-0057668.
PR 05-SEP-1997; 97US-0057762.
PR 05-SEP-1997; 97US-0057765.
PR 05-SEP-1997; 97US-0057771.
PR 05-SEP-1997; 97US-0057776.
PR 06-JUN-1997; 97US-0048876.
PR 06-JUN-1997; 97US-0048880.
PR 06-JUN-1997; 97US-0048883.
PR 06-JUN-1997; 97US-0048892.
PR 06-JUN-1997; 97US-0048895.
PR 06-JUN-1997; 97US-0048898.
PR 06-JUN-1997; 97US-0048901.
PR 06-JUN-1997; 97US-0048917.
PR 06-JUN-1997; 97US-0048963.
PR 06-JUN-1997; 97US-0048971.
PR 06-JUN-1997; 97US-0049019.
PR 06-JUN-1997; 97US-0049374.
PR 05-SEP-1997; 97US-0057627.
PR 05-SEP-1997; 97US-0057634.
PR 05-SEP-1997; 97US-0057643.
PR 05-SEP-1997; 97US-0057646.
PR 05-SEP-1997; 97US-0057649.
PR 05-SEP-1997; 97US-0057654.
PR 05-SEP-1997; 97US-0057666.
PR 05-SEP-1997; 97US-0057760.
PR 05-SEP-1997; 97US-0057763.
PR 05-SEP-1997; 97US-0057769.
PR 05-SEP-1997; 97US-0057774.
PR 05-SEP-1997; 97US-0057777.
XX

```

```

PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Brewer LA, Carter KC, Dillon PJ, Ebner R, Endress GA;
PI Fan P, Feng P, Ferris AM, Fischer CL, Florence C;
PI Florence K, Greene JM, Hu J, Kraw H, Lafleur DW;
PI Li Y, Moore PA, Ni J, Olsen HS, Rosen CA, Ruben SM;
PI Shi Y, Soppet DR, Wei Y, Young P, Yu G, Zeng Z;
XX
DR WPI; 1999-059865/05.
DR N-PSDB; AAV84521.
XX
PT New isolated human genes and the secreted polypeptides they encode -
PT useful for diagnosis and treatment of e.g. cancers, neurological
PT disorders, immune diseases, inflammation or blood disorders
PS
PS
XX
XX Claim 11; Page 542; 772pp; English.
CC The invention relates to nucleic acid sequences (AAV84411 to AAV84633)
CC encoding human secreted proteins (AAV88534 to AAV88756). The secreted
CC protein gene sequences are deposited with the ATCC under deposit numbers
CC ATCC 97979, 97974, 97975, 97976, 97977, 209007, 209008, 209009, 209010,
CC 209011, 209080, 209081, 209082, 209083, 209084, 209085, 209511. Host
CC cells comprising recombinant vectors containing the nucleic acid
CC sequences are used for the recombinant production of the secreted
CC proteins. The polynucleotide and amino acid sequences are useful for are
CC useful for preventing, treating or ameliorating medical conditions e.g.
CC by protein or gene therapy. Pathological conditions can be also
CC diagnosed by determining the amount of the new polypeptides in a sample
CC or by determining the presence of mutations in the new polynucleotides.
CC Specific uses are described for each of the polynucleotides, based on
CC which tissues they are most highly expressed in, and include developing
CC products for the diagnosis or treatment of cancer, neurodegenerative
CC disorders, developmental abnormalities and foetal deficiencies, blood
CC disorders, tumours, leukemias, diseases of the immune system, autoimmune
CC diseases, hepatic and renal disease, lymphomas, inflammation, allergies,
CC ischemic shock, Alzheimer's and cognitive disorders, schizophrenia,
CC restenosis, prostate diseases, obesity, disorders involving osteoclasts
CC such as osteoporosis, arthritis or malignancies, diseases of testes,
CC lung or thymus, digestive/endocrine disorders, infections and AIDS. The
CC polypeptides are also useful for identifying their binding partners.
CC The present sequence represents human secreted protein (see descriptor
CC line for gene number and clone identification).
XX
XX Sequence 56 AA:
SQ
Query Match 89.5%; Score 34; DB 20; Length 56;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 LAMSW 5
DB 9 LAMSW 13
RESULT 10
ABBS0411
ID ABB50411 standard; Protein; 56 AA.
AC ABB50411;
XX
XX 07-FEB-2002 (first entry)
DT
XX
XX Human secreted protein encoded by gene 111 SEQ ID NO:359.
DE
XX
XX Human; secreted protein; immunomodulatory; antisclerotic; anti-HIV;
XX dermatological; immunosuppressive; antiinflammatory; immunostimulant;
XX cytototoxic; cardiant; anti-angiogenic; ophthalmological;
XX neuroprotective; nootropic; anticonvulsant; antialzheimers; vulnery;
XX antiparkinsonian; antimicrobial; gene therapy; vaccine; immune disorder;
XX multiple sclerosis; systemic lupus erythematosus; HIV infection; cancer;
XX human immunodeficiency virus; hyperproliferative disorder; wound healing;
XX Chagha's disease; cardiovascular disease; Schittler syndrome; chemotaxis;
XX Chaga's cardiomyopathy; coronary arteriosclerosis; angiogenic disorder;
XX

```

KW corneal graft neovascularisation; diabetic retinopathy; regeneration;  
 KW neurological disorder; Huntington's chorea; Alzheimer's disease;  
 KW Parkinson's disease; infectious disease; chromosome 10.  
 OS Homo sapiens.  
 XX  
 XX WO200162891-A2.  
 PD 30-AUG-2001.  
 XX  
 XX 21-FEB-2001; 2001WO-US05614.  
 PF  
 XX 24-FEB-2000; 2000US-184836P.  
 PR 29-MAR-2000; 2000US-193170P.  
 XX  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 PA  
 PI NJ J. Ebner R, Lafleur DW, Moore PA, Olsen HS, Rosen CA;  
 PI Ruben SM, Soppet DR, Young PE, Shi Y, Florence KA, Wei Y,  
 PI Florence C, Hu Y, Kyaw H, Fischer CL, Ferrle AM, Fan P;  
 PI Feng P, Endress GA, Dillon PJ, Carter KC, Brewer LA, Yu G;  
 PI Zeng Z, Greene JM;  
 XX  
 XX WPI: 2001-625724/72.  
 DR N-PSDB; ABA83304.  
 XX  
 XX Nucleic acids encoding 207 human secreted polypeptides, useful for  
 PT preventing, diagnosing and/or treating, e.g. cancers, Parkinson's  
 PT disease and diabetic retinopathy -  
 XX  
 XX Claim 11: Page 1140; 1533pp; English.  
 PS  
 XX ABA50301 to ABA51287 and ABA83194 to ABA83441 represent human secreted  
 CC proteins (I) and polynucleotide (II) sequences. (I) and (II) have various  
 CC activities based on the tissues and cells the genes are expressed in.  
 CC Example of these activities include: immunomodulatory; antisclerotic;  
 CC dermatological; immunosuppressive; antiinflammatory; immunostimulant;  
 CC anti-HIV; cytostatic; cardiant; anti-angiogenic; ophthalmological;  
 CC neuroprotective; nootropic; anticonvulsant; antialzheimers; vascular;  
 CC antiparkinsonian; antimicrobial; and vulnary. (I) and (II) can be used  
 CC in gene therapy and vaccine production. (I) and (II) can be used in the  
 CC prevention, diagnosis and treatment of immune disorders (e.g. multiple  
 CC sclerosis, systemic lupus erythematosus and human immunodeficiency virus  
 CC (HIV) infections), hyperproliferative disorders (e.g. cancers and  
 CC Gaucher's disease), cardiovascular diseases (e.g. Scimitar syndrome,  
 CC Chaga's cardiomyopathy and coronary arteriosclerosis), angioclinic  
 CC disorders (e.g. corneal graft neovascularisation and diabetic  
 CC retinopathy), neurological disorders (e.g. Huntington's chorea,  
 CC Alzheimer's disease and Parkinson's disease), infectious diseases and/or  
 CC for promoting wound healing, regeneration and/or chemotaxis. ABA83185 to  
 CC ABA83193 and ABA50300 represent sequences used in the exemplification of  
 CC the present invention.  
 CC  
 XX  
 SO Sequence 56 AA;  
 Query Match 89.5%; Score 34; DB 22; Length 56;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 LAMSW 5  
 DB 9 LAMSW 13  
 DE  
 RESULT 11  
 ID ABB39983  
 AC ABB39983 standard; peptide; 64 AA.  
 XX  
 AC ABB39983;  
 XX  
 DT 04-FEB-2002 (first entry)  
 XX  
 DE Peptide #7489 encoded by human foetal liver single exon probe.

XX  
 XX Human; foetal liver; gene expression; single exon nucleic acid probe.  
 KW  
 XX Homo sapiens.  
 OS  
 XX WO200157277-A2.  
 PD 09-AUG-2001.  
 XX  
 XX 30-JAN-2001; 2001WO-US00669.  
 PF  
 XX 04-FEB-2000; 2000US-0180312.  
 PR 26-MAY-2000; 2000US-0207456.  
 PR 30-JUN-2000; 2000US-0608408.  
 PR 03-AUG-2000; 2000US-0632366.  
 PR 21-SEP-2000; 2000US-0234687.  
 PR 27-SEP-2000; 2000US-0236359.  
 PR 04-OCT-2000; 2000GB-0024263.  
 XX  
 XX (MOLE-) MOLECULAR DYNAMICS INC.  
 PA  
 PI Penn SG, Hanzel DK, Chen W, Rank DR;  
 XX  
 XX WPI: 2001-483447/52.  
 DR  
 XX Human genome-derived single exon nucleic acid probes useful for  
 PT analyzing gene expression in human fetal liver -  
 PT  
 XX  
 XX Claim 27: SEQ ID NO 32618; 639pp + sequence listing; English.  
 PS  
 XX The invention relates to a single exon nucleic acid probe for  
 CC measuring human gene expression in a sample derived from human foetal  
 CC liver. The single exon nucleic acid probes may be used for predicting,  
 CC measuring and displaying gene expression in samples derived from human  
 CC fetal liver. The present sequence is a peptide encoded by a single exon  
 CC nucleic acid probe of the invention.  
 CC Note: The sequence data for this patent did not form part of the  
 CC printed specification, but was obtained in electronic format directly  
 CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.  
 CC  
 XX  
 SO Sequence 64 AA;  
 Query Match 89.5%; Score 34; DB 22; Length 64;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 LAMSW 5  
 DB 33 LAMSW 37  
 DE  
 RESULT 12  
 ID ABB24510  
 AC ABB24510 standard; protein; 64 AA.  
 XX  
 AC ABB24510;  
 XX  
 DT 23-JAN-2002 (first entry)  
 XX  
 DE Protein #6509 encoded by probe for measuring heart cell gene expression.  
 XX  
 XX Human; gene expression; heart; microarray; vascular system;  
 KW cardiovascular disease; hypertension; cardiac arrhythmia;  
 KW congenital heart disease.  
 XX  
 XX Homo sapiens.  
 OS  
 XX WO200157274-A2.  
 PD 09-AUG-2001.  
 XX  
 DE 30-JAN-2001; 2001WO-US00666.  
 XX

PR 04-FEB-2000; 2000US-0180312.  
 PR 26-MAY-2000; 2000US-0207456.  
 PR 30-JUN-2000; 2000US-0608408.  
 PR 03-AUG-2000; 2000US-0632366.  
 PR 21-SEP-2000; 2000US-0234687.  
 PR 27-SEP-2000; 2000US-0236359.  
 PR 04-OCT-2000; 2000GB-0024263.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 PI Penn SG, Hanzel DK, Chen W, Rank DR;  
 DR WPI: 2001-488899/53.  
 PT Single exon nucleic acid probes for analyzing gene expression in human  
 PT hearts -  
 PS Claim 15; SEQ ID NO 26280; 530pp; English.  
 CC The present invention relates to single exon nucleic acid probes for  
 CC measuring human gene expression in a sample derived from human heart (see  
 CC ABA21535-ABA41305). The present sequence is a protein encoded by one such  
 CC probe. The probes may be used for predicting, measuring and displaying  
 CC gene expression in samples derived from the human heart via microarrays.  
 CC By measuring gene expression, the probes are useful for predicting,  
 CC diagnosing, grading, staging, monitoring and prognosing diseases of the  
 CC human heart and vascular system e.g. cardiovascular disease,  
 CC hypertension, cardiac arrhythmias and congenital heart disease.  
 CC Note: The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences.  
 SQ Sequence 64 AA:  
 Query Match 89.5%; Score 34; DB 22; Length 64;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LAMSW 5  
 DB 33 LAMSW 37  
 RESULT 13  
 AAM60730  
 ID AAM60730 standard; Protein; 64 AA.  
 AC AAM60730;  
 XX  
 XX AAM60730;  
 DT 05-NOV-2001 (first entry)  
 DE Human brain expressed single exon probe encoded protein SEQ ID NO: 32835.  
 XX  
 KW Human; brain expressed exon; gene expression analysis; probe;  
 KW microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;  
 KW epilepsy; cancer.  
 OS Homo sapiens.  
 XX  
 OS WO200157275-A2.  
 PN  
 XX  
 PD 09-AUG-2001.  
 PD 30-JAN-2001; 2001WO-US00667.  
 PF 04-FEB-2000; 2000US-0180312.  
 PR 26-MAY-2000; 2000US-0207456.  
 PR 30-JUN-2000; 2000US-0608408.  
 PR 03-AUG-2000; 2000US-0632366.  
 PR 21-SEP-2000; 2000US-0234687.  
 PR 27-SEP-2000; 2000US-0236359.  
 PR 04-OCT-2000; 2000GB-0024263.  
 XX

PA (MOLE-) MOLECULAR DYNAMICS INC.  
 PI Penn SG, Hanzel DK, Chen W, Rank DR;  
 DR WPI: 2001-483446/52.  
 PT Single exon nucleic acid probes for analyzing gene expression in human  
 PT brains -  
 PS Example 4; SEQ ID NO: 32835; 650pp + Sequence Listing; English.  
 CC The present invention provides a number of single exon nucleic acid  
 CC probes which are derived from genomic sequences expressed in the human  
 CC brain. They can be used to measure gene expression in brain cell samples,  
 CC which may enable the diagnosis and improved treatment of nervous system  
 CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,  
 CC epilepsy and cancer. The present sequence is a protein encoded by one of  
 CC the probes of the invention.  
 SQ Sequence 64 AA:  
 Query Match 89.5%; Score 34; DB 22; Length 64;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LAMSW 5  
 DB 33 LAMSW 37  
 RESULT 14  
 AAM73401  
 ID AAM73401 standard; Protein; 64 AA.  
 AC AAM73401;  
 XX  
 XX AAM73401;  
 DT 06-NOV-2001 (first entry)  
 DE Human bone marrow expressed probe encoded protein SEQ ID NO: 33707.  
 XX  
 KW Human; bone marrow expressed exon; gene expression analysis; probe;  
 KW microarray; cancer; leukemia; lymphoma; myeloma.  
 OS Homo sapiens.  
 XX  
 OS WO200157276-A2.  
 PN  
 XX  
 PD 09-AUG-2001.  
 PD 30-JAN-2001; 2001WO-US00668.  
 PF 04-FEB-2000; 2000US-0180312.  
 PR 26-MAY-2000; 2000US-0207456.  
 PR 30-JUN-2000; 2000US-0608408.  
 PR 03-AUG-2000; 2000US-0632366.  
 PR 21-SEP-2000; 2000US-0234687.  
 PR 27-SEP-2000; 2000US-0236359.  
 PR 04-OCT-2000; 2000GB-0024263.  
 XX  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 PI Penn SG, Hanzel DK, Chen W, Rank DR;  
 DR WPI: 2001-488900/53.  
 PT Human genome-derived single exon nucleic acid probes useful for  
 PT analyzing gene expression in human bone marrow -  
 PS Example 4; SEQ ID NO: 33707; 658pp + Sequence Listing; English.  
 CC The present invention provides a number of single exon nucleic acid  
 CC probes which are derived from genomic sequences expressed in the human  
 CC bone marrow. They can be used to measure gene expression in bone marrow

CC samples, which may enable the improved diagnosis and treatment of cancers  
 CC such as lymphoma, leukaemia and myeloma. The present sequence is a  
 CC protein encoded by one of the probes of the invention.  
 XX

SO Sequence 64 AA;

Query Match 89.5%; Score 34; DB 22; Length 64;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LAWSW 5  
 |||||  
 Db 33 LAWSW 37

RESULT 15  
 AAM33604  
 ID AAM33604 standard; Protein; 64 AA.  
 XX

AC AAM33604;

DT 17-OCT-2001 (first entry)

DE Peptide #7641 encoded by probe for measuring placental gene expression.

XX Probe: microarray; human; placenta; antenatal diagnosis;  
 KW genetic disorder.

XX Homo sapiens.

PN MO200157272-A2.

PD 09-AUG-2001.

PF 30-JAN-2001; 2001MO-US00663.

PR 04-FEB-2000; 2000US-0180312.

PR 26-MAY-2000; 2000US-0207456.

PR 30-JUN-2000; 2000US-0608408.

PR 03-AUG-2000; 2000US-0632366.

PR 21-SEP-2000; 2000US-0234687.

PR 27-SEP-2000; 2000US-0236359.

PR 04-OCT-2000; 2000GB-0024263.

XX

PA (MOLE-) MOLECULAR DYNAMICS INC.

PI Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-488897/53.

DR

XX

PT Human genome-derived single exon nucleic acid probes useful for

PT analyzing gene expression in human placenta -

XX

PS Claim 27; SEQ ID NO 33873; 654bp; English.

XX

CC The present invention relates to single exon nucleic acid probes (SENP;

CC see AAI31315-AI3157546). The present sequence is a peptide encoded by one

CC such probe. The probes are useful for producing a microarray for

CC predicting, measuring and displaying gene expression in samples derived

CC from human placenta. The probes are useful for antenatal diagnosis of

CC human genetic disorders.

XX

SO Sequence 64 AA;

Query Match 89.5%; Score 34; DB 22; Length 64;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LAWSW 5  
 |||||  
 Db 33 LAWSW 37

Search completed: May 30, 2003, 14:49:45  
 Job time : 21.7529 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 30, 2003, 14:32:11 ; Search time 14.7632 Seconds

(without alignments)  
83.741 Million cell updates/sec

Title: US-09-643-260-7

Perfect score: 38

Sequence: 1 LAWSWL 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 08  
Maximum Match 1008

Listing first 45 summaries

Database :

1: SP\_ARCHAEA:\*  
2: SP\_BACTERIA:\*  
3: SP\_FUNGI:\*  
4: SP\_HUMAN:\*  
5: SP\_INVERTEBRATE:\*  
6: SP\_MAMMAL:\*  
7: SP\_MHC:\*  
8: SP\_ORGANELLE:\*  
9: SP\_PHAGE:\*  
10: SP\_PLANT:\*  
11: SP\_RODENT:\*  
12: SP\_VIRUS:\*  
13: SP\_VERTEBRATE:\*  
14: SP\_UNCLASSIFIED:\*  
15: SP\_VIRUS:\*  
16: SP\_BACTERIAP:\*  
17: SP\_ARCHAEP:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	36	94.7	488	10	Q9SEJ7 lupinus alb
2	36	94.7	675	17	Q26849 026849 methanobact
3	35	92.1	91	16	Q98C88 098C88 rhizobium l
4	35	92.1	116	2	Q68039 068039 rhodobacter
5	35	92.1	135	2	Q05744 005744 mycobacter
6	35	92.1	172	2	Q9KK81 09KK81 mycobacter
7	35	92.1	196	16	Q50005 050005 mycobacter
8	35	92.1	197	2	Q8RSV7 08RSV7 unclutered
9	35	92.1	210	16	Q86317 086317 mycobacter
10	35	92.1	321	5	Q94515 094515 drosophila
11	35	92.1	329	5	Q9VFY8 09VFY8 rhizobium m
12	35	92.1	422	16	Q92ND3 092ND3 agrobacteri
13	35	92.1	438	16	Q8UDU6 08UDU6 bruceella me
14	35	92.1	441	16	Q8YBVO 08YBVO arabidopsis
15	35	92.1	1055	10	Q9S722 09S722 arabidopsis
16	35	92.1	1057	10	Q9FI17 09FI17 arabidopsis

17	35	92.1	1058	10	Q9FLR5 09FLR5 arabidopsis
18	34	89.5	50	2	Q49396 049396 mycobacteri
19	34	89.5	77	2	Q9KIK2 09KIK2 pseudomonas
20	34	89.5	88	12	Q88800 088800 eastern equ
21	34	89.5	88	12	Q88801 088801 eastern equ
22	34	89.5	88	12	Q88802 088802 eastern equ
23	34	89.5	88	12	Q88803 088803 eastern equ
24	34	89.5	88	12	Q88804 088804 eastern equ
25	34	89.5	88	12	Q88805 088805 eastern equ
26	34	89.5	88	12	Q88806 088806 eastern equ
27	34	89.5	88	12	Q88807 088807 eastern equ
28	34	89.5	88	12	Q88808 088808 eastern equ
29	34	89.5	88	12	Q88809 088809 eastern equ
30	34	89.5	88	12	Q88810 088810 eastern equ
31	34	89.5	88	12	Q88811 088811 eastern equ
32	34	89.5	88	12	Q88812 088812 eastern equ
33	34	89.5	88	12	Q88813 088813 eastern equ
34	34	89.5	88	12	Q88814 088814 eastern equ
35	34	89.5	88	12	Q88815 088815 eastern equ
36	34	89.5	88	12	Q88816 088816 eastern equ
37	34	89.5	88	12	Q88817 088817 eastern equ
38	34	89.5	88	12	Q88818 088818 eastern equ
39	34	89.5	88	12	Q88819 088819 eastern equ
40	34	89.5	88	12	Q88820 088820 eastern equ
41	34	89.5	88	12	Q88821 088821 eastern equ
42	34	89.5	88	12	Q88822 088822 eastern equ
43	34	89.5	88	12	Q88823 088823 eastern equ
44	34	89.5	136	16	Q8ZH91 08ZH91 yersinia pe
45	34	89.5	151	16	Q8YRA0 08YRA0 anabaena sp

#### ALIGNMENTS

RESULT 1

Q9SEJ7 ID Q9SEJ7 PRELIMINARY; PRT; 488 AA.

AC Q9SEJ7; 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DT 01-MAY-2000 (TREMBLrel. 20, Last annotation update)

DE 1-aminocyclopropane-1-carboxylate synthase 3 (EC 4.4.1.14).

GN ACS3.

OS Lupinus albus (White lupine).

OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

OC eurosids I; Fabales; Fabaceae; Papilionoideae; Genisteae; Lupinus.

OX NCBI\_TaxID=3870;

RN (1)

RP SEQUENCE FROM N.A.

RC STRAIN=CV. ULTRA;

RA MEDLINE=20539411; PubMed=11089679;

RA Bekman E.P., Salbo N.J., Di Cataldo A., Regalado A.P., Ricardo C.P.,

RA Rodrigues-Pousada C.,

RT Differential expression of four genes encoding 1-aminocyclopropane-1-

RT carboxylate synthase in Lupinus albus during germination, and in

RT response to indole-3-acetic acid and wounding.";

RL Planta 211:663-672(2000).

CC -1- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).

CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).

CC -1- MISCELLANEOUS: IN EUKARYOTES THERE ARE TWO ISOZYMES: A CYTOPLASMIC

CC ONE AND A MITOCHONDRIAL ONE (BY SIMILARITY).

CC -1- SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDNT

CC AMINOTRANSFERASES.

DR EMBL: AF119413; AAF22111.1; -.

DR HSSP: P37821; 1B8C.

DR InterPro: IPR001176; ACQ\_synthase.

DR InterPro: IPR004839; Aminoctransf1/2.

DR InterPro: IPR004838; NHTransf\_1.

DR Pfam: PF00155; aminotran\_1.2; 1.

DR PRINTS: PR00753; ACQSYNTHASE.

DR PROSITE: PS00105; AA-TRANSFER\_CLASS\_1; 1.

KW Lyase; Pyridoxal phosphate.

SO SEQUENCE 488 AA; 55026 MW; 5EB0640DD129970 CRC64;

Query Match  
Best Local Similarity 94.7%; Score 36; DB 10; Length 488;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LAMSWL 6  
:|||||  
DB 479 LAMSWL 484

## RESULT 2

ID 026849 PRELIMINARY; PRT; 675 AA.

AC 026849;  
DT 01-JAN-1998 (TREMBLrel. 05, Created)  
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)  
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
DE Heavy metal transporting CPX-type ATPase.  
GN MTH755.

OS Methanobacterium thermoautotrophicum.  
OC Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;  
OC Methanobacteriaceae; Methanothermobacter.  
OX NCBI\_TaxID=187420;

RN [1]  
RP SEQUENCE FROM N.A.

RC STRAIN-DELTA H;  
RX MEDLINE-98037514; PubMed-9371463;

RA Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois J.,  
RA Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,  
RA Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D.,  
RA Spadafora R., Viare R., Wang Y., Wierzbowski J., Gibson R.,  
RA Iwani N., Caruso A., Bush D., Sater H., Patwell D., Prabhakar S.,  
RA McDougall S., Shmer G., Goyal A., Pietrovski S., Church G.M.,  
RA Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.;  
RT "Complete genome sequence of Methanobacterium thermoautotrophicum  
deltaH: functional analysis and comparative genomics.";

RL J. Bacteriol. 179:7135-7155(1997).

DR EMBL; AE000854; AAB85258.1; -

DR InterPro; IPR002106; AtcRNA\_LigaseII.

DR InterPro; IPR00157; ATPase\_E1-E2.

DR InterPro; IPR001454; Hlgase/hydriase.

DR Pfam; PF00122; E1-E2\_ATPase; 1.

DR Pfam; PF00702; Hydrolase; 1.

DR PRINTS; PR00119; CAYATPASE.

DR PROSITE; PS00339; AA\_TRNA\_LIGASE\_II\_2; UNKNOWN\_1.

DR PROSITE; PS00154; ATPase\_E1-E2; UNKNOWN\_1.

DR Complete proteome.  
KW SEQUENCE 675 AA; 72337 MW; 56A5D4C175C0CC6F CRC64;

Query Match  
Best Local Similarity 94.7%; Score 36; DB 17; Length 675;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LAMSWL 6  
:|||||  
DB 299 LAMSWL 304

## RESULT 3

ID 098C88 PRELIMINARY; PRT; 91 AA.

AC 098C88;  
DT 01-OCT-2001 (TREMBLrel. 18, Created)  
DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)  
DT 01-OCT-2001 (TREMBLrel. 18, Last annotation update)  
DE Exopolysaccharide production repressor, ExoX.  
GN MUR5253.

OS Rhizobium loti (Mesorhizobium loti).

OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;

OC Phyllobacteriaceae; Mesorhizobium.

OX NCBI\_TaxID=381;  
RN [1]

RP SEQUENCE FROM N.A.  
RC STRAIN-MAFF303099;

RX MEDLINE-21082930; PubMed-11214968;

RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,  
RA Watanabe A., Idegawa K., Ishikawa A., Kawashima K., Kimura T.,  
RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,  
RA Mochizuki Y., Yamada M., Nakazaki N., Shimo S., Sugimoto M.,  
RA Takeuchi C., Yamada M., Tabata S.;

RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium  
Mesorhizobium loti.";

RL DNA Res. 7:331-338(2000).

DR EMBL; AP003006; BAB51733.1; -

KW Complete proteome.  
SQ SEQUENCE 91 AA; 9887 MW; 10F09237249B37F0 CRC64;

Query Match  
Best Local Similarity 92.1%; Score 35; DB 16; Length 91;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LAMSWL 6  
:|||||  
DB 18 LAMSWL 23

## RESULT 4

ID 068039 PRELIMINARY; PRT; 116 AA.

AC 068039;

DT 01-AUG-1998 (TREMBLrel. 07, Created)  
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)  
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)

DE Hypothetical 12.6 kDa protein.

OS Rhodospirillum rubrum (Rhodospirillum rubrum).

OC Bacteria; Proteobacteria; alpha subdivision; Rhodospirillum group;

OC Rhodospirillum.

OX NCBI\_TaxID=1061;

RN [1]  
RP SEQUENCE FROM N.A.

RC STRAIN-SB1003;

RX MEDLINE-97404404; PubMed-9256491;  
VLICK C., Paces V., Maltsev N., Paces J., Haselkorn R., Feinstein M.;

RT "Sequence of a 189-kb segment of the chromosome of Rhodospirillum  
rubrum.";

RL Proc. Natl. Acad. Sci. U.S.A. 94:9384-9388(1997).

DR EMBL; AF010436; AAC16125.1; -

DR InterPro; IPR005133; Phag\_MnHg\_YuFB.

DR Pfam; PF03334; Phag\_MnHg\_YuFB; 1.

DR TIGRFAMs; TIGR01300; CPA3\_mnHg\_phag; 1.

DR Hypothetical protein.  
KW SEQUENCE 116 AA; 12553 MW; FFB91E726D421996 CRC64;

Query Match  
Best Local Similarity 92.1%; Score 35; DB 2; Length 116;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LAMSWL 6  
:|||||  
DB 63 LAMSWL 68

## RESULT 5

ID 005744 PRELIMINARY; PRT; 135 AA.

AC 005744;  
DT 01-JUL-1997 (TREMBLrel. 04, Created)  
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)  
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)  
DE Hypothetical 14.5 kDa protein.

GN MCB85.12.

OS Mycobacterium leprae.

OC Bacteria; Firmicutes; Actinobacteria; Actinobacteriales;  
OC Actinomycetales; Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.

OX NCBI\_TaxID=1769;

[1]  
 RP SEQUENCE FROM N.A.  
 RA Badcock K., Churcher C.M.;  
 RL Submitted (May-1997) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Parkhill J., Barrell B.G., Randal M.A.;  
 RL Submitted (May-1997) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE-9318700; Pubmed-8446027;  
 RA Elgimeier K., Honore N., Woods S.A., Caudron B., Cole S.T.;  
 RT "Use of an ordered cosmid library to deduce the genomic organization  
 of Mycobacterium leprae."  
 RL Mol. Microbiol. 7:197-206(1993).  
 DR EMBL: Z95151; CAB08408.1; -  
 KW Hypothetical protein.  
 SQ SEQUENCE 135 AA; 14516 MW; E7B32E2379C4888C CRC64;

Query Match 92.1%; Score 35; DB 2; Length 135;  
 Best Local Similarity 83.3%; Pred. No. 1.9e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LANSWL 6  
 DB 23 LANSWL 28

## RESULT 6

O9KR81 PRELIMINARY; PRT; 172 AA.  
 AC O9KR81;  
 DT 01-OCT-2000 (TREMblrel. 15, Created)  
 DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)  
 DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)  
 DE Hypothetical 18.8 kDa protein.  
 GN CRK.  
 OS Brevibacterium linens.  
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;  
 OC Actinomycetales; Micrococcales; Brevibacteriaceae; Brevibacterium.  
 OX NCBI\_TaxId-1703;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-DSM 20426;  
 RX MEDLINE-20279196; Pubmed-10821176;  
 RA Krubasik P., Sandmann G.;  
 RT "A carotenogenic gene cluster from Brevibacterium linens with novel  
 carotenoid genes involved in the synthesis of aromatic  
 carotenoids."  
 RL Mol. Gen. Genet. 263:423-432(2000).  
 DR EMBL: AF139916; AAF65585.1; -  
 DR InterPro: IPR000230; RiboSomaL\_S12.  
 DR InterPro: IPR004307; TSP0\_MBR.  
 DR Pfam: PF03073; TSP0\_MBR.1.  
 DR PROSITE: PS00055; RIBOSOMAL\_S12; UNKNOWN\_1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 172 AA; 18808 MW; 9F6BD848E95875F5 CRC64;

Query Match 92.1%; Score 35; DB 2; Length 172;  
 Best Local Similarity 83.3%; Pred. No. 2.4e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LANSWL 6  
 DB 91 VAMSWL 96

## RESULT 7

O50005 PRELIMINARY; PRT; 196 AA.  
 AC O50005;  
 DT 01-NOV-1996 (TREMblrel. 01, Created)  
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)

DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)  
 DE U1764V (Hypothetical protein ML1041).  
 GN ML1041.  
 OS Mycobacterium leprae.  
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;  
 OC Actinomycetales; Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.  
 OX NCBI\_TaxId-1769;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Smith D.R., Robison K.;  
 RL Submitted (Apr-1995) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.

RC STRAIN-TN;  
 RX MEDLINE-21128732; Pubmed-11234002;  
 RA Cole S.T., Elgimeier K., Parkhill J., James K.D., Thomson N.R.,  
 RA Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,  
 RA Mungall K., Basham D., Brown D., Chillingworth T., Connor R.,  
 RA Davies R.M., Devlin K., Duthoy S., Felwell T., Fraser A., Hamlin N.,  
 RA Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,  
 RA Murphy L., Oliver K., Quail M.A., Randal M.A., Rutherford K.M.,  
 RA Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,  
 RA Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,  
 RA Barrell B.G.;  
 RT "Massive gene decay in the leprosy bacillus."  
 RL Nature 409:1007-1011(2001).  
 DR EMBL: U15181; AAA62925.1; -  
 DR EMBL: AL583920; CAC31422.1; -  
 DR Leproma: ML1041; -  
 KW Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 196 AA; 21186 MW; 15DAF7CDE53936 CRC64;

Query Match 92.1%; Score 35; DB 16; Length 196;  
 Best Local Similarity 83.3%; Pred. No. 2.8e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LANSWL 6  
 DB 109 VAMSWL 114

## RESULT 8

O8RSV7 PRELIMINARY; PRT; 197 AA.  
 AC O8RSV7;  
 DT 01-JUN-2002 (TREMblrel. 21, Created)  
 DT 01-JUN-2002 (TREMblrel. 21, Last sequence update)  
 DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)  
 DE Matutase (Fragment).  
 OS uncultured marine bacterium.  
 OC Bacteria; environmental samples.  
 OX NCBI\_TaxId-56765;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Podar M., Mullineaux L., Sogin M.L., Perlman P.S.;  
 RT "Bacterial group II introns in a deep sea hydrothermal vent  
 environment."  
 RL Submitted (Jan-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AY075118; AAL78689.1; -  
 FT NON\_TER  
 SQ SEQUENCE 197 AA; 24010 MW; FA76F629B3D836A CRC64;

Query Match 92.1%; Score 35; DB 2; Length 197;  
 Best Local Similarity 83.3%; Pred. No. 2.8e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LANSWL 6  
 DB 172 LANSWL 177

## RESULT 9

O86317

ID 086317 PRELIMINARY: PRT: 210 AA.  
 AC 086317  
 DT 01-NOV-1998 (TREMBlrel. 08, Created)  
 DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)  
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)  
 DE Hypothetical protein RV2680.  
 GN RV2680 OR MT2754 OR MT010.04.  
 OS Mycobacterium tuberculosis.  
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;  
 OC Actinomycetales; Corynebacteriaceae; Mycobacterium.  
 NCBI\_TaxID=1773;  
 [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-H37RV:  
 RX MEDLINE=96295987; PubMed=9634230;  
 RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,  
 RA Gordon S.V., Eigmeier K., Gas S., Barry C.E. III, Tekala F.,  
 RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,  
 RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,  
 RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,  
 RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,  
 RA Rutter S., Seeger K., Skelton S., Squares R., Squares J.,  
 RA Sultun J.E., Taylor K., Whitehead S., Barrett B.G.,  
 RA "Deciphering the biology of Mycobacterium tuberculosis from the  
 RT complete genome sequence."  
 RL Nature 393:537-544(1998).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-CDC 1551 / OSHKOSH;  
 RA Fleischnann R.D., Alland D., Eisen J.A., Carpenter L., White O.,  
 RA Peterson J., Debey R., Dodson R., Gwinn M., Haft D., Hickey E.,  
 RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L.,  
 RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,  
 RA Bishai W.;  
 RT "Whole genome comparison of Mycobacterium tuberculosis clinical and  
 RT laboratory strains."  
 RL Submitted (APR-2001) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: Z96072; CAB09496.1; -  
 DR EMBL: AE007105; AAK47069.1; ALT\_INIT.  
 DR TIGR: MT2754; -  
 DR Tuberculist; RV2680; -  
 KW Hypothetical protein: Complete proteome.  
 SQ SEQUENCE 210 AA: 22573 MW: 2D9429BF1FE0956A CRC64;  
 Query Match 92.1%; Score 35; DB 16; Length 210;  
 Best Local Similarity 83.3%; Pred. No. 3e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 LAMSWL 6 :|||||  
 DB 123 VAMSWL 128  
 RESULT 10  
 094515 PRELIMINARY: PRT: 321 AA.  
 AC 094515.  
 DT 01-FEB-1997 (TREMBlrel. 02, Created)  
 DT 01-FEB-1997 (TREMBlrel. 02, Last sequence update)  
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)  
 DE IFC protein (LD15458P) (Sphingolipid delta 4 desaturase protein  
 DE Des-1).  
 GN IFC OR DES1 OR CG9078.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 DE Ephydroidea; Drosophilidae; Drosophila.  
 NCBI\_TaxID=7227;  
 [1]  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BERKELEY;  
 RX MEDLINE=20196006; PubMed=10731132;  
 RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
 RA Ballew R.M., Basu A., Baxendale J., Bayraktiroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S.,  
 RA Borrova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,  
 RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
 RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Glodek K., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeagwam C.,  
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson J.,  
 RA Merulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusser D.R., Pacle J.M.,  
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svirska R., Tector C., Turner R., Ventler E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of Drosophila melanogaster."  
 RL Science 287:2185-2195(2000).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-OREGON R;  
 RX MEDLINE=97156918; PubMed=9003299;  
 RA Endo K., Akiyama T., Kobayashi S., Okada M.;  
 RT "Degenerative spermatocyte, a novel gene encoding a transmembrane  
 RT protein required for the initiation of meiosis in Drosophila  
 RT spermatogenesis."  
 RL Mol. Gen. Genet. 253:157-165(1996).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BERKELEY;  
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,  
 RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,  
 RA Gonzalez M., Guartin H., Li P., Liao G., Miranda A., Mungall C.J.,  
 RA Nuncio J., Pacle J., Paragas V., Park S., Phouanavong S., Wan K.,  
 RA Yu C., Lewis S.E., Rubin G.M., Celinker S.;  
 RT Submitted (OCT-2001) to the EMBL/Genbank/DBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-WHOLE BODY;  
 RA Terres P., Franke S., Zaehlinger U., Sperling P., Heinz E.;  
 RT "Identification and Characterization of a Sphingolipid delta4-  
 RT desaturase Family.";  
 RL J. Biol. Chem. 277:10000-10006(2002).  
 DR EMBL: AE003612; AAF52318.1; -  
 DR EMBL: X94180; CAA63889.1; -  
 DR EMBL: AY061196; AAL28744.1; -  
 DR EMBL: AF466379; AAM12535.1; -  
 DR FLYBASE: FBgn0001941; ffc.  
 DR InterPro: IPR001064; Crystalin.  
 DR InterPro: IPR001225; FA\_desaturase.  
 DR InterPro: IPR000130; Zn\_Mpseptase.  
 DR Pfam: PF00487; FA\_desaturase; 1.  
 DR PROSITE: PS00225; CRYSTALLIN\_BETAGAMMA; UNKNOWN\_1.  
 DR PROSITE: PS00142; ZINC\_PROTEASE; UNKNOWN\_1.

KW Transmembrane.  
 SQ SEQUENCE 321 AA; 37213 MW; B8DB1361BF5F38E CRC64;  
 Query Match  
 Best Local Similarity 92.1%; Score 35; DB 5; Length 321;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LANSWL 6  
 Db 64 LANSWL 69

RESULT 11  
 ID Q9VEY8 PRELIMINARY; PRT; 329 AA.  
 AC Q9VEY8;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE CG10148 protein.  
 GN CG10148.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 NCBI\_Taxid=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BERKELEY;  
 RX MEDLINE=20196006; PubMed=10731132;  
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,  
 Man K.H., Doyle C., Baxter E.G., Helt J.G., Nelson C.R., Miklos G.L.G.,  
 Abril J.F., Aghayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
 Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 Beeson K.Y., Benos P.V., Bertone B.P., Bhandari D., Bolshakov S.,  
 Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,  
 Burks K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 Cherry J.M., Chew S., Dahlke C., Davenport L.B., Davies P., de  
 Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 Dodson K., Dou P.L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,  
 Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
 Hostin D., Houston K.A., Howland T.J., Wei M.-H., Idegawa C.,  
 Jalali M., Kalush F., Karpen G.H., Ke Z., Kenlison J.A., Ketchum K.A.,  
 Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
 Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,  
 Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 Reibert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 Wang Z.-Y., Wasserman D., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RA "The genome sequence of Drosophila melanogaster.";  
 RL Science 287:2185-2195(2000).  
 DR EMBL; AEO03698; AAF54907.1; -;  
 DR FLYBase; FBgn0038120; CG10148.  
 DR InterPro; IPR001611; LRR.  
 DR InterPro; IPR003592; LRR\_out.  
 DR InterPro; IPR003591; LRR\_tyr.

DR Pfam; PF00560; LRR; 4.  
 DR PRINTS; PR00019; LEURICHRPT.  
 DR SMART; SM00370; LRR; 3.  
 DR SMART; SM00369; LRR\_tyr; 1.  
 SQ SEQUENCE 329 AA; 37165 MW; C4106348E5C334DA CRC64;  
 Query Match  
 Best Local Similarity 92.1%; Score 35; DB 5; Length 329;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LANSWL 6  
 Db 17 LANSWL 22

RESULT 12  
 ID Q92NU3 PRELIMINARY; PRT; 422 AA.  
 AC Q92NU3;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE Putative NADH dehydrogenase transmembrane protein (EC 1.6.99.3).  
 GN NDH OR R02079 OR SMC04452.  
 OS Rhizobium meliloti (Sinorhizobium meliloti).  
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;  
 OC Rhizobiaceae; Sinorhizobium.  
 NCBI\_Taxid=382;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=1021;  
 RX MEDLINE=21396507; PubMed=11481430;  
 RA Capela D., Barley-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,  
 Bostard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,  
 Godrie T., Goffeau A., Kahn D., Kiss E., Lelaire V., Masuy D.,  
 Pohl T., Portetalle D., Puehler A., Purnelle B., Rampeger U.,  
 Renard C., Thebaud P., Vandenbol M., Weidner S., Gallibert F.,  
 RT "Analysis of the chromosome sequence of the legume symbiont  
 Sinorhizobium meliloti strain 1021.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).  
 DR EMBL; AL591789; CAC46658.1; -;  
 DR InterPro; IPR001327; FAD\_DYR\_redox.  
 DR Pfam; PF00070; PYR\_redox; 1.  
 KW Oxidoreductase; Complete proteome.  
 SQ SEQUENCE 422 AA; 46023 MW; 1490D9AC1EA517DB CRC64;  
 Query Match  
 Best Local Similarity 92.1%; Score 35; DB 16; Length 422;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LANSWL 6  
 Db 394 VANSWL 399

RESULT 13  
 ID Q8UDU6 PRELIMINARY; PRT; 438 AA.  
 AC Q8UDU6;  
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE NADH dehydrogenase.  
 GN NDH OR ATU0203 OR AGR\_C3667.  
 OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).  
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;  
 OC Rhizobiaceae; Rhizobium.  
 NCBI\_Taxid=176299;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21608550; PubMed=11743193;  
 RA Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,  
 Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,

RA Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Boyce D. St.,  
 RA Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,  
 RA Kutyavin T., Levy R., Li M.-J., McClelland E., Palmeri A.,  
 RA Raymond C., Rouse G., Saenphitachak C., Wu Z., Romero P., Gordon D.,  
 RA Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,  
 RA Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,  
 RA Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,  
 RA Nester E.W.;  
 RT "The genome of the natural genetic engineer *Agrobacterium tumefaciens*  
 C58.";  
 RL Science 294:2317-2323(2001).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-21608551; PubMed-11743194;  
 RA Goodner B., Hunkle G., Gattung S., Miller N., Blanchard M.,  
 RA Quicilo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,  
 RA Houtmel K., Gordon J., Vaudin M., Iarchouk O., Epp A., Liu F.,  
 RA Wollam C., Allinger M., Doughy D., Scott C., Lapps C., Marzel B.,  
 RA Flanagan C., Crowell C., Gursen J., Lomo C., Sear C., Strub G.,  
 RA Cleio C., Slater S.;  
 RT "Genome sequence of the plant pathogen and biotechnology agent  
*Agrobacterium tumefaciens* C58.";  
 RL Science 294:2323-2328(2001).  
 DR EMBL: AE009153; AAL43015.1: ALU-INT.  
 DR EMBL: AE008119; AAK6777.1; -  
 KW Complete proteome.  
 SQ SEQUENCE 438 AA; 47993 MW; B857CB84D03D9E7B CRC64;

Query Match 92.1%; Score 35; DB 16; Length 438;  
 Best Local Similarity 83.3%; Pred. No. 6.2e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LAMSWL 6  
 DB 410 VAMSWL 415

RESULT 14  
 O8YBV0 PRELIMINARY; PRT; 441 AA.  
 AC O8YBV0;  
 DT 01-MAR-2002 (TREMBLrel. 20, Created)  
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE NAH dehydrogenase (EC 1.6.99.3).  
 GN BME10786.  
 GN Brucella melitensis.  
 OS Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;  
 OC Brucellaceae; Brucella.  
 OX NCBI\_TaxID=29459;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX STRAIN-16W / ATCC 23456 / BIOTYPE 1;  
 RX MEDLINE-20020109; PubMed-11756688;  
 RA Delvecchio V.G., Kapatal V., Redkar R.J., Patra G., Mijer C., Los T.,  
 RA Ivanova N., Anderson I., Bhattacharya A., Lykidis A., Reznik G.,  
 RA Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goldsman E.,  
 RA Seikov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,  
 RA Haselkorn R., Kyripides N., Overbeek R.;  
 RT "The genome sequence of the facultative intracellular pathogen  
*Brucella melitensis*.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).  
 DR EMBL: AE009713; AAL54028.1; -  
 DR InterPro: IPR001327; FAD\_Pyr\_redox.  
 DR Pfam: PF00070; Pyr\_redox; 1.  
 KW Oxidoreductase; Complete proteome.  
 SQ SEQUENCE 441 AA; 48477 MW; E9D846904C6CB5D7 CRC64;

Query Match 92.1%; Score 35; DB 16; Length 441;  
 Best Local Similarity 83.3%; Pred. No. 6.3e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LAMSWL 6

DB 413 VAMSWL 418

RESULT 15  
 O9S722 PRELIMINARY; PRT; 1055 AA.  
 AC O9S722;  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE SMC-like protein.  
 GN MIM.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 OX NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX STRAIN-CV. COLUMBIA;  
 RX MEDLINE-99380167; PubMed-10449416;  
 RA Mengiste T., Revenkova E., Bechtold N., Paszkowski J.;  
 RT "An SMC-like protein is required for efficient homologous  
 recombination in arabidopsis.";  
 RL EMBL J. 18:4505-4512(1999).  
 DR EMBL: AF120933; AAD54770.1; -  
 DR EMBL: AF120932; AAD54769.1; -  
 DR InterPro: IPR003439; ABC\_transport.  
 DR InterPro: IPR003395; SMC\_N.  
 DR Pfam: PF02463; SMC\_N; 1.  
 SQ SEQUENCE 1055 AA; 121349 MW; E9F0C0427FB602E4 CRC64;

Query Match 92.1%; Score 35; DB 10; Length 1055;  
 Best Local Similarity 83.3%; Pred. No. 1.5e+03;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LAMSWL 6  
 DB 248 LAMSWV 253

Search completed: May 30, 2003, 14:38:50  
 Job time : 22.7632 secs

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OM protein - protein search, using sw model

Run on: May 30, 2003, 14:41:40 ; Search time 3.11842 Seconds

(without alignments)  
79.803 Million cell updates/sec

Title: US-09-643-260-7

Perfect score: 38

Sequence: 1 LAMSWL 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	34	89.5	338 1	GALE_MYCPN
2	34	89.5	1239 1	P08768 eastern egu
3	34	89.5	1240 1	P08768 eastern egu
4	34	89.5	1402 1	P08768 eastern egu
5	33	86.8	1118 1	YE16_HAEMIN
6	33	86.8	1053 1	HMDR_SCHPO
7	33	86.8	1564 1	N184_SCHPO
8	32	84.2	60 1	YMER_ECOLI
9	32	84.2	136 1	Y07C_BPPI4
10	32	84.2	252 1	Y410_RHISN
11	32	84.2	446 1	NU4M_CERCA
12	32	84.2	471 1	MELE_ENTAE
13	32	84.2	471 1	MELE_ENTAE
14	32	84.2	592 1	NDCL_HUMAN
15	32	84.2	745 1	IKRA_HUMAN
16	32	84.2	745 1	IKRA_MOUSE
17	32	84.2	756 1	IKRB_HUMAN
18	32	84.2	757 1	IKRB_MOUSE
19	32	84.2	757 1	IKRB_MOUSE
20	32	84.2	842 1	AMPN_LACDL
21	32	84.2	981 1	RREO_HANNV
22	32	84.2	982 1	RREO_HANNV
23	32	84.2	982 1	RREO_HANNV
24	32	84.2	982 1	RREO_HANNV
25	32	84.2	982 1	RREO_HANNV
26	32	84.2	982 1	RREO_HANNV
27	32	84.2	982 1	RREO_HANNV
28	32	84.2	982 1	RREO_HANNV
29	32	84.2	982 1	RREO_HANNV
30	32	84.2	982 1	RREO_HANNV
31	32	84.2	982 1	RREO_HANNV
32	32	84.2	982 1	RREO_HANNV
33	32	84.2	982 1	RREO_HANNV

34	31	81.6	443 1	FD6C_BRANA	P48627 brassica na
35	31	81.6	447 1	FD6C_SPIOL	P48629 spiniacia ol
36	31	81.6	448 1	FD6C_ARATH	P46312 arabidopsis
37	31	81.6	483 1	VE2_HPVI4	P36783 human papil
38	31	81.6	493 1	VE2_HPVI9	P36786 human papil
39	31	81.6	497 1	VE2_HPVI20	P50766 human papil
40	31	81.6	502 1	VE2_HPVI25	P36787 human papil
41	31	81.6	503 1	VE2_HPVI21	P50767 human papil
42	31	81.6	646 1	T3MO_BPPI	P08763 bacterioph
43	31	81.6	726 1	VNCS_PAVBO	P07296 bovine parv
44	31	81.6	838 1	PTFL_XANCP	P45597 x multilipos
45	31	81.6	870 1	FTMD_SALTY	P37924 salmonella

## ALIGNMENTS

RESULT 1  
GALE\_MYCPN STANDARD; PRT; 338 AA.  
ID GALE\_MYCPN  
AC P75517;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE UDP-glucose 4-epimerase (EC 5.1.3.2) (Galactowaldenase) (UDP-  
galactose 4-epimerase).  
GN GALE OR MPN257 OR MP576.  
OS Mycoplasma pneumoniae.  
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.  
OX NCBI\_TaxID=2104;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-ATCC 29342 / M129;  
RX MEDLINE-97105885; PubMed-8948633;  
RA Himmelreich R., Hilbert H., Plagens H., Pirkl E., Li B.-C.,  
Herrmann R.;  
RT "Complete sequence analysis of the genome of the bacterium Mycoplasma  
pneumoniae."  
RL Nucleic Acids Res. 24:4420-4449(1996).  
CC -1- CATALYTIC ACTIVITY: UDP-glucose -> UDP-galactose.  
CC -1- COFACTOR: NAD.  
CC -1- PATHWAY: Galactose metabolism; third step.  
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).  
CC -1- SIMILARITY: BELONGS TO THE SUGAR EPIMERASE FAMILY.  
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CC  
DR EMBL; AE000056; AAB96224.1; -  
DR HSP; P09147; IKVS.  
DR InterPro; IPR001509; Epimerase\_Dh.  
DR Pfam; PF01370; Epimerase; 1.  
DR TIGRFAMs; TIGR01179; gale; 1.  
KW Isomerase; NAD; Galactose metabolism; Complete proteome.  
FT NP\_BIND 338 AA; 38132 MW; 9C50FF3856E8C03 CRC64;  
SQ  
Query Match 89.5%; Score 34; DB 1; Length 338;  
Best Local Similarity 83.3%; Pred. No. 1;e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

ID POLS\_EEEV3 STANDARD: PRT: 1239 AA.  
 AC P08768:  
 DT 01-NOV-1988 (Rel. 09, Created)  
 DT 01-NOV-1988 (Rel. 09, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Structural polypeptide (P130) [Contains: Coat protein C (EC 3.4.21.-)]  
 DE (Capsid protein C): Spike glycoprotein E3; Spike glycoprotein E2;  
 DE 6 kDa peptide; Spike glycoprotein E1.  
 OS Eastern equine encephalitis virus (Eastern equine encephalomyelitis virus).  
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Togaviridae;  
 OC Alphavirus.  
 OX NCBI\_TaxID=11021;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-82V-2137;  
 RX MEDLINE-8728265; PubMed-2886548;  
 RA Chang G.-J., Trent D.W.;  
 RT "Nucleotide sequence of the genome region encoding the 26S mRNA of eastern equine encephalomyelitis virus and the deduced amino acid sequence of the viral structural proteins."  
 RL J. Gen. Virol. 68:2129-2142(1987).  
 CC -1- FUNCTION: THE CAPSID PROTEIN IS AN AUTO-PROTEASE.  
 CC -1- PTM: SPECIFIC ENZYMAIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS.  
 CC -1- MISCELLANEOUS: THE 6 kDa POLYPEPTIDE PROBABLY SERVES AS THE SIGNAL SEQUENCE FOR THE MEMBRANE GLYCOPROTEIN E1, WHICH IS THE VIRAL HEMAGGLUTININ.  
 CC -1- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY S3.  
 CC -----  
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 CC -----  
 DR EMBL: X05816; CAA29261.1; -  
 DR PIR: A26816; VHWYEE.  
 DR HSSP: P03315; IYCP.  
 DR MEROPS: S03.001; -  
 DR InterPro: IPR002548; Alpha\_E1\_glycop.  
 DR InterPro: IPR000936; Alpha\_E2\_glycop.  
 DR InterPro: IPR002533; Alpha\_E3\_glycop.  
 DR InterPro: IPR001836; Alpha\_core.  
 DR InterPro: IPR000930; Togavirin.  
 DR Pfam: PF009443; Alpha\_E2\_glycop; 1.  
 DR Pfam: PF00944; Alpha\_core; 1.  
 DR Pfam: PF01563; Alpha\_E3\_glycop; 1.  
 DR Pfam: PF01589; Alpha\_E1\_glycop; 1.  
 DR PRINTS: PR00798; TOGAVIRIN.  
 KW Coat protein; Polypeptide; Transmembrane; glycoprotein; Hydrolyase; Serine protease.  
 KM  
 FT CHAIN 1 259 COAT PROTEIN C.  
 FT CHAIN 260 322 SPIKE GLYCOPROTEIN E3.  
 FT CHAIN 323 742 SPIKE GLYCOPROTEIN E2.  
 FT CHAIN 743 798 6 kDa peptide.  
 FT CHAIN 799 1239 SPIKE GLYCOPROTEIN E1.  
 FT ACT\_SITE 136 136 CHARGE RELAY SYSTEM (BY SIMILARITY).  
 FT ACT\_SITE 142 142 CHARGE RELAY SYSTEM (BY SIMILARITY).  
 FT ACT\_SITE 210 210 CHARGE RELAY SYSTEM (BY SIMILARITY).  
 FT TRANSMEM 261 277 POTENTIAL.  
 FT TRANSMEM 684 701 POTENTIAL.  
 FT TRANSMEM 727 737 POTENTIAL.  
 FT TRANSMEM 777 798 POTENTIAL.  
 FT TRANSMEM 1211 1235 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 49 49 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 637 637 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 932 932 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SO SEQUENCE 1239 AA; 137431 MW; 8C7664A405D2D41C CRC64;  
 Query Match 89.5%; Score 34; DB 1; Length 1239;  
 Best Local Similarity 100.0%; Pred. No. 3.7e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 2 ANSWL 6  
 Db 1205 ANSWL 1209  
 RESULT 3  
 ID POLS\_EEEV3 STANDARD: PRT: 1240 AA.  
 AC P27284;  
 DT 01-AUG-1992 (Rel. 23, Created)  
 DT 01-AUG-1992 (Rel. 23, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Structural polypeptide (P130) [Contains: Coat protein C (EC 3.4.21.-)]  
 DE (Capsid protein C): Spike glycoprotein E3; Spike glycoprotein E2;  
 DE 6 kDa peptide; Spike glycoprotein E1.  
 OS Eastern equine encephalitis virus (strain va33(ten breck)) (Eastern equine encephalomyelitis virus).  
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Togaviridae;  
 OC Alphavirus.  
 OX NCBI\_TaxID=11022;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-91220727; PubMed-2024496;  
 RA Weaver S.C., Scott T.W., Rico-Hesse R.;  
 RT "Molecular evolution of eastern equine encephalomyelitis virus in North America."  
 RL Virology 182:774-784(1991).  
 CC -1- FUNCTION: THE CAPSID PROTEIN IS AN AUTO-PROTEASE.  
 CC -1- PTM: SPECIFIC ENZYMAIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS.  
 CC -1- MISCELLANEOUS: THE 6 kDa POLYPEPTIDE PROBABLY SERVES AS THE SIGNAL SEQUENCE FOR THE MEMBRANE GLYCOPROTEIN E1, WHICH IS THE VIRAL HEMAGGLUTININ.  
 CC -1- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY S3.  
 CC -----  
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 CC -----  
 DR EMBL: M69094; AAA42980.1; -  
 DR PIR: A39992; VHWYEV.  
 DR HSSP: P03315; IYCP.  
 DR MEROPS: S03.001; -  
 DR InterPro: IPR002548; Alpha\_E1\_glycop.  
 DR InterPro: IPR000936; Alpha\_E2\_glycop.  
 DR InterPro: IPR002533; Alpha\_E3\_glycop.  
 DR InterPro: IPR001836; Alpha\_core.  
 DR InterPro: IPR000930; Togavirin.  
 DR Pfam: PF009443; Alpha\_E2\_glycop; 1.  
 DR Pfam: PF00944; Alpha\_core; 1.  
 DR Pfam: PF01563; Alpha\_E3\_glycop; 1.  
 DR Pfam: PF01589; Alpha\_E1\_glycop; 1.  
 DR PRINTS: PR00798; TOGAVIRIN.  
 KW Coat protein; Polypeptide; Transmembrane; glycoprotein; Hydrolyase; Serine protease.  
 KM  
 FT CHAIN 1 260 COAT PROTEIN C.  
 FT CHAIN 261 323 SPIKE GLYCOPROTEIN E3.  
 FT CHAIN 324 743 SPIKE GLYCOPROTEIN E2.  
 FT CHAIN 744 799 6 kDa peptide.  
 FT CHAIN 800 1240 SPIKE GLYCOPROTEIN E1.  
 FT ACT\_SITE 137 137 CHARGE RELAY SYSTEM (BY SIMILARITY).  
 FT ACT\_SITE 143 143 CHARGE RELAY SYSTEM (BY SIMILARITY).  
 FT ACT\_SITE 211 211 CHARGE RELAY SYSTEM (BY SIMILARITY).  
 FT TRANSMEM 259 276 POTENTIAL.  
 FT TRANSMEM 695 712 POTENTIAL.  
 FT TRANSMEM 722 738 POTENTIAL.  
 FT TRANSMEM 781 799 POTENTIAL.  
 FT TRANSMEM 1212 1236 POTENTIAL.

FT CARBOHYD 49 49 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 638 638 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 834 834 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 933 933 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SO SEQUENCE 1240 AA; 137290 MW; ABBEB1599D083045 CRC64;

Query Match 89.5%; Score 34; DB 1; Length 1240;  
 Best Local Similarity 100.0%; Pred. No. 3.7e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 AWSWL 6  
 DB 1206 AWSWL 1210

RESULT 4  
 Y197\_MOUSE  
 ID Y197\_MOUSE STANDARD; PRT; 1402 AA.

AC 0920W3;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Protein KIAA0197 (GTL-13).

GN KIAA0197 OR GTL1-13.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RC STRAIN-129/SVJ;  
 RA Van de Putte T., Cozijnsen M., Dewulf N., Tydzanowski P., Lonnoy O.,  
 RA Huybrecock D.;  
 RT \*Mus musculus mRNA for gtl-13 (gene trap locus-13), similar to human  
 RT KIAA0197 gene (D83781), complete cds.\*;  
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.

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CC EMBL; AF104415; AAD17922.2; -  
 DR MGD; MGI:1926227; Gtl1-13.  
 SO SEQUENCE 1402 AA; 158230 MW; 3BF5D9F057D28772 CRC64;

Query Match 89.5%; Score 34; DB 1; Length 1402;  
 Best Local Similarity 100.0%; Pred. No. 4.1e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 AWSWL 6  
 DB 1230 AWSWL 1234

RESULT 5  
 YE16\_HAEIN  
 ID YE16\_HAEIN STANDARD; PRT; 118 AA.

AC P44188;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Hypothetical protein H11416 precursor.

GN H11416.  
 OS Haemophilus influenzae.  
 OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;  
 OC Haemophilus.  
 OX NCBI\_TaxID=727;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RC STRAIN-Rd / KW20 / ATCC 51907;  
 RX MEDLINE=95350630; PubMed=7542800;  
 RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,  
 RA Keriavene A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,  
 RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,  
 RA Scott J.D., Shrivley R., Liu L.-I., Glodek A., Kelley J.M.,  
 RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,  
 RA Usterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,  
 RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,  
 RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,  
 RA Venter J.C.;  
 RT "Whole-genome random sequencing and assembly of Haemophilus influenzae  
 RT Rd.";  
 RL Science 269:496-512(1995).

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CC EMBL; U32821; AAC23067.1; -  
 DR TIGR; H11416; -  
 KW Hypothetical protein; Signal; Complete proteome.  
 FT SIGNAL 1 27  
 FT CHAIN 28 118  
 SO SEQUENCE 118 AA; 13516 MW; 96CE5D469D8E2EB CRC64;

Query Match 86.8%; Score 33; DB 1; Length 118;  
 Best Local Similarity 83.3%; Pred. No. 62;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 LAWSWL 6  
 DB 11 LAWSWL 16

RESULT 6  
 HMDL\_SCHPO  
 ID HMDL\_SCHPO STANDARD; PRT; 1053 AA.

AC Q10283; 074425;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE 3-hydroxy-3-methylglutaryl-coenzyme A reductase (EC 1.1.1.34) (HMG-CoA  
 DE reductase).

GN HMG1 OR SPC162.09C.  
 OS Schizosaccharomyces pombe (fission yeast).  
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;  
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;  
 OX NCBI\_TaxID=4896;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RA MEDLINE=97051601; PubMed=8896278;  
 RA Lum P.Y., Edwards S., Wright R.;  
 RT "Molecular, functional and evolutionary characterization of the gene  
 RT encoding HMG-CoA reductase in the fission yeast, Schizosaccharomyces  
 RT pombe.";  
 RL Yeast 12:1107-1124(1996).  
 RN [2]  
 RP SEQUENCE FROM N.A.

RC STRAIN-972;  
 RX MEDLINE=21848401; PubMed=11859360;  
 RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,  
 RA Sgourou J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,  
 RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,  
 RA Collins M., Connor R., Cronin A., Davis P., Feltham C.M., Fraser A.,  
 RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,  
 RA Holtroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,  
 RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,

Query Match	Similarity	Score	DB 1	Length
Best Local	56.7%	Pred No. 4	5e+02	
Matches	4; Conservative	2; Mismatches	0; Indels	0; Gaps

  

QY	1	I	I	I	I	I
Db	177	ISMSWL	182			

  

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RESULT 7
ID N184_SCHPO STANDARD: PRT; 1564 AA.
AC 09P7M8; 09Y8G4;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Nucleoporin nup184 (Nuclear pore protein nup184) .
GN NUP184 OR SPAP27G11.10C.
OS Schizosaccharomyces pombe (fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomyces.
XX NCBI_taxid=4896;
XX [1]
XX
XX SEQUENCE FROM N.A., FUNCTION, AND SUBCELLULAR LOCATION.
XX
XX STRAIN=972;
XX MEDLINE=99318821; PubMed=10388805;
XX Whalen W.A., Yoon J.H., Shen R., Dhar R.;
XX "Regulation of mRNA export by nutritional status in fission yeast.";
XX Genetics 152:827-838(1999).
XX [2]
XX
XX SEQUENCE FROM N.A.
XX STRAIN=972;
XX MEDLINE=21848401; PubMed=11859360;
XX Wood V., Williams R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
XX Sgouros J., Beatt N., Hayles J., Baker S., Basham D., Bowman S.,
XX Brooks K., Brown D., Brown S., Chillingworth T., Church C.M.,
XX Collins M., Connor R., Cronin A., Davis P., Fellwell T., Fraser A.,
XX Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
XX Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
XX James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
XX Oliver P., O'Neill S., Mungall K., Murphy L., Niblett D., Odell C.,
XX Olyver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
XX Rutherford J., Rutter S., Saunders D., Seeger K., Sharp S.,
XX Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
XX Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
XX Williams J., Volckaert G., Aert R., Robben J., Grymoprez B.,
XX Welljeds I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
XX Gabell C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
XX Borzym K., Langer I., Beck A., Lehnach H., Reinhardt R., Pohl T.M.,
XX Eger P., Zimmermann W., Medler H., Wambutt R., Purnelle B.,
XX Goffeau A., Cadieu E., Dreano S., Gloux S., Laeure V., Mottier S.,
XX Galibert F., Aves S.-J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
XX Lucas M., Rochet M., Galliardin C., Tallada V.A., Rayon A., Thode G.,
XX Dugas R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Bento J.,
XX Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
XX Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
XX Shpakovski G.V., Ussery D., Barrett B.G., Nurse P.;
XX "The genome sequence of Schizosaccharomyces pombe.";
XX Nature 415:871-880(2002).
XX
XX -I- FUNCTION: INTERACTS WITH POM152 IN THE CORE STRUCTURE OF THE
XX NUCLEAR PORE COMPLEX (NPC). INVOLVED IN THE EXPORT OF mRNA.
XX -I- SUBCELLULAR LOCATION: Nuclear pore complex.
XX -I- CAUTION: REF.1 SEQUENCE DIFFERS FROM THAT SHOWN FROM POSITION 1560
XX ONWARD AND IS LONGER (1628 AA) DUE TO A FRAMESHIFT.
XX
XX -----
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CC -----  
 DR EMBL: AF055035; AAD43830.1; ALT\_FRAME.  
 DR EMBL: AL157917; CAB76031.1; -  
 KW Nuclear protein; Transport.  
 FT CONFIRM 1219 1219 S -> P (IN REF. 1).  
 SQ SEQUENCE 1564 AA; 176962 MW; 248F3AEF38C30B7 CRC64;

Query Match  
 Best Local Similarity 86.8%; Score 33; DB 1; Length 1564;  
 Best Local Similarity 66.7%; Pred. No. 6.4e+02;  
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 LAMSWL 6  
 DB 6 LAMSWL 11

# RESULT 8

YMF8\_FCOLI STANDARD; PRT; 60 AA.

AC P75979;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Hypothetical protein ymf8.  
 GN YMF8 OR B1150.  
 OS Escherichia coli.  
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
 OC Escherichia.  
 OX NCBI\_TaxID=562;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-K12 / MG1655;  
 RX MEDLINE=97426617; PubMed=9278503;  
 RA Blatner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,  
 RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,  
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,  
 RA Mau B., Shao Y.;  
 RT "The complete genome sequence of Escherichia coli K-12.";  
 RL Science 277:1453-1474(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-K12;  
 RX MEDLINE=97061202; PubMed=8905232;  
 RA Oshima T., Alba H., Baba T., Fujita K., Hayashi K., Honjo A.,  
 RA Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,  
 RA Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,  
 RA Mori H., Motomura K., Nakamura Y., Nishimoto H., Nishio Y., Saito N.,  
 RA Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,  
 RA Yano W., Horinouchi T.;  
 RT "A 718-kb DNA sequence of the Escherichia coli K-12 genome  
 corresponding to the 12.7-28.0 min region on the linkage map.";  
 RL DNA Res. 3:137-155(1996).  
 CC -1 SUBCELLULAR LOCATION: Integral membrane protein (Potential).

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CC EMBL: AE000214; AAC74234.1; -  
 DR EMBL: D90749; BAA35976.1; -  
 DR EMBL: D90750; BAA35988.1; -  
 DR Ecogene: EG14336; ymf8.  
 KW Hypothetical protein; Transmembrane; Complete proteome.  
 FT TRANSMEM 5 25 POTENTIAL.  
 FT TRANSNEM 26 46  
 SQ SEQUENCE 60 AA; 6381 MW; AA1487AAFEED364A CRC64;

Query Match 84.2%; Score 32; DB 1; Length 60;

Best Local Similarity 83.3%; Pred. No. 47;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 LAMSWL 6  
 DB 39 LAMSWL 44

# RESULT 9

Y07C\_BPT4 STANDARD; PRT; 136 AA.

AC P13323;  
 DT 01-JAN-1990 (Rel. 13, Created)  
 DT 01-JAN-1990 (Rel. 13, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Hypothetical 16.0 kDa protein in segB-*lpi* intergenic region (ORF3).  
 GN Y07C OR *lpi*-2 OR TRNA.3.  
 OS Bacteriophage T4.  
 OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;  
 OC T4-like viruses.  
 OX NCBI\_TaxID=10665;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=86037230; PubMed=4057254;  
 RA Broda J., Abelson J.;  
 RT "Sequence organization and control of transcription in the  
 RT bacteriophage T4 RNA region.";  
 RL J. Mol. Biol. 185:545-563(1985).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Kutter E., Arisaka F., Kunisawa T., Tsugita A., Mosig G.,  
 RA Mesyanzhinov V., Ruger W., Stidham T., Thomas E.;  
 RT "Bacteriophage T4 genome analysis";  
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.

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CC EMBL: X03016; CAA26805.1; -  
 DR EMBL: AF158101; AAD42681.1; -  
 KW Hypothetical protein.  
 SQ SEQUENCE 136 AA; 16034 MW; 02ED3B4D8D274D9A CRC64;

Query Match 84.2%; Score 32; DB 1; Length 136;  
 Best Local Similarity 80.0%; Pred. No. 99;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 AMSWL 6  
 DB 35 AMSWL 39

# RESULT 10

Y4IO\_RHISN STANDARD; PRT; 252 AA.

AC P55496;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE Hypothetical 28.6 kDa protein y4io.  
 GN Y4IO.  
 OS Rhizobium sp. (strain NGR234).

OG Plasmid sym pNGR234a.  
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;  
 OC Rhizobiaceae; Rhizobium.  
 OX NCBI\_TaxID=394;  
 RN [1]  
 RP SEQUENCE FROM N.A.

```

RX MEDLINE-97305956; PubMed-9163424;
RA Freiberg C.A., Fellay R., Bairoch A., Broughton W.J., Rosenthal A.,
RA Perret X.;
RT "Molecular basis of symbiosis between Rhizobium and Legumes.";
RL Nature 387:394-401(1997).
CC -1- SIMILARITY: LOW SIMILARITY TO THE IS1111A/IS1328/IS1533 FAMILY OF
CC TRANSPOSASES.
CC -1- SIMILARITY: HIGH TO F13; SOME, TO Y4PF/Y4SB AND Y4QE.
CC -----
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CC -----
DR EMBL; AE000079; AAB91710.1;
DR InterPro; IPR003346; Transposase_20.
DR Pfam; PF02371; Transposase_20; 1.
RW Hypothetical protein; Plasmid.
SQ SEQUENCE 252 AA; 28552 MW; D993C7DA03E15190 CRC64;

Query March 84.2%; Score 32; DB 1; Length 252;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LAWSWL 6
Db 190 LAWSWL 195

RESULT 11
NU4M_CERCA
ID NU4M_CERCA STANDARD; PRT; 446 AA.
AC 034048; 034053;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE NADH-ubiquinone oxidoreductase chain 4 (EC 1.6.5.3).
GN NDA.
OS Ceratitidis capitata (Mediterranean fruit fly).
OC Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
OC Muscomorpha; Tephritidae; Tephritidae; Ceratitidis.
OX NCBI_TaxID=7213;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-Guatemala laboratory colony, and Hawaii laboratory colony;
RX MEDLINE-95261546; PubMed-7742977;
RA Gasparich G.E., Sheppard W.S., Han H.Y., McPherson B.A., Steck G.J.;
RT "Analysis of mitochondrial DNA and development of PCR-based
RT diagnostic molecular markers for Mediterranean fruit fly (Ceratitidis
RT capitata) populations.";
RL Insect Mol. Biol. 4:61-67(1995).
CC -1- CATALYTIC ACTIVITY: NADH + ubiquinone -> NAD(+) + ubiquinol.
CC -----
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CC -----
DR EMBL; U12925; AAA85797.1;
DR EMBL; U12924; AAA85796.1;
DR InterPro; IPR003918; NADHdb_oxred4.
DR InterPro; IPR001150; Oxidored_g1.
DR InterPro; IPR000260; Oxidored_g5_N.
DR Pfam; PF00361; Oxidored_g1_1.
DR Pfam; PF01059; Oxidored_g5_N; 1.

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DR PRINTS; PRO1437; NUCXDRDTASE4.
RW Oxidoreductase; NAD; Ubiquinone; Mitochondrion.
SQ SEQUENCE 446 AA; 50967 MW; E9AAAC06796897FD CRC64;

Query March 84.2%; Score 32; DB 1; Length 446;
Best Local Similarity 66.7%; Pred. No. 2.9e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LAWSWL 6
Db 374 VSMWL 379

RESULT 12
MELB_ENTAE
ID MELB_ENTAE STANDARD; PRT; 471 AA.
AC 007366;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Melibiose carrier protein (Thiomethylgalactoside permease II)
DE (Melibiose permease) (Nat (L1+)/melibiose symporter) (Melibiose
DE transporter).
GN MELB.
OS Enterobacter aerogenes (Aerobacter aerogenes).
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Enterobacter.
OX NCBI_TaxID=548;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-97332569; PubMed-9188803;
RA Okazaki N., Kuroda M., Shimamoto T., Tsuchiya T.;
RT "Characteristics of the melibiose transporter and its primary
RT structure in Enterobacter aerogenes.";
RL Biochim. Biophys. Acta 1326:83-91(1997).
CC -1- FUNCTION: PROTEIN RESPONSIBLE FOR MELIBIOSE TRANSPORT. IT IS
CC CAPABLE OF USING HYDROGEN AND LITHIUM CATIONS AS COUPLING CATIONS
CC FOR COTRANSPORT, DEPENDENT ON THE PARTICULAR SUGAR TRANSPORTED
CC (SYMPORT SYSTEM).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane.
CC -1- SIMILARITY: BELONGS TO THE SODIUM:GALACTOSIDE SYMPORTER FAMILY
CC (SGF).
CC -----
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CC -----
DR EMBL; D86576; BAA20461.1;
DR InterPro; IPR001927; Na/Gal_symp.
DR TIGRfam; TIGR00792; gph; 1.
DR PROSITE; PS00872; NA.GALACTOSIDE_SYMP; 1.
KM Transport; Sugar transport; Transmembrane; Inner membrane; Symport.
FT DOMAIN 1 11 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 12 32 POTENTIAL.
FT DOMAIN 33 36 PERIPLASMIC (POTENTIAL).
FT DOMAIN 37 57 POTENTIAL.
FT DOMAIN 58 79 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 80 100 POTENTIAL.
FT DOMAIN 101 106 PERIPLASMIC (POTENTIAL).
FT DOMAIN 107 127 POTENTIAL.
FT DOMAIN 128 149 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 150 170 POTENTIAL.
FT TRANSMEM 171 175 PERIPLASMIC (POTENTIAL).
FT TRANSMEM 176 196 POTENTIAL.
FT TRANSMEM 197 234 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 235 255 POTENTIAL.
FT TRANSMEM 256 266 PERIPLASMIC (POTENTIAL).
FT TRANSMEM 267 287 POTENTIAL.
FT DOMAIN 288 296 CYTOPLASMIC (POTENTIAL).

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FT TRANSMEM 297 317 POTENTIAL.  
 FT DOMAIN 318 323 PERIPLASMIC (POTENTIAL).  
 FT TRANSMEM 324 344 POTENTIAL.  
 FT DOMAIN 324 344 POTENTIAL.  
 FT TRANSMEM 345 373 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 374 394 POTENTIAL.  
 FT TRANSMEM 395 411 PERIPLASMIC (POTENTIAL).  
 FT DOMAIN 412 432 POTENTIAL.  
 FT TRANSMEM 433 471 POTENTIAL.  
 FT DOMAIN 471 52214 MW; 9755D85D91828106 CRC64;  
 SQ SEQUENCE

Query Match 84.2%; Score 32; DB 1; Length 471;  
 Best Local Similarity 83.3%; Pred. No. 3e+02;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LANSWL 6  
 11111  
 Db 106 LAMVWL 111

RESULT 13  
 MELB\_KLEPN STANDARD; PRT; 471 AA.  
 ID MELB\_KLEPN  
 AC 002581;  
 DT 01-JUL-1993 (Rel. 26, Last sequence update)  
 DT 01-JUL-1993 (Rel. 26, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Melbiose carrier protein (Thiomethylgalactoside permease II)  
 DE (Melbiose permease) (Na<sup>+</sup> (H<sup>+</sup>)/melbiose symporter) (melbiose  
 DE transporter).  
 GN MELB  
 OS Klebsiella pneumoniae.  
 OS Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
 OC Klebsiella.  
 OX NCBI\_TaxID=573;  
 [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=2002;  
 RA MEDLINE=92406738; PubMed=1339436;  
 RA Hama H., Wilson T.H.;  
 RT "Primary structure and characteristics of the melbiose carrier of  
 RT Klebsiella pneumoniae."  
 RL J. Biol. Chem. 267:18371-18376(1992).  
 CC -1- FUNCTION: PROTEIN RESPONSIBLE FOR MELBIOSE TRANSPORT. IT IS  
 CC CAPABLE OF USING HYDROGEN AND LITHIUM CATIONS AS COUPLING CATIONS  
 CC FOR CORTRANSORT, DEPENDING ON THE PARTICULAR SUGAR TRANSPORTED  
 CC (SYMPORT SYSTEM). IT CATALYZES HYDROGEN CATION-MELBIOSE, LITHIUM  
 CC CATION-LACTOSE, & HYDROGEN/LITHIUM CATIONS-METHYL-1-THIO-BETA-D-  
 CC GALACTOPYRANOSIDE (TMG) CORTRANSORT. THIS PROTEIN SEEMS TO BE  
 CC LACKING THE ABILITY TO RECOGNIZE SODIUM CATIONS.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane.  
 CC -1- SIMILARITY: BELONGS TO THE SODIUM-GALACTOSIDE SYMPORTER FAMILY  
 CC (SGF).  
 CC -----  
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 CC -----  
 CC EMBL: M97257; AAA25067.1; -  
 CC PIR: B44166; B44166.  
 CC InterPro: IPR001927; Na/Gal\_symp.  
 CC TIGRPFAMs: TIGR00792; gph. 1.  
 CC PROSITE: PS00872; NA.GALACTOSIDE\_SYMP. 1.  
 CC TRANSMEM 111  
 CC DOMAIN 111  
 CC TRANSMEM 112 332 CYTOPLASMIC (POTENTIAL).  
 CC TRANSMEM 33 36 PERIPLASMIC (POTENTIAL).  
 CC TRANSMEM 37 57 POTENTIAL.  
 CC TRANSMEM 58 79 CYTOPLASMIC (POTENTIAL).  
 CC TRANSMEM 80 100 POTENTIAL.

FT DOMAIN 101 106 PERIPLASMIC (POTENTIAL).  
 FT TRANSMEM 107 127 POTENTIAL.  
 FT DOMAIN 128 149 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 150 170 POTENTIAL.  
 FT DOMAIN 171 175 PERIPLASMIC (POTENTIAL).  
 FT TRANSMEM 176 196 POTENTIAL.  
 FT DOMAIN 197 234 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 235 255 POTENTIAL.  
 FT DOMAIN 256 266 PERIPLASMIC (POTENTIAL).  
 FT TRANSMEM 267 287 POTENTIAL.  
 FT DOMAIN 288 296 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 297 317 POTENTIAL.  
 FT DOMAIN 318 323 PERIPLASMIC (POTENTIAL).  
 FT TRANSMEM 324 344 POTENTIAL.  
 FT DOMAIN 345 373 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 374 394 POTENTIAL.  
 FT DOMAIN 395 411 PERIPLASMIC (POTENTIAL).  
 FT TRANSMEM 412 432 POTENTIAL.  
 FT DOMAIN 433 471 POTENTIAL.  
 FT TRANSMEM 471 52329 MW; 6D373D09FABAEC7 CRC64;  
 SQ SEQUENCE

Query Match 84.2%; Score 32; DB 1; Length 471;  
 Best Local Similarity 83.3%; Pred. No. 3e+02;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LANSWL 6  
 11111  
 Db 106 LAMVWL 111

RESULT 14  
 NDC1\_HUMAN STANDARD; PRT; 592 AA.  
 ID NDC1\_HUMAN  
 AC Q3183;  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Renal sodium/dicarboxylate cotransporter (Na<sup>+</sup>)/dicarboxylate  
 DE cotransporter).  
 GN SLC13A2 OR NADC1.  
 OS Homo sapiens (Human).  
 OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Kidney;  
 RA MEDLINE=9619379; PubMed=8967342;  
 RA Pafor A.N.;  
 RT "Molecular cloning and functional expression of a sodium/dicarboxylate  
 RT cotransporter from human kidney."  
 RL Am. J. Physiol. 270:F642-F648(1996).  
 CC -1- FUNCTION: CORTRANSORT OF SODIUM AND DICARBOXYLATES SUCH AS  
 CC SUCCINATE AND CITRATE.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).  
 CC -1- SIMILARITY: BELONGS TO THE NADC/P/PHO87 FAMILY OF TRANSPORTERS.  
 CC NADC SUBFAMILY.  
 CC -----  
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 CC -----  
 CC EMBL: U26209; AAA96504.1; -  
 CC Genew; HGNC:10917; SLC13A2.  
 CC MIM; 604148; -  
 CC InterPro: IPR001898; Na/sulf\_symp.  
 CC Pfam; PF00939; Na\_sulph\_symp. 1.  
 CC TIGRPFAMs: TIGR00785; dass. 1.  
 CC PROSITE: PS01271; NA\_SULFATE. 1.

KW TRANSMEM 13 33 POTENTIAL. Sodium transport; Symport.  
 FT TRANSMEM 53 73 POTENTIAL.  
 FT TRANSMEM 86 106 POTENTIAL.  
 FT TRANSMEM 114 134 POTENTIAL.  
 FT TRANSMEM 221 241 POTENTIAL.  
 FT TRANSMEM 274 294 POTENTIAL.  
 FT TRANSMEM 324 344 POTENTIAL.  
 FT TRANSMEM 371 391 POTENTIAL.  
 FT TRANSMEM 450 470 POTENTIAL.  
 FT TRANSMEM 482 502 POTENTIAL.  
 FT TRANSMEM 511 531 POTENTIAL.  
 FT TRANSMEM 565 585 POTENTIAL.  
 SQ SEQUENCE 592 AA; 64410 MW; 41137D6621A0872A CRC64;  
 Query Match 84.2%; Score 32; DB 1; Length 592;  
 Best Local Similarity 83.3%; Pred. No. 3.7e+02;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 LAMSWL 6  
 DB 280 LAMSWL 285  
 RESULT 15  
 IKKA\_HUMAN  
 ID IKKA\_HUMAN STANDARD; PRT; 745 AA.  
 AC O15111; O14666; Q13132; Q92467;  
 DT 16-OCT-2001 (Rel. 40; Created)  
 DT 16-OCT-2001 (Rel. 40; Last sequence update)  
 DT 15-JUN-2002 (Rel. 41; Last annotation update)  
 DE Inhibitor of nuclear factor kappa-B kinase alpha subunit (EC 2.7.1.-)  
 DE (I-kappa-B kinase alpha) (IKK $\alpha$ ) (IKK-A) (Ikappab kinase)  
 DE (I-kappa-B kinase 1) (IKK1) (Conserved helix-loop-helix ubiquitous  
 kinase) (Nuclear factor NF-kappaB inhibitor kinase alpha) (NFKBIA).  
 GN IKKA OR CHUK  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 NX NCBI\_Taxid=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-44.  
 RC TISSUE-T-cell;  
 RX MEDLINE-9738461; PubMed-9244310;  
 RA Regnier C.H., Song H.Y., Gao X., Goeddel D.V., Cao Z., Rothe M.;  
 RT "Identification and characterization of an Ikappab kinase.";  
 RL Cell 90:373-383(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
 RX MEDLINE-97394468; PubMed-9252186;  
 RA D'Imorto J.A., Hayakawa M., Rothwarf D.M., Zandi E., Karin M.;  
 RT "A cytokine-responsive Ikappab kinase that activates the transcription  
 factor NF-kappaB.";  
 RL Nature 388:548-554(1997).  
 RN [3]  
 RP SEQUENCE FROM N.A., PARTIAL SEQUENCE, AND MUTAGENESIS OF LYS-44 AND  
 SER-176  
 RC TISSUE-Cervical carcinoma;  
 RX MEDLINE-98008813; PubMed-9346484;  
 RA Mercutio F., Zhu H., Murray B.W., Shevchenko A., Bennett B.L.,  
 RA Li J.W., Young D.B., Barbosa M., Mann M., Manning A., Rao A.;  
 RT "IKK-1 and IKK-2: cytokine-activated Ikappab kinases essential for  
 NF-kappaB activation.";  
 RL Science 278:860-866(1997).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-Heart;  
 RX MEDLINE-99032998; PubMed-9813230;  
 RA Hu M.C.-T., Wang Y.-P.;  
 RT "Ikappab kinase-alpha and -beta genes are coexpressed in adult and  
 embryonic tissues but localized to different human chromosomes.";  
 RL Gene 222:31-40(1998).  
 RN [5]

RP SEQUENCE OF 32-745 FROM N.A.  
 RC TISSUE-Cervical carcinoma;  
 RX MEDLINE-96258427; PubMed-8777433;  
 RA Connolly M.A., Marcu K.B.;  
 RT "CHUK, a new member of the helix-loop-helix and leucine zipper  
 families of interacting proteins, contains a serine-threonine kinase  
 catalytic domain.";  
 RL Cell. Mol. Biol. Res. 41:537-549(1995).  
 RN [6]  
 RP PHOSPHORYLATION BY MAP3K14/NIK, AND MUTAGENESIS OF S-176; T-179 AND  
 S-180.  
 RX MEDLINE-98188283; PubMed-9520446;  
 RA Ling L., Cao Z., Goeddel D.V.;  
 RT "NF-kappaB-inducing kinase activates IKK-alpha by phosphorylation of  
 Ser-176.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 95:3792-3797(1998).  
 RN [7]  
 RP PHOSPHORYLATION BY AKT, AND MUTAGENESIS OF THR-23.  
 RX MEDLINE-99413720; PubMed-10485710;  
 RA Ozes O.N., Mayo L.D., Gustin J.A., Pfeffer S.R., Pfeffer L.M.,  
 RA Donner D.B.;  
 RT "NF-kappaB activation by tumour necrosis factor requires the Akt  
 serine-threonine kinase.";  
 RL Nature 401:82-85(1999).  
 RN [8]  
 RP IKKA-IKKB BINDING.  
 RX MEDLINE-99212141; PubMed-10195894;  
 RA Delnase M., Hayakawa M., Chen Y., Karin M.;  
 RT "Positive and negative regulation of Ikappab kinase activity through  
 IKKbeta subunit phosphorylation.";  
 RL Science 284:309-313(1999).  
 RN [9]  
 RP IKK PHOSPHORYLATION.  
 RX MEDLINE-99038238; PubMed-9819420;  
 RA Nemoto S., D'Imorto J.A., Lin A.;  
 RT "Coordinate regulation of Ikappab kinases by mitogen-activated protein  
 kinase kinase kinase 1 and NF-kappaB-inducing kinase.";  
 RL Mol. Cell. Biol. 18:7336-7343(1998).  
 RN [10]  
 RP REVIEW.  
 RX MEDLINE-20178139; PubMed-10712233;  
 RA Tobin C., Sartor R.B.;  
 RT "The I kappa B/NF-kappa B system: a key determinant of mucosal  
 inflammation and protection.";  
 RL Am. J. Physiol. 278:C451-C462(2000).  
 CC [1]  
 CC FUNCTION: PHOSPHORYLATES INHIBITORS OF NF-KAPPA-B THUS LEADING TO  
 THE DISSOCIATION OF THE INHIBITOR/NF-KAPPA-B COMPLEX AND  
 ULTIMATELY THE DEGRADATION OF THE INHIBITOR.  
 CC [2]  
 CC ENZYME REGULATION: ACTIVATED WHEN PHOSPHORYLATED AND INACTIVATED  
 WHEN DEPHOSPHORYLATED.  
 CC [3]  
 CC SUBUNIT: PREFERENTIALLY FOUND AS A HETERODIMER WITH IKK-BETA BUT  
 ALSO AS AN HOMODIMER. DIRECTLY INTERACTS WITH IKK-GAMMA/IKK- $\gamma$ .  
 CC HETERODIMERS FORM THE ACTIVE COMPLEX. THE TRIPARTITE COMPLEX CAN  
 ALSO BIND TO MAP3K14/NIK, MEK1, IKAP AND IKK-ALPHA-P65-P50  
 COMPLEX. A WEAK INTERACTION WITH TRAF2 CANNOT BE EXCLUDED.  
 CC [4]  
 CC SUBCELLULAR LOCATION: Cytoplasmic.  
 CC [5]  
 CC TISSUE SPECIFICITY: WIDELY EXPRESSED.  
 CC [6]  
 CC PTM: PHOSPHORYLATED BY MAP3K14/NIK, AKT AND TO A LESSER EXTENT BY  
 MEK1, AND DEPHOSPHORYLATED BY PP2A. AUTOPHOSPHORYLATED.  
 CC [7]  
 CC SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 CC IKAPAB KINASE SUBFAMILY.  
 CC [8]  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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 or send an email to [license@sdb.ch](mailto:license@sdb.ch)).  
 CC [9]  
 CC EMBL; AF012890; AAC51662.1;  
 CC EMBL; AF009225; AAC51671.1;  
 CC EMBL; AF080157; AAD08996.1;

DR EMBL: U22512; AAC50713.1; -.  
DR HSSP; Q63450; 1A06.  
DR Genew; HGNC:1974; CHOK.  
DR MIM; 600664; -.  
DR InterPro: IPR000719; Euk\_kinase.  
DR InterPro: IPR002290; Ser\_thr\_kinase.  
DR Pfam; PF00069; kinase; 1.  
DR ProDom; PD000001; Euk\_kinase; 1.  
DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
KM Transferase: Serine/threonine-protein kinase; ATP-binding;  
Phosphorylation.  
KW DOMAIN 15 302 PROTEIN KINASE.  
FT DOMAIN 455 476 LEUCINE-ZIPPER (POTENTIAL).  
FT DOMAIN 738 743 NEMO-BINDING.  
FT NP\_BIND 21 29 ATP (BY SIMILARITY).  
FT BINDING 44 44 ATP (BY SIMILARITY).  
FT ACT\_SITE 144 144 BY SIMILARITY.  
FT MOD\_RES 23 23 PHOSPHORYLATION (BY PKB/AKT1).  
FT MOD\_RES 176 176 PHOSPHORYLATION (BY MAP3K14).  
FT MUTAGEN 23 23 T->A: LOSS OF PHOSPHORYLATION AND  
DECREASE OF KINASE ACTIVITY.  
FT MUTAGEN 44 44 K->A: LOSS OF KINASE ACTIVITY.  
FT MUTAGEN 44 44 K->M: LOSS OF AUTOPHOSPHORYLATION.  
FT MUTAGEN 176 176 S->A: LOSS OF PHOSPHORYLATION AND OF  
ACTIVITY.  
FT MUTAGEN 176 176 S->E: FULL ACTIVATION.  
FT MUTAGEN 179 179 T->A: NO CHANGE IN PHOSPHORYLATION.  
FT MUTAGEN 180 180 S->A: NO CHANGE IN PHOSPHORYLATION.  
FT CONFLICT 543 543 E->G (IN REF. 2).  
FT CONFLICT 604 604 L->R (IN REF. 5).  
FT CONFLICT 679 680 TS->AY (IN REF. 5).  
FT CONFLICT 684 684 P->A (IN REF. 3 AND 5).  
FT CONFLICT 686 687 TS->DL (IN REF. 5).  
SQ SEQUENCE 745 AA; 84653 MW; 7A90B59BC98A56C2 CRC64;

Query Match 84.28; Score 32; DB 1; Length 745;  
Best Local Similarity 83.3%; Pred. No. 4.6e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 LAWSWL 6  
DB 738 LDMSWL 743

Search completed: May 30, 2003, 15:48:52  
Job time : 4.11842 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 30, 2003, 14:32:12 ; Search time 6.5921 Seconds  
(without alignments)  
87.500 Million cell updates/sec

Title: US-09-643-260-7

Perfect score: 38

Sequence: 1 LAMSWL 6

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

1: PIR1:\*  
2: PIR2:\*  
3: PIR3:\*  
4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	36	94.7	675	2	H69200 heavy-metal transp
2	35	92.1	116	2	T03472 conserved hypotet
3	35	92.1	172	2	T51122 critr protein (limp
4	35	92.1	196	2	C87039 conserved hypotet
5	35	92.1	210	2	C70528 hypothetical prote
6	35	92.1	421	2	A12824 NADH dehydrogenase
7	35	92.1	438	2	H97602 probable NADH dehy
8	35	92.1	441	2	A13607 NADH2 dehydrogenas
9	34	89.5	136	2	A10124 probable prepillin
10	34	89.5	151	2	AE2249 hypothetical prote
11	34	89.5	162	2	B83635 conserved hypotet
12	34	89.5	207	2	A48608 EI glycoprotein -
13	34	89.5	224	2	C48652 transfer protein s
14	34	89.5	264	2	H83224 phosphonate transp
15	34	89.5	266	2	C83602 prolipoprotein dia
16	34	89.5	296	2	E83292 conserved hypotet
17	34	89.5	338	2	S73902 UDP-glucose 4-epim
18	34	89.5	357	2	C97564 hypothetical prote
19	34	89.5	446	2	A83355 hypothetical prote
20	34	89.5	516	2	JEO134 mannan endo-1,4-be
21	34	89.5	709	2	F75584 hypothetical prote
22	34	89.5	1147	1	T35781 hypothetical prote
23	34	89.5	1239	1	VHWVEE structural polypo
24	34	89.5	1240	1	VHWVEE structural polypo
25	34	89.5	1241	2	S26373 genome polypolyp
26	34	89.5	1242	2	S72350 structural polyp
27	34	89.5	1242	2	A56605 structural polyp
28	34	89.5	1315	2	T05300 hypothetical prote
29	34	89.5	1411	2	T48529 hypothetical prote

30	34	89.5	4924	2	T50176 probable peptide s
31	33	86.8	65	2	E83492 hypothetical prote
32	33	86.8	72	2	AD2464 hypothetical prote
33	33	86.8	118	2	I64028 hypothetical prote
34	33	86.8	306	2	G82256 conserved hypotet
35	33	86.8	311	2	AE3169 hypothetical prote
36	33	86.8	335	2	F70983 probable serine pr
37	33	86.8	420	2	E72357 sugar ABC transpor
38	33	86.8	433	2	E70968 hypothetical prote
39	33	86.8	440	2	D87076 probable conserved
40	33	86.8	661	2	F83342 probable cation-tr
41	33	86.8	685	1	A48289 neurotrophic recep
42	33	86.8	919	2	T37062 probable transcrip
43	33	86.8	1053	2	S72194 hydroxymethylgluta
44	33	86.8	1628	2	T43682 nucleoporin - firs
45	33	86.8	2121	2	T27406 hypothetical prote

#### ALIGNMENTS

##### RESULT 1

H69200 heavy-metal transporting CPX-type ATPase - Methanobacterium thermoautotrophicum (stra

C:Species: Methanobacterium thermoautotrophicum

C:Date: 05-Dec-1997 #sequence\_rev1sion 05-Dec-1997 #text\_change 22-Oct-1999

C:Accession: H69200

R:Smith, D.R.; Doucette-Stamm, L.A.; Delouhery, C.; Lee, H.; Dubois, J.; Aldredge, T

K1, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.

J. Bacteriol. 179, 7135-7155, 1997

A:Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: fu

A:Reference number: A690000; MUID:98037514; PMID:9371463

A:Accession: H69200

A>Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-675 <MTH>

A:Cross-references: GB:AE000854; GB:AE000666; NID:g2621839; PIDN:AAB85258.1; PID:g262

A:Experimental source: strain Delta H

C:Genetics:

A:Gene: MTH755

C:Superfamily: Enterococcus copper-transporting ATPase copB; ATPase nucleotide-bindin

F/76-413/Domain: ATPase transnucleotide-binding domain homology <ATN>

F/484-626/Domain: ATPase nucleotide-binding domain homology <ATN>

Query Match 94.7%; Score 36; DB 2; Length 675;  
Best Local Similarity 83.3%; Pred. No. 2.1e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LAMSWL 6

Db 299 IAMSWL 304

RESULT 2

T03472

conserved hypothetical protein - Rhodobacter capsulatus

C:Species: Rhodobacter capsulatus

C:Date: 24-Mar-1999 #sequence\_rev1sion 24-Mar-1999 #text\_change 08-Oct-1999

C:Accession: T03472

R:Vlcek, C.; Paces, V.; Maltsev, N.; Paces, J.; Haselkorn, R.; Fomstein, M.

Proc. Natl. Acad. Sci. U.S.A. 94, 9384-9388, 1997

A:Title: Sequence of a 189-kb segment of the chromosome of Rhodobacter capsulatus SRI

A:Reference number: Z14955; MUID:97404404; PMID:9256491

A:Accession: T03472

A>Status: preliminary; translated from GB/EMBL/DDDBJ

A:Molecule type: DNA

A:Residues: 1-116 <VLC>

A:Cross-references: EMBL:AF010496; NID:g3128256; PIDN:AC16125.1; PID:g3128273

C:Genetics:

A:Map position: 1

Query Match 92.1%; Score 35; DB 2; Length 116;

Best Local Similarity 83.3%; Pred. No. 57;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LAMSWL 6  
DB 63 LAMSWL 68

## RESULT 3

151122

crk protein [Imported] - Brevibacterium linens

C:Species: Brevibacterium linens

C>Date: 28-Jul-2000 #sequence\_revision 28-Jul-2000 #text\_change 28-Jul-2000

C:Accession: J51122

R:Kribasik, P.; Sandmann, G.

Mol. Gen. Genet. 263, 423-432, 2000

A:Title: A carotenogenic gene cluster from Brevibacterium linens with novel lycopene cyc

A:Reference number: 225303; MUID:20279196; PMID:10821176

A:Accession: J51122

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-172 <R0>

A:Cross-references: EMBL:AF139916; PIDN:AAF65585.1

A:Experimental source: DSM 20426; ATCC9175

A:Gene: crk

## Query Match

Best Local Similarity 92.1%; Score 35; DB 2; Length 172;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LAMSWL 6  
DB 91 VAMSWL 96

## RESULT 4

C87039

conserved hypothetical protein ML1041 [Imported] - Mycobacterium leprae

C:Species: Mycobacterium leprae

C>Date: 20-Apr-2001 #sequence\_revision 20-Apr-2001 #text\_change 10-May-2001

C:Accession: C87039

R:Cole, S.T.; Eigmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Ho

R.; Davies, R.M.; Devlin, K.; Duthey, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd,

eam, M.A.; Rutherford, K.M.

Nature 409, 1007-1011, 2001

A:Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sc

A:Title: Massive gene decay in the leprosy bacillus.

A:Reference number: A86909; MUID:21128732; PMID:11234002

A:Accession: C87039

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-196 <STO>

A:Cross-references: GB:AL450380; NID:G13093055; PIDN:CAC31422.1; GSPDB:GN00147

C:Gene: ML1041

C:Superfamily: Mycobacterium tuberculosis hypothetical protein Rv2680

## Query Match

Best Local Similarity 92.1%; Score 35; DB 2; Length 196;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LAMSWL 6  
DB 109 VAMSWL 114

## RESULT 5

C70528

hypothetical protein Rv2680 - Mycobacterium tuberculosis (strain H37RV)

C:Species: Mycobacterium tuberculosis

C>Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 15-Sep-2000

C:Accession: C70528

R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon  
; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd,

Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.

Nature 393, 537-544, 1998

A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete geno

A:Reference number: A70500; MUID:96295987; PMID:9634230

A:Accession: C70528

A>Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Cross-references: GB:Z96072; GB:AL123456; NID:G3261793; PIDN:CAB09496.1; PID:el3000

A:Experimental source: strain H37RV

C:Gene: Rv2680

C:Superfamily: Mycobacterium tuberculosis hypothetical protein Rv2680

## Query Match

Best Local Similarity 92.1%; Score 35; DB 2; Length 210;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LAMSWL 6  
DB 123 VAMSWL 128

## RESULT 6

A12824

NADH dehydrogenase ndh [Imported] - Agrobacterium tumefaciens (strain C58, Dupont)

C:Species: Agrobacterium tumefaciens

C>Date: 11-Jan-2002 #sequence\_revision 11-Jan-2002 #text\_change 01-Feb-2002

C:Accession: A12824

R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo

erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavlin, T.; Levy, R.; Li, M.; McCl

; Karp, P.; Romero, P.; Zhang, S.

Science 294, 2317-2323, 2001

A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kam

ster, E.W.

A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

A:Reference number: AB2577; PMID:11743193

A:Accession: A12824

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-421 <K0>

A:Cross-references: GB:AE006688; PIDN:AA143015.1; PID:G17740478; GSPDB:GN00186

A:Experimental source: strain C58 (Dupont)

C:Gene: ndh

A:Map position: circular chromosome

C:Superfamily: NADH dehydrogenase

## Query Match

Best Local Similarity 92.1%; Score 35; DB 2; Length 421;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LAMSWL 6  
DB 393 VAMSWL 398

## RESULT 7

H97602

Probable NADH dehydrogenase (Y09899) [Imported] - Agrobacterium tumefaciens (strain C

C:Species: Agrobacterium tumefaciens

C>Date: 30-Sep-2001 #sequence\_revision 30-Sep-2001 #text\_change 11-Jan-2002

C:Accession: H97602

R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldm

A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Dappas, C.; Markelz,

Science 294, 2323-2328, 2001

A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium

A:Reference number: A97359; PMID:11743194

A:Accession: H97602

A>Status: preliminary

A:Molecule type: DNA  
 A:Residues: 1-438 <KUR>  
 A:Cross-references: GB:AE007869; PIDN:AAK87777.1; PID:g15157148; GSPDB:GN00169  
 C:Genetics:  
 A:Gene: AGR\_C\_3667  
 A:Map position: circular chromosome  
 C:Superfamily: NADH dehydrogenase

Query Match 92.1%; Score 35; DB 2; Length 438;  
 Best Local Similarity 83.3%; Pred. No. 2e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LAMSWL 6  
 DB 410 VAMSWL 415

## RESULT 8

AI3607  
 NADH2 dehydrogenase (EC 1.6.99.3) [Imported] - Brucella melitensis (strain 16M)

C:Species: Brucella melitensis  
 C:Date: 01-Feb-2002 #sequence\_revision 01-Feb-2002 #text\_change 03-Jun-2002

C:Accession: AI3607

R:Bellocchio, V.G.; Kapetral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, M.; Mazur, M.; Goldsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letessier, P.; Natl. Acad. Sci. U.S.A. 99, 443-448, 2002

A:Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis  
 A:Reference number: AD3252; PMID:11756688

A:Accession: AI3607

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-441 <KUR>

A:Cross-references: GB:AE008918; PIDN:AAI54028.1; PID:g17984981; GSPDB:GN00191

A:Experimental source: strain 16M

C:Genetics:

A:Map position: 11

C:Superfamily: NADH dehydrogenase

C:Keywords: oxidoreductase

Query Match 92.1%; Score 35; DB 2; Length 441;  
 Best Local Similarity 83.3%; Pred. No. 2e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LAMSWL 6  
 DB 413 VAMSWL 418

RESULT 9  
 AI0124  
 probable prepilin peptidase dependent protein YPO1017 [Imported] - Yersinia pestis (strain C:Species: Yersinia pestis

C:Date: 02-Nov-2001 #sequence\_revision 02-Nov-2001 #text\_change 02-Nov-2001

C:Accession: AI0124  
 R:Farhah, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.; deno-Parraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; 11. M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 523-527, 2001

A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.  
 A:Reference number: AB0001; MUID:21470413; PMID:11586360

A:Accession: AI0124

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-136 <KUR>

A:Cross-references: GB:AL590842; PIDN:CAC89860.1; PID:g15979085; GSPDB:GN00175

C:Genetics:  
 A:Gene: YPO1017

Query Match 89.5%; Score 34; DB 2; Length 136;  
 Best Local Similarity 100.0%; Pred. No. 94;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 LAMSWL 6  
 DB 68 VAMSWL 72

## RESULT 10

AE2249  
 hypothetical protein alr3548 [Imported] - Nostoc sp. (strain PCC 7120)

C:Species: Nostoc sp.  
 A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120

C:Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 30-Jun-2002

C:Accession: AE2249

R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriku Nakazaki, N.; Shimo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata DNA Res. 8, 205-213, 2001

A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium

A:Reference number: AB1807; MUID:21595285; PMID:11759840

A:Accession: AE2249

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-151 <KUR>

A:Cross-references: GB:BA000019; PIDN:BAV5247.1; PID:g17132681; GSPDB:GN00179

A:Experimental source: strain PCC 7120

C:Genetics:  
 A:Gene: alr3548

Query Match 89.5%; Score 34; DB 2; Length 151;  
 Best Local Similarity 100.0%; Pred. No. 1e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LAMSW 5  
 DB 18 LAMSW 22

## RESULT 11

B83635  
 conserved hypothetical protein PA0085 [Imported] - Pseudomonas aeruginosa (strain PAO

C:Species: Pseudomonas aeruginosa  
 C:Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 31-Dec-2000

C:Accession: B83635

R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Miroguchi, S.D.; Watterer, P.; Hickey, M.J.; adman, S.; Yun, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L. Nature 406, 959-964, 2000

A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa

A:Reference number: A82950; MUID:20437337; PMID:10984043

A:Accession: B83635

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-162 <STO>

A:Cross-references: GB:AE004447; GB:AE004091; NID:9945902; PIDN:AG03475.1; GSPDB:GN

A:Experimental source: strain PA01

C:Genetics:  
 A:Gene: PA0085

Query Match 89.5%; Score 34; DB 2; Length 162;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LAMSW 5  
 DB 28 LAMSW 32

RESULT 12  
 A48608  
 E1 glycoprotein - eastern equine encephalomyelitis virus (fragment)

C:Species: eastern equine encephalomyelitis virus  
 C:Date: 16-Feb-1994 #sequence\_revision 18-Nov-1994 #text\_change 26-Aug-1999

C:Accession: A48608  
 R:Maaver, S.C.; Bellaw, L.A.; Gousset, L.; Repik, P.M.; Scott, T.W.; Holland, J.J. Virology 195, 700-709, 1993

A:Title: Diversity within natural populations of eastern equine encephalomyelitis virus.  
A:Reference number: A48606; MUID:9331728; PMID:8101674  
A:Contents: 215-85, MD85B  
A:Accession: A48608  
A:Status: preliminary  
A:Molecule type: nucleic acid  
A:Residues: 1-207 <WEA>  
A:Cross-references: GB:S63996; NID:9400551; PIDN:AAB27576.1; PID:9400552  
A>Note: sequence extracted from NCBI backbone (NCBIN:135481, NCBI:135482)  
C:Superfamily: togavirus structural polypeptide  
C:Keywords: glycoprotein

Query Match 89.5%; Score 34; DB 2; Length 207;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 LAMSW 6  
|||||  
DB 173 LAMSW 177

## RESULT 13

transfer protein apda - Streptomyces ambofaciens plasmid psAM2  
C:Species: Streptomyces ambofaciens  
C:Date: 03-May-1994 #sequence\_revision 03-May-1994 #text\_change 22-Oct-1999  
C:Accession: C48652; S33428  
R:Haage, J.; Pernodet, J.L.; Sezonov, G.; Gerbad, C.; Friedmann, A.; Guerineau, M.  
J. Bacteriol. 175, 5529-5538, 1993  
A:Title: Transfer functions of the conjugative integrating element psAM2 from Streptomyces  
A:Reference number: A48652; MUID:93374848; PMID:8366038  
A:Accession: C48652  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-224 <HAG>  
A:Cross-references: EMBL:Z19593; NID:9298051; PIDN:CAA79641.1; PID:9298054  
C:Genetics:

Query Match 89.5%; Score 34; DB 2; Length 224;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LAMSW 5  
|||||  
DB 66 LAMSW 70

## RESULT 14

H83224  
phosphonate transport protein PhnE PA3382 [Imported] - Pseudomonas aeruginosa (strain PA  
C:Species: Pseudomonas aeruginosa  
C:Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 31-Dec-2000  
C:Accession: H83224  
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Br  
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lardig, K.; Lim,  
.; Lory, S.; Olson, M.V.  
Nature 406, 959-964, 2000  
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho  
A:Reference number: A82950; MUID:20437337; PMID:10984043  
A:Accession: H83224  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-264 <STO>  
A:Cross-references: GB:AE004759; GB:AE004091; NID:99949500; PIDN:AAG06770.1; GSPDB:GN001  
A:Experimental source: strain PA01  
C:Genetics:  
A:Gene: phnE; PA3382  
C:Superfamily: phnE protein

Query Match 89.5%; Score 34; DB 2; Length 264;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LAMSW 5  
|||||  
DB 31 LAMSW 35

## RESULT 15

C83602  
prolipoprotein diacylglycerol transferase PA0341 [Imported] - Pseudomonas aeruginosa  
C:Species: Pseudomonas aeruginosa  
C:Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 31-Dec-2000  
C:Accession: C83602  
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.;  
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lardig, K.; L  
.; Lory, S.; Olson, M.V.  
Nature 406, 959-964, 2000  
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa  
A:Reference number: A82950; MUID:20437337; PMID:10984043  
A:Accession: C83602  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-266 <STO>  
A:Cross-references: GB:AE004472; GB:AE004091; NID:99946188; PIDN:AAG03730.1; GSPDB:GN  
C:Genetics:  
A:Gene: lgt; PA0341  
C:Superfamily: prolipoprotein diacylglycerol transferase

Query Match 89.5%; Score 34; DB 2; Length 266;  
Best Local Similarity 83.3%; Pred. No. 1.8e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 LAMSW 6  
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DB 229 LAMSW 234

Search completed: May 30, 2003, 14:52:45  
Job time : 10.5921 secs

GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: May 30, 2003, 14:50:13 ; Search time 10.4605 Seconds  
(without alignments)  
58.060 Million cell updates/sec

Title: US-09-643-260-7  
Perfect score: 38  
Sequence: 1 LAMSWL 6

Scoring table: BL0SUM62  
Gapop 10.0 , Gapext 0.5

Searched: 383519 seqs, 101223694 residues

Total number of hits satisfying chosen parameters: 383519

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications, AA:\*

- 1: /cgn2\_6/ptodata/1/pubppa/US08\_NEW\_PUB pep:\*
- 2: /cgn2\_6/ptodata/1/pubppa/PCT\_NEW\_PUB pep:\*
- 3: /cgn2\_6/ptodata/1/pubppa/US06\_NEW\_PUB pep:\*
- 4: /cgn2\_6/ptodata/1/pubppa/US06\_PUBCOMB pep:\*
- 5: /cgn2\_6/ptodata/1/pubppa/US07\_NEW\_PUB pep:\*
- 6: /cgn2\_6/ptodata/1/pubppa/US07\_PUBCOMB pep:\*
- 7: /cgn2\_6/ptodata/1/pubppa/PCTUS\_PUBCOMB pep:\*
- 8: /cgn2\_6/ptodata/1/pubppa/US08\_PUBCOMB pep:\*
- 9: /cgn2\_6/ptodata/1/pubppa/US09\_NEW\_PUB pep:\*
- 10: /cgn2\_6/ptodata/1/pubppa/US09\_PUBCOMB pep:\*
- 11: /cgn2\_6/ptodata/1/pubppa/US10\_NEW\_PUB pep:\*
- 12: /cgn2\_6/ptodata/1/pubppa/US10\_PUBCOMB pep:\*
- 13: /cgn2\_6/ptodata/1/pubppa/US60\_NEW\_PUB pep:\*
- 14: /cgn2\_6/ptodata/1/pubppa/US60\_PUBCOMB pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	38	100.0	6	9	US-09-847-940B-7
2	38	100.0	6	9	US-09-847-946A-7
3	35	92.1	10	10	US-09-759-667A-3
4	34	89.5	56	9	US-10-023-282-359
5	34	89.5	64	10	US-09-864-761-39808
6	34	89.5	544	9	US-10-067-668-8
7	34	89.5	544	9	US-10-175-696-8
8	33	86.8	6	9	US-09-847-940B-8
9	33	86.8	6	9	US-09-847-946A-8
10	33	86.8	288	10	US-09-820-893-74
11	33	86.8	323	10	US-09-820-893-131
12	33	86.8	350	10	US-09-820-893-132
13	33	86.8	355	9	US-09-712-363-161
14	33	86.8	1369	9	US-10-108-605-303
15	32	84.2	6	9	US-09-847-940B-2
16	32	84.2	6	9	US-09-847-940B-9
17	32	84.2	6	9	US-09-847-946A-2
18	32	84.2	6	9	US-09-847-946A-9
19	32	84.2	6	9	US-09-847-946A-33

20	32	84.2	7	9	US-09-847-946A-37	Sequence 37, Appl
21	32	84.2	8	9	US-09-847-946A-30	Sequence 30, Appl
22	32	84.2	8	9	US-09-847-946A-38	Sequence 38, Appl
23	32	84.2	9	9	US-09-847-946A-29	Sequence 29, Appl
24	32	84.2	9	9	US-09-847-946A-32	Sequence 32, Appl
25	32	84.2	9	9	US-09-847-946A-35	Sequence 35, Appl
26	32	84.2	9	9	US-09-847-946A-36	Sequence 36, Appl
27	32	84.2	10	9	US-09-847-946A-31	Sequence 31, Appl
28	32	84.2	10	9	US-09-847-946A-34	Sequence 34, Appl
29	32	84.2	11	9	US-09-847-946A-28	Sequence 28, Appl
30	32	84.2	11	9	US-09-847-946A-132	Sequence 132, Appl
31	32	84.2	11	9	US-09-847-946A-140	Sequence 140, Appl
32	32	84.2	13	9	US-09-847-946A-143	Sequence 143, Appl
33	32	84.2	13	9	US-09-847-946A-144	Sequence 144, Appl
34	32	84.2	13	9	US-09-847-946A-145	Sequence 145, Appl
35	32	84.2	13	9	US-09-847-946A-148	Sequence 148, Appl
36	32	84.2	17	9	US-09-847-946A-141	Sequence 141, Appl
37	32	84.2	17	9	US-09-847-946A-142	Sequence 142, Appl
38	32	84.2	17	9	US-09-847-946A-146	Sequence 146, Appl
39	32	84.2	17	9	US-09-847-946A-147	Sequence 147, Appl
40	32	84.2	18	9	US-09-847-946A-131	Sequence 131, Appl
41	32	84.2	18	9	US-09-847-946A-135	Sequence 135, Appl
42	32	84.2	18	9	US-09-847-946A-136	Sequence 136, Appl
43	32	84.2	22	9	US-09-847-946A-133	Sequence 133, Appl
44	32	84.2	22	9	US-09-847-946A-134	Sequence 134, Appl
45	32	84.2	22	9	US-09-847-946A-137	Sequence 137, Appl

## ALIGNMENTS

RESULT 1  
US-09-847-940B-7  
Sequence 7, Application US/09847940B  
Patent No. US20020156000A1  
GENERAL INFORMATION:  
APPLICANT: Ghosh, Sankar  
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
FILE REFERENCE: PFI-117CP  
CURRENT APPLICATION NUMBER: US/09/847,940B  
CURRENT FILING DATE: 2001-05-02  
PRIOR APPLICATION NUMBER: 09/643,260  
PRIOR FILING DATE: 2000-08-22  
NUMBER OF SEQ ID NOS: 27  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 7  
LENGTH: 6  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: NBD mutants  
US-09-847-940B-7

Query Match 100.0%; Score 38; DB 9; Length 6;  
Best Local Similarity 100.0%; Pred. No. 3.4e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LAMSWL 6  
DB 1 LAMSWL 6

RESULT 2  
US-09-847-946A-7  
Sequence 7, Application US/09847946A  
Publication No. US20030054999A1

GENERAL INFORMATION:  
APPLICANT: May, Michael J

APPLICANT: Ghosh, Sankar  
APPLICANT: Fildels, Mark A  
APPLICANT: Phillips, Kathryn  
APPLICANT: Hannig, Gerhard

;; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
;; FILE REFERENCE: PPI-119  
;; CURRENT APPLICATION NUMBER: US/09/847,946A  
;; CURRENT FILING DATE: 2001-05-02  
;; PRIOR APPLICATION NUMBER: 60/201,261  
;; PRIOR FILING DATE: 2000-05-02  
;; PRIOR APPLICATION NUMBER: 09/643,260  
;; PRIOR FILING DATE: 2000-08-22  
;; NUMBER OF SEQ ID NOS: 160  
;; SOFTWARE: PatentIn Ver. 2.0  
;; SEQ ID NO 7  
;; LENGTH: 6  
;; TYPE: PRT  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Description of Artificial Sequence:NBD peptide  
US-09-847-946A-7

Query Match 100.0%; Score 38; DB 9; Length 6;  
Best Local Similarity 100.0%; Pred. No. 3.4e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LAMSWL 6  
|||||  
DB 1 LAMSWL 6

RESULT 3  
US-09-759-667A-3  
;; Sequence 3, Application US/09759667A  
;; Patent No. US20020064777A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Mengiste, Tesaye  
;; APPLICANT: Paszkowski, Jerzy  
;; TITLE OF INVENTION: Recombination Repair Gene, MIM, from Arabidopsis thaliana  
;; FILE REFERENCE: S-30568A  
;; CURRENT APPLICATION NUMBER: US/09/759,667A  
;; CURRENT FILING DATE: 2001-01-12  
;; PRIOR APPLICATION NUMBER: 9815485.9  
;; PRIOR FILING DATE: 1998-07-16  
;; PRIOR APPLICATION NUMBER: 9900760.1  
;; PRIOR FILING DATE: 1999-01-14  
;; NUMBER OF SEQ ID NOS: 15  
;; SOFTWARE: PatentIn version 3.0  
;; SEQ ID NO 3  
;; LENGTH: 1055  
;; TYPE: PRT  
;; ORGANISM: Arabidopsis thaliana  
US-09-759-667A-3

Query Match 92.1%; Score 35; DB 10; Length 1055;  
Best Local Similarity 83.3%; Pred. No. 1.2e+03;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 LAMSWL 6  
|||||  
DB 248 LAMSWL 253

RESULT 4  
US-10-023-282-359  
;; Sequence 359, Application US/10023282  
;; Publication No. US20030092893A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Young et al.  
;; TITLE OF INVENTION: 207 Human Secreted Proteins  
;; FILE REFERENCE: P2007P1  
;; CURRENT APPLICATION NUMBER: US/10/023,282  
;; CURRENT FILING DATE: 2001-12-20  
;; EARLIER APPLICATION NUMBER: 09/205,258  
;; EARLIER FILING DATE: 1998-12-04  
;; EARLIER APPLICATION NUMBER: PCT/US98/11422  
;; EARLIER FILING DATE: 1998-06-04

;; EARLIER APPLICATION NUMBER: 60/048,885  
;; EARLIER FILING DATE: 1997-06-06  
;; EARLIER APPLICATION NUMBER: 60/049,375  
;; EARLIER FILING DATE: 1997-06-06  
;; EARLIER APPLICATION NUMBER: 60/048,881  
;; EARLIER FILING DATE: 1997-06-06  
;; EARLIER APPLICATION NUMBER: 60/048,880  
;; EARLIER FILING DATE: 1997-06-06  
;; EARLIER APPLICATION NUMBER: 60/048,896  
;; EARLIER FILING DATE: 1997-06-06  
;; EARLIER APPLICATION NUMBER: 60/049,020  
;; EARLIER FILING DATE: 1997-06-06  
;; EARLIER APPLICATION NUMBER: 60/048,876  
;; EARLIER FILING DATE: 1997-06-06  
;; EARLIER APPLICATION NUMBER: 60/048,895  
;; EARLIER FILING DATE: 1997-06-06  
;; EARLIER APPLICATION NUMBER: 60/048,884  
;; EARLIER FILING DATE: 1997-06-06  
;; EARLIER APPLICATION NUMBER: 60/048,894  
;; EARLIER FILING DATE: 1997-06-06  
;; EARLIER APPLICATION NUMBER: 60/048,971  
;; EARLIER FILING DATE: 1997-06-06  
;; EARLIER APPLICATION NUMBER: 60/048,964  
;; EARLIER FILING DATE: 1997-06-06  
;; EARLIER APPLICATION NUMBER: 60/048,882  
;; EARLIER FILING DATE: 1997-06-06  
;; EARLIER APPLICATION NUMBER: 60/048,899  
;; EARLIER FILING DATE: 1997-06-06  
;; EARLIER APPLICATION NUMBER: 60/048,893  
;; EARLIER FILING DATE: 1997-06-06  
;; EARLIER APPLICATION NUMBER: 60/048,900  
;; EARLIER FILING DATE: 1997-06-06  
;; EARLIER APPLICATION NUMBER: 60/048,901  
;; EARLIER FILING DATE: 1997-06-06  
;; EARLIER APPLICATION NUMBER: 60/048,892  
;; EARLIER FILING DATE: 1997-06-06  
;; EARLIER APPLICATION NUMBER: 60/048,915  
;; EARLIER FILING DATE: 1997-06-06  
;; EARLIER APPLICATION NUMBER: 60/049,019  
;; EARLIER FILING DATE: 1997-06-06  
;; EARLIER APPLICATION NUMBER: 60/048,970  
;; EARLIER FILING DATE: 1997-06-06  
;; EARLIER APPLICATION NUMBER: 60/048,972  
;; EARLIER FILING DATE: 1997-06-06  
;; EARLIER APPLICATION NUMBER: 60/048,916  
;; EARLIER FILING DATE: 1997-06-06  
;; EARLIER APPLICATION NUMBER: 60/049,373  
;; EARLIER FILING DATE: 1997-06-06  
;; EARLIER APPLICATION NUMBER: 60/048,875  
;; EARLIER FILING DATE: 1997-06-06  
;; EARLIER APPLICATION NUMBER: 60/049,374  
;; EARLIER FILING DATE: 1997-06-06  
;; EARLIER APPLICATION NUMBER: 60/048,917  
;; EARLIER FILING DATE: 1997-06-06  
;; EARLIER APPLICATION NUMBER: 60/048,949  
;; EARLIER FILING DATE: 1997-06-06  
;; EARLIER APPLICATION NUMBER: 60/048,974  
;; EARLIER FILING DATE: 1997-06-06  
;; EARLIER APPLICATION NUMBER: 60/048,883  
;; EARLIER FILING DATE: 1997-06-06  
;; EARLIER APPLICATION NUMBER: 60/048,897  
;; EARLIER FILING DATE: 1997-06-06  
;; EARLIER APPLICATION NUMBER: 60/048,898  
;; EARLIER FILING DATE: 1997-06-06  
;; EARLIER APPLICATION NUMBER: 60/048,962  
;; EARLIER FILING DATE: 1997-06-06  
;; EARLIER APPLICATION NUMBER: 60/048,963  
;; EARLIER FILING DATE: 1997-06-06  
;; EARLIER APPLICATION NUMBER: 60/048,877  
;; EARLIER FILING DATE: 1997-06-06  
;; EARLIER APPLICATION NUMBER: 60/048,878  
;; EARLIER FILING DATE: 1997-06-06  
;; EARLIER APPLICATION NUMBER: 60/070,923

EARLIER FILING DATE: 1997-12-18  
EARLIER APPLICATION NUMBER: 60/092,921  
EARLIER FILING DATE: 1998-07-15  
EARLIER APPLICATION NUMBER: 60/094,657  
EARLIER FILING DATE: 1998-07-30  
NUMBER OF SEQ ID NOS: 1227  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 359  
LENGTH: 56  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: SITE  
LOCATION: (56)  
OTHER INFORMATION: Xaa equals stop translation  
US-10-023-282-359

Query Match 89.5%; Score 34; DB 9; Length 56;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LAMSW 5  
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DB 9 LAMSW 13

RESULT 5  
US-09-864-761-39808  
Sequence 39808, Application US/09864761  
Patent No. US20020048763A1  
GENERAL INFORMATION:  
APPLICANT: Penn, Sharon G.  
APPLICANT: Rank, David R.  
APPLICANT: Hanzel, David K.  
APPLICANT: Chen, Wensheng  
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
FILE REFERENCE: Aecm1ca-X-1  
CURRENT FILING DATE: 2001-05-23  
PRIOR APPLICATION NUMBER: US 60/180,312  
PRIOR FILING DATE: 2000-02-04  
PRIOR APPLICATION NUMBER: US 60/207,456  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: US 09/632,366  
PRIOR FILING DATE: 2000-08-03  
PRIOR APPLICATION NUMBER: GB 24263.6  
PRIOR FILING DATE: 2000-10-04  
PRIOR APPLICATION NUMBER: US 60/236,359  
PRIOR FILING DATE: 2000-09-27  
PRIOR APPLICATION NUMBER: PCT/US01/00666  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00667  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00664  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00669  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00665  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00668  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00663  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00662  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00661  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00670  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: US 60/234,687  
PRIOR FILING DATE: 2000-09-21  
PRIOR APPLICATION NUMBER: US 09/608,408

PRIOR FILING DATE: 2000-06-30  
PRIOR APPLICATION NUMBER: US 09/774,203  
PRIOR FILING DATE: 2001-01-29  
NUMBER OF SEQ ID NOS: 49117  
SOFTWARE: Anomax Sequence Listing Engine vers. 1.1  
SEQ ID NO 39808  
LENGTH: 64  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: MAP TO AC004596.1  
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.2  
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.4  
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.8  
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.3  
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.2  
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.3  
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.3  
OTHER INFORMATION: EST\_HUMAN HIT: BB91286.1, EVALUATE 3.00e-33  
OTHER INFORMATION: SWISSPROT HIT: P14528, EVALUATE 4.50e+00  
US-09-864-761-39808

Query Match 89.5%; Score 34; DB 10; Length 64;  
Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LAMSW 5  
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DB 33 LAMSW 37

RESULT 6  
US-10-067-668-8  
Sequence 8, Application US/10067668  
Publication No. US20030022334A1  
GENERAL INFORMATION:  
APPLICANT: Glucksmann, Maria Alexandra  
TITLE OF INVENTION: 33312, 33303, 32579, NOVEL HUMAN  
FILE REFERENCE: 10448-136001  
CURRENT FILING DATE: 2002-02-04  
PRIOR APPLICATION NUMBER: 60/266,140  
PRIOR FILING DATE: 2001-02-02  
NUMBER OF SEQ ID NOS: 12  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 8  
LENGTH: 544  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-067-668-8

Query Match 89.5%; Score 34; DB 9; Length 544;  
Best Local Similarity 83.3%; Pred. No. 9.3e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 LAMSW 6  
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DB 46 LAMSW 51

RESULT 7  
US-10-175-696-8  
Sequence 8, Application US/10175696  
Publication No. US20030092658A1  
GENERAL INFORMATION:  
APPLICANT: Glucksmann, Maria Alexandra  
APPLICANT: Meyers, Rachel  
APPLICANT: Rudolph-Owen, Laura A.  
TITLE OF INVENTION: NOVEL HUMAN ENZYME FAMILY MEMBERS AND USES THEREOF  
FILE REFERENCE: 10448-193001  
CURRENT FILING DATE: 2002-06-20  
US-10-175-696-8

PRIOR APPLICATION NUMBER: 10/067,668  
PRIOR FILING DATE: 2002-02-04  
PRIOR APPLICATION NUMBER: 60/266,140  
PRIOR FILING DATE: 2001-02-02  
PRIOR APPLICATION NUMBER: 09/823,901  
PRIOR FILING DATE: 2001-03-30  
PRIOR APPLICATION NUMBER: PCT/US01/10720  
PRIOR FILING DATE: 2001-04-02  
PRIOR APPLICATION NUMBER: 60/193,920  
PRIOR FILING DATE: 2000-03-31  
PRIOR APPLICATION NUMBER: 09/862,658  
PRIOR FILING DATE: 2001-05-21  
PRIOR APPLICATION NUMBER: PCT/US01/16380  
PRIOR FILING DATE: 2001-05-21  
PRIOR APPLICATION NUMBER: 60/205,675  
PRIOR FILING DATE: 2000-05-19  
PRIOR APPLICATION NUMBER: 09/882,837  
PRIOR FILING DATE: 2001-06-15  
PRIOR APPLICATION NUMBER: PCT/US01/19319  
PRIOR FILING DATE: 2001-06-15  
PRIOR APPLICATION NUMBER: 60/211,727  
PRIOR FILING DATE: 2000-06-15  
NUMBER OF SEQ ID NOS: 31  
SOFTWARE: FASTSEQ for Windows Version 4.0  
SEQ ID NO: 8  
LENGTH: 544  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-175-696-8

Query Match 89.5%; Score 34; DB 9; Length 544;  
Best Local Similarity 83.3%; Pred. No. 9.3e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LAMSWL 6  
| | | | |  
DB 46 LAMSWL 51

RESULT 8  
US-09-847-940B-8  
Sequence 8, Application US/09847940B  
Patent No. US20020156000A1  
GENERAL INFORMATION:  
APPLICANT: May, Michael J.  
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
FILE REFERENCE: PFI-117CP  
CURRENT APPLICATION NUMBER: US/09/847,940B  
PRIOR FILING DATE: 2001-05-02  
PRIOR APPLICATION NUMBER: 09/643,260  
PRIOR FILING DATE: 2000-08-22  
NUMBER OF SEQ ID NOS: 27  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO: 8  
LENGTH: 6  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: NBD mutants  
US-09-847-940B-8

Query Match 86.8%; Score 33; DB 9; Length 6;  
Best Local Similarity 83.3%; Pred. No. 3.4e+05;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LAMSWL 6  
| | | | |  
DB 1 LAMSWL 6

RESULT 9  
US-09-847-946A-8

Sequence 8, Application US/09847946A  
Publication No. US20030054999A1  
GENERAL INFORMATION:  
APPLICANT: May, Michael J.  
APPLICANT: Ghosh, Sankar  
APPLICANT: Phillips, Mark A  
APPLICANT: Phillips, Kathryn  
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
FILE REFERENCE: PFI-119  
CURRENT APPLICATION NUMBER: US/09/847,946A  
PRIOR FILING DATE: 2001-05-02  
PRIOR APPLICATION NUMBER: 60/201,261  
PRIOR FILING DATE: 2000-05-02  
PRIOR APPLICATION NUMBER: 09/643,260  
PRIOR FILING DATE: 2000-08-22  
NUMBER OF SEQ ID NOS: 160  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO: 8  
LENGTH: 6  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: NBD peptide  
US-09-847-946A-8

Query Match 86.8%; Score 33; DB 9; Length 6;  
Best Local Similarity 83.3%; Pred. No. 3.4e+05;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LAMSWL 6  
| | | | |  
DB 1 LAMSWL 6

RESULT 10  
US-09-820-893-74  
Sequence 74, Application US/09820893  
Patent No. US2002076705A1  
GENERAL INFORMATION:  
APPLICANT: Rosen et al.  
TITLE OF INVENTION: 31 Human Secreted Proteins  
FILE REFERENCE: P2033PI  
CURRENT APPLICATION NUMBER: US/09/820,893  
PRIOR FILING DATE: 2001-03-30  
PRIOR APPLICATION NUMBER: 09/531,119  
PRIOR FILING DATE: 2000-03-20  
PRIOR APPLICATION NUMBER: 60/102,895  
PRIOR FILING DATE: 1998-10-02  
NUMBER OF SEQ ID NOS: 140  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO: 74  
LENGTH: 288  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: SITE  
LOCATION: (288)  
OTHER INFORMATION: Xaa equals stop translation  
US-09-820-893-74

Query Match 86.8%; Score 33; DB 10; Length 288;  
Best Local Similarity 83.3%; Pred. No. 7.4e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LAMSWL 6  
| | | | |  
DB 28 LAMSWL 33

RESULT 11  
US-09-820-893-131  
Sequence 131, Application US/09820893

Patent No. US20020076705A1  
GENERAL INFORMATION:  
APPLICANT: Rosen et al.  
TITLE OF INVENTION: 31 Human Secreted Proteins  
FILE REFERENCE: P2033P1  
CURRENT APPLICATION NUMBER: US/09/820,893  
PRIOR FILING DATE: 2001-03-30  
PRIOR APPLICATION NUMBER: 09/531,119  
PRIOR FILING DATE: 2000-03-20  
PRIOR APPLICATION NUMBER: 60/102,895  
PRIOR FILING DATE: 1998-10-02  
NUMBER OF SEQ ID NOS: 140  
SOFTWARE: Patentln Ver. 2.0  
SEQ ID NO 131  
LENGTH: 323  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-820-893-131

Query Match  
Best Local Similarity 86.8%; Score 33; DB 10; Length 323;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LAMSWL 6  
|||  
Db 64 LAMRWL 69

RESULT 12  
US-09-820-893-132  
Sequence 132, Application US/09820893  
Patent No. US20020076705A1  
GENERAL INFORMATION:  
APPLICANT: Rosen et al.  
TITLE OF INVENTION: 31 Human Secreted Proteins  
FILE REFERENCE: P2033P1  
CURRENT APPLICATION NUMBER: US/09/820,893  
PRIOR FILING DATE: 2001-03-30  
PRIOR APPLICATION NUMBER: 09/531,119  
PRIOR FILING DATE: 2000-03-20  
PRIOR APPLICATION NUMBER: 60/102,895  
PRIOR FILING DATE: 1998-10-02  
NUMBER OF SEQ ID NOS: 140  
SOFTWARE: Patentln Ver. 2.0  
SEQ ID NO 132  
LENGTH: 350  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-820-893-132

Query Match  
Best Local Similarity 86.8%; Score 33; DB 10; Length 350;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LAMSWL 6  
|||  
Db 91 LAMRWL 96

RESULT 13  
US-09-712-363-161  
Sequence 161, Application US/09712363  
Patent No. US20020164588A1  
GENERAL INFORMATION:  
APPLICANT: Eisenberg, David  
APPLICANT: Rotstein, Sergio H.  
APPLICANT: Marcotte, Edward M.  
TITLE OF INVENTION: DETERMINING THE FUNCTIONS AND  
FILE REFERENCE: 07419-032001  
CURRENT APPLICATION NUMBER: US/09/712,363  
PRIOR FILING DATE: 2000-11-13  
PRIOR APPLICATION NUMBER: PCT/US00/02246

PRIOR FILING DATE: 2000-01-28  
PRIOR APPLICATION NUMBER: 60/179,531  
PRIOR FILING DATE: 2000-02-01  
PRIOR APPLICATION NUMBER: 60/117,844  
PRIOR FILING DATE: 1999-01-29  
PRIOR APPLICATION NUMBER: 60/118,206  
PRIOR FILING DATE: 1999-02-01  
PRIOR APPLICATION NUMBER: 60/126,593  
PRIOR FILING DATE: 1999-03-26  
PRIOR APPLICATION NUMBER: 60/134,093  
PRIOR FILING DATE: 1999-05-14  
PRIOR APPLICATION NUMBER: 60/134,092  
PRIOR FILING DATE: 1999-05-14  
PRIOR APPLICATION NUMBER: 60/165,124  
PRIOR FILING DATE: 1999-11-12  
PRIOR APPLICATION NUMBER: 60/165,086  
PRIOR FILING DATE: 1999-11-12  
NUMBER OF SEQ ID NOS: 292  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 161  
LENGTH: 355  
TYPE: PRT  
ORGANISM: Mycobacterium tuberculosis  
US-09-712-363-161

Query Match  
Best Local Similarity 86.8%; Score 33; DB 9; Length 355;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LAMSWL 6  
|||  
Db 9 LAMRWL 14

RESULT 14  
US-10-108-605-303  
Sequence 303, Application US/10108605  
Patent No. US20020160934A1  
GENERAL INFORMATION:  
APPLICANT: Broadus, Julie  
APPLICANT: Stram, Lynn  
APPLICANT: Bachmann, Jane  
TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FROM DROSOPHILA MELANOGASTER THAT ENCODE  
FILE REFERENCE: 31133B  
CURRENT APPLICATION NUMBER: US/10/108,605  
PRIOR FILING DATE: 2002-03-27  
PRIOR APPLICATION NUMBER: US 09/761,142  
PRIOR FILING DATE: 2001-01-16  
PRIOR APPLICATION NUMBER: US 60/176,418  
PRIOR FILING DATE: 2000-01-14  
NUMBER OF SEQ ID NOS: 361  
SOFTWARE: Patentln Ver. 2.1  
SEQ ID NO 303  
LENGTH: 1569  
TYPE: PRT  
ORGANISM: Drosophila melanogaster  
US-10-108-605-303

Query Match  
Best Local Similarity 86.8%; Score 33; DB 9; Length 1569;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LAMSWL 6  
|||  
Db 657 LAMRWL 662

RESULT 15  
US-09-847-940B-2  
Sequence 2, Application US/09847940B  
Patent No. US20020156000A1

GENERAL INFORMATION:  
APPLICANT: May, Michael J.  
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
FILE REFERENCE: PPI-117CP  
CURRENT APPLICATION NUMBER: US/09/847,940B  
CURRENT FILING DATE: 2001-05-02  
PRIOR APPLICATION NUMBER: 09/643,260  
PRIOR FILING DATE: 2000-08-22  
NUMBER OF SEQ ID NOS: 27  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 2  
LENGTH: 6  
TYPE: prt  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: NBD mutants  
US-09-847-940B-2

Query Match 84.2%; Score 32; DB 9; Length 6;  
Best Local Similarity 83.3%; Pred. NO. 3.4e+05;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Oy 1 LAMSWL 6  
| | | | |  
Db 1 LDMSWL 6

Search completed: May 30, 2003, 15:53:16  
Job time : 10.4605 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

# OM protein - protein search, using sw model

Run on: May 30, 2003, 14:32:12 ; Search time 6.03947 Seconds  
(Without alignments)  
29.231 Million cell updates/sec

Title: US-09-643-260-7  
Perfect score: 38  
Sequence: 1 LAMSWL 6

Scoring table: BIOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 08  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/prodata/1/1aa/5A\_COMB.pep:\*  
2: /cgn2\_6/prodata/1/1aa/5B\_COMB.pep:\*  
3: /cgn2\_6/prodata/1/1aa/6A\_COMB.pep:\*  
4: /cgn2\_6/prodata/1/1aa/6B\_COMB.pep:\*  
5: /cgn2\_6/prodata/1/1aa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/prodata/1/1aa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	34	89.5	468	4	US-09-485-648-4
2	34	89.5	468	4	US-09-503-565-4
3	34	89.5	468	4	US-09-485-649-4
4	34	89.5	468	4	US-09-485-648-2
5	34	89.5	468	4	US-09-503-565-2
6	34	89.5	468	4	US-09-485-649-2
7	34	89.5	468	4	US-08-818-112-79
8	34	89.5	468	4	US-08-818-111-80
9	34	89.5	468	4	US-09-056-556-79
10	34	89.5	468	4	US-09-072-596-80
11	34	89.5	468	4	US-08-137-117D-31
12	34	89.5	468	4	US-08-436-717-31
13	34	89.5	468	4	US-08-887-518-3
14	34	89.5	468	4	US-09-023-321-3
15	34	89.5	468	4	US-08-890-853-4
16	34	89.5	468	4	US-09-032-475-3
17	34	89.5	468	4	US-09-099-125A-4
18	34	89.5	468	4	US-09-099-124A-4
19	34	89.5	468	4	US-09-032-476-4
20	34	89.5	468	4	US-08-890-854-4
21	34	89.5	468	4	US-09-023-324-4
22	34	89.5	468	4	US-09-168-629-2
23	34	89.5	468	4	US-08-910-820-10
24	34	89.5	468	4	US-08-810-131A-2
25	34	89.5	468	4	US-08-887-518-4
26	34	89.5	468	4	US-09-023-321-4
27	34	89.5	468	4	US-09-023-321-4

28	32	84.2	756	2	US-08-890-853-2	Sequence 2, Appl
29	32	84.2	756	2	US-09-032-475-4	Sequence 4, Appl
30	32	84.2	756	2	US-09-099-125A-2	Sequence 2, Appl
31	32	84.2	756	2	US-09-099-124A-2	Sequence 2, Appl
32	32	84.2	756	4	US-08-890-854-2	Sequence 2, Appl
33	32	84.2	756	4	US-09-023-324-2	Sequence 2, Appl
34	32	84.2	756	4	US-09-168-629-15	Sequence 15, Appl
35	32	84.2	756	4	US-08-910-820-9	Sequence 9, Appl
36	32	84.2	756	4	US-08-137-117D-64	Sequence 64, Appl
37	31	81.6	123	1	US-08-436-717-64	Sequence 64, Appl
38	31	81.6	123	2	US-08-137-117D-69	Sequence 69, Appl
39	31	81.6	138	1	US-08-436-717-69	Sequence 69, Appl
40	31	81.6	138	2	PCT-US94-01321-72	Sequence 72, Appl
41	31	81.6	418	5	US-09-161-994A-3	Sequence 3, Appl
42	31	81.6	443	4	US-09-172-841-55	Sequence 38, Appl
43	31	81.6	519	4	US-08-637-670-38	
44	31	81.6	593	4		
45	31	81.6				

## ALIGNMENTS

RESULT 1  
US-09-485-648-4  
Sequence 4, Application US/09485648  
Patent No. 6376445  
GENERAL INFORMATION:  
APPLICANT: Showell, Jean-Luc P.  
TITLE OF INVENTION: Detergent Compositions Comprising a Mannanase and a  
FILE REFERENCE: Mannanase and protease  
CURRENT APPLICATION NUMBER: US/09/485, 648  
CURRENT FILING DATE: 2000-04-05  
PRIOR APPLICATION NUMBER: PCT/US98/11996  
PRIOR FILING DATE: 1998-06-10  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 4  
LENGTH: 468  
TYPE: PRT  
ORGANISM: Bacillus sp.  
US-09-485-648-4

Query Match 89.5%; Score 34; DB 4; Length 468;  
Best Local Similarity 100.0%; Pred. No. 4.4e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LAMSW 5  
DB 280 LAMSW 284

RESULT 2  
US-09-503-565-4  
Sequence 4, Application US/09503565  
Patent No. 6420331  
GENERAL INFORMATION:  
APPLICANT: Bettiol, Jean-Luc P.  
TITLE OF INVENTION: Detergent Compositions Comprising a Mannanase and a  
FILE REFERENCE: Mannanase and cationic surfactant  
CURRENT APPLICATION NUMBER: US/09/503, 565  
CURRENT FILING DATE: 2001-02-14  
PRIOR APPLICATION NUMBER: PCT/US98/12025  
PRIOR FILING DATE: 1998-06-10  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 4  
LENGTH: 468  
TYPE: PRT  
ORGANISM: Bacillus sp.

US-09-503-565-4

Query Match 89.5%; Score 34; DB 4; Length 468;  
Best Local Similarity 100.0%; Pred. No. 4.4e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LAMSW 5

DB 280 LAMSW 284

RESULT 3  
US-09-485-649-4  
; Sequence 4, Application US/09485649  
; Patent No. 6440911  
; GENERAL INFORMATION:  
; APPLICANT: Bettiol, Jean-Luc P.  
; APPLICANT: Joos, Conny E.A.  
; TITLE OF INVENTION: Enzymatic Cleaning Compositions  
; FILE REFERENCE: Enzymatic Cleaning  
; CURRENT APPLICATION NUMBER: US/09/485,649  
; CURRENT FILING DATE: 2000-03-17  
; PRIOR APPLICATION NUMBER: PCT/US98/11993  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 468  
; TYPE: PRT  
; ORGANISM: Bacillus sp.  
US-09-485-649-4

Query Match 89.5%; Score 34; DB 4; Length 468;  
Best Local Similarity 100.0%; Pred. No. 4.4e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LAMSW 5

DB 280 LAMSW 284

RESULT 4  
US-09-485-648-2  
; Sequence 2, Application US/09485648  
; Patent No. 6376445  
; GENERAL INFORMATION:  
; APPLICANT: Bettiol, Jean-Luc P.  
; APPLICANT: Showell, Michael S.  
; TITLE OF INVENTION: Detergent Compositions Comprising a Mannanase and a  
; FILE REFERENCE: Mannanase and protease  
; CURRENT APPLICATION NUMBER: US/09/485,648  
; CURRENT FILING DATE: 2000-04-05  
; PRIOR APPLICATION NUMBER: PCT/US98/11996  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 493  
; TYPE: PRT  
; ORGANISM: Bacillus sp.  
US-09-485-648-2

Query Match 89.5%; Score 34; DB 4; Length 493;  
Best Local Similarity 100.0%; Pred. No. 4.7e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LAMSW 5

DB 280 LAMSW 284

RESULT 5

US-09-503-565-2

; Sequence 2, Application US/09503565  
; Patent No. 6420331  
; GENERAL INFORMATION:  
; APPLICANT: Bettiol, Jean-Luc P.  
; TITLE OF INVENTION: Detergent Compositions Comprising a Mannanase and a  
; FILE REFERENCE: Cationic Surfactant  
; CURRENT APPLICATION NUMBER: US/09/503,565  
; CURRENT FILING DATE: 2001-02-14  
; PRIOR APPLICATION NUMBER: PCT/US98/12025  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 493  
; TYPE: PRT  
; ORGANISM: Bacillus sp.  
US-09-503-565-2

Query Match 89.5%; Score 34; DB 4; Length 493;  
Best Local Similarity 100.0%; Pred. No. 4.7e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LAMSW 5

DB 280 LAMSW 284

RESULT 6  
US-09-485-649-2  
; Sequence 2, Application US/09485649  
; Patent No. 6440911  
; GENERAL INFORMATION:  
; APPLICANT: Bettiol, Jean-Luc P.  
; APPLICANT: Joos, Conny E.A.  
; TITLE OF INVENTION: Enzymatic Cleaning Compositions  
; FILE REFERENCE: Enzymatic Cleaning  
; CURRENT APPLICATION NUMBER: US/09/485,649  
; CURRENT FILING DATE: 2000-03-17  
; PRIOR APPLICATION NUMBER: PCT/US98/11993  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 493  
; TYPE: PRT  
; ORGANISM: Bacillus sp.  
US-09-485-649-2

Query Match 89.5%; Score 34; DB 4; Length 493;  
Best Local Similarity 100.0%; Pred. No. 4.7e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LAMSW 5

DB 280 LAMSW 284

RESULT 7  
US-08-818-112-79  
; Sequence 79, Application US/08818112  
; Patent No. 6290969  
; GENERAL INFORMATION:  
; APPLICANT: Reed, Steven G.  
; APPLICANT: Skelky, Yasir A.W.  
; APPLICANT: Dillon, Davin C.  
; APPLICANT: Campos-Neto, Antonio  
; APPLICANT: Houghton, Raymond  
; APPLICANT: Hedrick, Thomas S.  
; APPLICANT: Twardzik, Daniel R.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY  
AND DIAGNOSIS OF TUBERCULOSIS

NUMBER OF SEQUENCES: 153  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SEED and BERRY LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/818,112  
FILING DATE: 13-MAR-1997  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Makl, David J.  
REGISTRATION NUMBER: 31,392  
REFERENCE/DOCKET NUMBER: 210121.411C6  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 79:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 355 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-818-112-79

Query Match  
Best Local Similarity 86.8%; Score 33; DB 4; Length 355;  
Pred. No. 4.7e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LAMSWL 6  
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|  
|  
|  
|  
Db 9 LRMSWL 14

RESULT 8  
US-08-818-111-80  
Sequence 80, Application US/08818111  
Patent No. 6338852  
GENERAL INFORMATION:  
APPLICANT: Reed, Steven G.  
APPLICANT: Skeiky, Yasir A.W.  
APPLICANT: Dillon, David C.  
APPLICANT: Campos-Neto, Antonia  
APPLICANT: Houghton, Raymond  
APPLICANT: Vedvick, Thomas S.  
APPLICANT: Twardzik, Daniel R.  
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF  
TUBERCULOSIS  
NUMBER OF SEQUENCES: 148  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SEED and BERRY LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/818,111  
FILING DATE: 13-MAR-1997  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Makl, David J.

REGISTRATION NUMBER: 31,392  
REFERENCE/DOCKET NUMBER: 210121.417C6  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 80:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 355 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-818-111-80

Query Match  
Best Local Similarity 86.8%; Score 33; DB 4; Length 355;  
Pred. No. 4.7e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LAMSWL 6  
|  
|  
|  
|  
|  
Db 9 LRMSWL 14

RESULT 9  
US-09-056-556-79  
Sequence 79, Application US/09056556  
Patent No. 6350456  
GENERAL INFORMATION:  
APPLICANT: Reed, Steven G.  
APPLICANT: Skeiky, Yasir A.W.  
APPLICANT: Dillon, David C.  
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE PREVENTION AND  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SEED and BERRY LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/056,556  
FILING DATE: 07-APR-1998  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Makl, David J.  
REGISTRATION NUMBER: 31,392  
REFERENCE/DOCKET NUMBER: 210121.457  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 79:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 355 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-056-556-79

Query Match  
Best Local Similarity 86.8%; Score 33; DB 4; Length 355;  
Pred. No. 4.7e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LAMSWL 6  
|  
|  
|  
|  
|  
Db 9 LRMSWL 14

RESULT 10

US-09-072-596-80  
Sequence 80, Application US/09072596  
Patent No. 6458366  
GENERAL INFORMATION:  
APPLICANT: Reed, Steven G.  
APPLICANT: Skelvy, Yasir A.W.  
APPLICANT: Dillon, Davin C.  
APPLICANT: Campos Neto, Antonia  
APPLICANT: Houghton, Raymond  
APPLICANT: Vedvyck, Thomas S.  
APPLICANT: Twardzik, Daniel R.  
APPLICANT: Lodes, Michael J.  
APPLICANT: Hendrickson, Ronald C.  
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF TUBERCULOSIS  
NUMBER OF SEQUENCES: 350  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SEED and BERRY LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/072.596  
FILING DATE: 05-MAY-1998  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: MAKI, David J.  
REGISTRATION NUMBER: 31,392  
REFERENCE/DOCKET NUMBER: 210121.417C9  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 80:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 355 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-072-596-80

Query Match 86.8%; Score 33; DB 4; Length 355;  
Best Local Similarity 83.3%; Pred. No. 4.7e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LAMSWL 6  
DB 9 LRMSWL 14

RESULT 11  
US-08-137-117D-31  
Sequence 31, Application US/08137117D  
Patent No. 5795965  
GENERAL INFORMATION:  
APPLICANT: TSUCHIYA, Masayuki  
APPLICANT: SATO, Koh  
APPLICANT: BENDIG, Mary  
APPLICANT: JONES, Steven  
APPLICANT: SALDANHA, Jose  
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN  
NUMBER OF SEQUENCES: 158  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.

COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/137.117D  
FILING DATE: 20-DEC-1993  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/JP92/00544  
FILING DATE: 24-APR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 4-32084  
FILING DATE: 19-FEB-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 3-95476  
FILING DATE: 25-APR-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: WEGNER, Harold C.  
REGISTRATION NUMBER: 25,258  
REFERENCE/DOCKET NUMBER: 53466/126/AAOK  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)672-5399  
TELEFAX: (202)672-5300  
INFORMATION FOR SEQ ID NO: 31:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 137 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-137-117D-31

Query Match 84.2%; Score 32; DB 1; Length 137;  
Best Local Similarity 80.0%; Pred. No. 2.7e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 AMSWL 6  
DB 52 AMSWI 56

RESULT 12  
US-08-436-717-31  
Sequence 31, Application US/08436717  
Patent No. 5817790  
GENERAL INFORMATION:  
APPLICANT: TSUCHIYA, Masayuki  
APPLICANT: SATO, Koh  
APPLICANT: BENDIG, Mary  
APPLICANT: JONES, Steven  
APPLICANT: SALDANHA, Jose  
TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN  
NUMBER OF SEQUENCES: 158  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/436.717  
FILING DATE:

CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/137,117  
FILING DATE: 20-DEC-1993  
APPLICATION NUMBER: WO PCT/JP92/00544  
FILING DATE: 24-APR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 4-32084  
FILING DATE: 19-FEB-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 3-95476  
FILING DATE: 25-APR-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: WESNER, Harold C.  
REGISTRATION NUMBER: 25,258  
REFERENCE/DOCKET NUMBER: 53466/126/AAOK  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 31:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 137 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-436-717-31

Query Match 84.2%; Score 32; DB 2; Length 137;  
Best Local Similarity 80.0%; Pred. No. 2.7e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 AMSWL 6  
DB 52 AMSWI 56

RESULT 13  
5217891-4  
PATENT NO. 5217891  
APPLICANT: BRAKE, ANTHONY J.; VAN DEN BERG, JOHAN A.  
TITLE OF INVENTION: DNA CONSTRUCTS CONTAINING A KLUYVEROMYCES  
A FACTOR LEADER SEQUENCE FOR DIRECTING SECRETION OF HETEROLOGOUS  
POLYPEPTIDES  
NUMBER OF SEQUENCES: 23  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/507,398  
FILING DATE: 09-APR-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 78,551  
FILING DATE: 28-JUL-1987  
SEQ ID NO: 4  
LENGTH: 187  
5217891-4

Query Match 84.2%; Score 32; DB 6; Length 187;  
Best Local Similarity 80.0%; Pred. No. 3.6e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 AMSWL 6  
DB 174 AMSWI 178

RESULT 14  
US-08-887-518-3  
Sequence 3, Application US/08887518  
Patent No. 5843721  
GENERAL INFORMATION:  
APPLICANT: Roche, Mike  
ATTORNEY/AGENT INFORMATION:  
NAME: MU, Lin  
REGISTRATION NUMBER: NIK Proteins, Nucleic Acids and Methods  
REFERENCE/DOCKET NUMBER: 4

CORRESPONDENCE ADDRESS:  
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
STREET: 268 BUSH STREET, SUITE 3200  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/887,518  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: OSMAN, RICHARD A.  
REGISTRATION NUMBER: 36,627  
REFERENCE/DOCKET NUMBER: T97-008  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 343-4341  
TELEFAX: (415) 343-4342  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 745 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-887-518-3

Query Match 84.2%; Score 32; DB 2; Length 745;  
Best Local Similarity 83.3%; Pred. No. 1.3e+03;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 LAMSWL 6  
DB 738 LDMSWL 743

RESULT 15  
US-09-023-321-3  
Sequence 3, Application US/09023321  
Patent No. 5844073  
GENERAL INFORMATION:  
APPLICANT: Roche, Mike  
ATTORNEY/AGENT INFORMATION:  
NAME: MU, Lin  
REGISTRATION NUMBER: NIK Proteins, Nucleic Acids and Methods  
REFERENCE/DOCKET NUMBER: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
STREET: 268 BUSH STREET, SUITE 3200  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/023,321  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/887,518  
ATTORNEY/AGENT INFORMATION:  
NAME: OSMAN, RICHARD A.  
REGISTRATION NUMBER: 36,627  
REFERENCE/DOCKET NUMBER: T97-008

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 343-4341  
TELEFAX: (415) 343-4342  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 745 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-023-321-3

Query Match 84.2%; Score 32; DB 2; Length 745;  
Best Local Similarity 83.3%; Pred. No. 1.3e+03;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 LAMSWL 6  
| | | | |  
DB 738 LDMSWL 743

Search completed: May 30, 2003, 14:41:25  
Job time : 7.03947 secs

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## OM protein - protein search, using sw model

Run on: May 30, 2003, 14:50:13 ; Search time 10.4605 Seconds

(without alignments)  
58.060 Million cell updates/sec

Title: US-09-643-260-6

Perfect score: 40

Sequence: 1 ADMSWA 6

Scoring table: BIOSUM62  
Gapop 10.0, Gapept 0.5

Searched: 383519 seqs, 101223694 residues

Total number of hits satisfying chosen parameters: 383519

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

## Database : Published Applications\_AA:\*

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2: /cgn2\_6/ptodata/1/pubppa/PCT\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptodata/1/pubppa/US06\_NEW\_PUB.pep:\*  
4: /cgn2\_6/ptodata/1/pubppa/US06\_PUBCOMB.pep:\*  
5: /cgn2\_6/ptodata/1/pubppa/US07\_NEW\_PUB.pep:\*  
6: /cgn2\_6/ptodata/1/pubppa/US07\_PUBCOMB.pep:\*  
7: /cgn2\_6/ptodata/1/pubppa/PCTUS\_PUBCOMB.pep:\*  
8: /cgn2\_6/ptodata/1/pubppa/US08\_PUBCOMB.pep:\*  
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12: /cgn2\_6/ptodata/1/pubppa/US10\_PUBCOMB.pep:\*  
13: /cgn2\_6/ptodata/1/pubppa/US60\_NEW\_PUB.pep:\*  
14: /cgn2\_6/ptodata/1/pubppa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40	100.0	6	9	US-09-847-946A-41
2	40	100.0	6	9	US-09-847-946A-73
3	40	100.0	7	9	US-09-847-946A-77
4	40	100.0	8	9	US-09-847-946A-70
5	40	100.0	8	9	US-09-847-946A-78
6	40	100.0	9	9	US-09-847-946A-69
7	40	100.0	9	9	US-09-847-946A-72
8	40	100.0	9	9	US-09-847-946A-75
9	40	100.0	9	9	US-09-847-946A-76
10	40	100.0	10	9	US-09-847-946A-74
11	40	100.0	10	9	US-09-847-946A-74
12	40	100.0	11	9	US-09-847-946A-68
13	37	92.5	885	10	US-09-815-242-5090
14	36	90.0	6	9	US-09-847-940B-4
15	36	90.0	6	9	US-09-847-940B-5
16	36	90.0	6	9	US-09-847-946A-4
17	36	90.0	6	9	US-09-847-946A-5
18	36	90.0	6	9	US-09-847-946A-39
19	36	90.0	6	9	US-09-847-946A-40

20	36	90.0	6	9	US-09-847-946A-51	Sequence 51, Appl
21	36	90.0	6	9	US-09-847-946A-62	Sequence 62, Appl
22	36	90.0	7	9	US-09-847-946A-55	Sequence 55, Appl
23	36	90.0	7	9	US-09-847-946A-66	Sequence 66, Appl
24	36	90.0	8	9	US-09-847-946A-48	Sequence 48, Appl
25	36	90.0	8	9	US-09-847-946A-56	Sequence 56, Appl
26	36	90.0	8	9	US-09-847-946A-59	Sequence 59, Appl
27	36	90.0	8	9	US-09-847-946A-67	Sequence 67, Appl
28	36	90.0	9	9	US-09-847-946A-47	Sequence 47, Appl
29	36	90.0	9	9	US-09-847-946A-50	Sequence 50, Appl
30	36	90.0	9	9	US-09-847-946A-53	Sequence 53, Appl
31	36	90.0	9	9	US-09-847-946A-54	Sequence 54, Appl
32	36	90.0	9	9	US-09-847-946A-58	Sequence 58, Appl
33	36	90.0	9	9	US-09-847-946A-61	Sequence 61, Appl
34	36	90.0	9	9	US-09-847-946A-64	Sequence 64, Appl
35	36	90.0	9	9	US-09-847-946A-65	Sequence 65, Appl
36	36	90.0	10	9	US-09-847-946A-49	Sequence 49, Appl
37	36	90.0	10	9	US-09-847-946A-52	Sequence 52, Appl
38	36	90.0	10	9	US-09-847-946A-57	Sequence 57, Appl
39	36	90.0	10	9	US-09-847-946A-60	Sequence 60, Appl
40	36	90.0	11	9	US-09-847-946A-63	Sequence 63, Appl
41	36	90.0	11	9	US-09-847-946A-63	Sequence 63, Appl
42	36	90.0	174	9	US-10-219-220-163	Sequence 163, App
43	36	90.0	225	9	US-10-219-220-162	Sequence 162, App
44	36	90.0	277	9	US-10-219-220-280	Sequence 280, App
45	36	90.0	378	9	US-10-219-220-158	Sequence 158, App

## ALIGNMENTS

RESULT 1  
US-09-847-946A-41  
Sequence 41, Application US/09847946A  
Publication No. US20030054999A1  
GENERAL INFORMATION:  
APPLICANT: May, Michael J  
APPLICANT: Ghosh, Sanjay  
APPLICANT: Flinders, Mark A  
APPLICANT: Phillips, Kathryn  
APPLICANT: Hannig, Gerhard  
TITLE OR INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
FILE REFERENCE: PFI-119  
CURRENT APPLICATION NUMBER: US/09/847, 946A  
CURRENT FILING DATE: 2001-05-02  
PRIOR APPLICATION NUMBER: 60/201,261  
PRIOR FILING DATE: 2000-05-02  
PRIOR APPLICATION NUMBER: 09/643,260  
PRIOR FILING DATE: 2000-08-22  
NUMBER OF SEQ ID NOS: 160  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 41  
LENGTH: 6  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: NEMO binding  
US-09-847-946A-41  
Query Match 100.0%; Score 40; DB 9; Length 6;  
Best Local Similarity 100.0%; Pred. No. 3.4e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 ADMSWA 6  
DB 1 ADMSWA 6  
RESULT 2  
US-09-847-946A-73  
Sequence 73, Application US/09847946A  
Publication No. US20030054999A1

```
GENERAL INFORMATION:
APPLICANT: May, Michael J
APPLICANT: Ghosh, Sankar
APPLICANT: Findels, Mark A
APPLICANT: Phillips, Kathryn
APPLICANT: Hannig, Gerhard
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 60/201,261
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 73
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
US-09-847-946A-73
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Query Match      100.0%; Score 40; DB 9; Length 6;
Best Local Similarity 100.0%; Pred. No. 3.4e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY      1 ADMSWA 6
        |||||
DB      1 ADMSWA 6
```

```
RESULT 3
US-09-847-946A-77
Sequence 77, Application US/09847946A
Publication No. US20030054999A1
GENERAL INFORMATION:
APPLICANT: May, Michael J
APPLICANT: Ghosh, Sankar
APPLICANT: Findels, Mark A
APPLICANT: Phillips, Kathryn
APPLICANT: Hannig, Gerhard
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 60/201,261
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 77
LENGTH: 7
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
US-09-847-946A-77
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Query Match      100.0%; Score 40; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 3.4e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 ADMSWA 6
        |||||
DB      1 ADMSWA 6
```

RESULT 4

```
US-09-847-946A-70
Sequence 70, Application US/09847946A
Publication No. US20030054999A1
GENERAL INFORMATION:
APPLICANT: May, Michael J
APPLICANT: Ghosh, Sankar
APPLICANT: Findels, Mark A
APPLICANT: Phillips, Kathryn
APPLICANT: Hannig, Gerhard
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 60/201,261
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 70
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
US-09-847-946A-70
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Query Match      100.0%; Score 40; DB 9; Length 8;
Best Local Similarity 100.0%; Pred. No. 3.4e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 ADMSWA 6
        |||||
DB      3 ADMSWA 8
```

```
RESULT 5
US-09-847-946A-78
Sequence 78, Application US/09847946A
Publication No. US20030054999A1
GENERAL INFORMATION:
APPLICANT: May, Michael J
APPLICANT: Ghosh, Sankar
APPLICANT: Findels, Mark A
APPLICANT: Phillips, Kathryn
APPLICANT: Hannig, Gerhard
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
FILE REFERENCE: PPI-119
CURRENT APPLICATION NUMBER: US/09/847,946A
CURRENT FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 60/201,261
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 09/643,260
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 160
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 78
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
US-09-847-946A-78
```

```
Query Match      100.0%; Score 40; DB 9; Length 8;
Best Local Similarity 100.0%; Pred. No. 3.4e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY      1 ADMSWA 6
        |||||
DB      1 ADMSWA 6
```

RESULT 6  
US-09-847-946A-69  
; Sequence 69, Application US/09847946A  
; Publication No. US20030054999A1  
; GENERAL INFORMATION:  
; APPLICANT: May, Michael J  
; APPLICANT: Ghosh, Sankar  
; APPLICANT: Findels, Mark A  
; APPLICANT: Phillips, Kathryn  
; APPLICANT: Hannig, Gerhard  
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
; FILE REFERENCE: PFI-119  
; CURRENT APPLICATION NUMBER: US/09/847,946A  
; CURRENT FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: 60/201,261  
; PRIOR FILING DATE: 2000-05-02  
; PRIOR APPLICATION NUMBER: 09/643,260  
; PRIOR FILING DATE: 2000-08-22  
; NUMBER OF SEQ ID NOS: 160  
; SOFTWARE: Patentln Ver. 2.0  
; SEQ ID NO 69  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding  
US-09-847-946A-69  
OTHER INFORMATION: sequence

Query Match 100.0%; Score 40; DB 9; Length 9;  
Best Local Similarity 100.0%; Pred. No. 3.4e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWA 6  
Db 1 ADMSWA 6

RESULT 7  
US-09-847-946A-72  
; Sequence 72, Application US/09847946A  
; Publication No. US20030054999A1  
; GENERAL INFORMATION:  
; APPLICANT: May, Michael J  
; APPLICANT: Ghosh, Sankar  
; APPLICANT: Findels, Mark A  
; APPLICANT: Phillips, Kathryn  
; APPLICANT: Hannig, Gerhard  
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
; FILE REFERENCE: PFI-119  
; CURRENT APPLICATION NUMBER: US/09/847,946A  
; CURRENT FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: 60/201,261  
; PRIOR FILING DATE: 2000-05-02  
; PRIOR APPLICATION NUMBER: 09/643,260  
; PRIOR FILING DATE: 2000-08-22  
; NUMBER OF SEQ ID NOS: 160  
; SOFTWARE: Patentln Ver. 2.0  
; SEQ ID NO 72  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding  
US-09-847-946A-72  
OTHER INFORMATION: sequence

Query Match 100.0%; Score 40; DB 9; Length 9;  
Best Local Similarity 100.0%; Pred. No. 3.4e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWA 6  
Db 1 ADMSWA 6

QY 1 ADMSWA 6  
Db 1 ADMSWA 6

RESULT 8  
US-09-847-946A-75  
; Sequence 75, Application US/09847946A  
; Publication No. US20030054999A1  
; GENERAL INFORMATION:  
; APPLICANT: May, Michael J  
; APPLICANT: Ghosh, Sankar  
; APPLICANT: Findels, Mark A  
; APPLICANT: Phillips, Kathryn  
; APPLICANT: Hannig, Gerhard  
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
; FILE REFERENCE: PFI-119  
; CURRENT APPLICATION NUMBER: US/09/847,946A  
; CURRENT FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: 60/201,261  
; PRIOR FILING DATE: 2000-05-02  
; PRIOR APPLICATION NUMBER: 09/643,260  
; PRIOR FILING DATE: 2000-08-22  
; NUMBER OF SEQ ID NOS: 160  
; SOFTWARE: Patentln Ver. 2.0  
; SEQ ID NO 75  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding  
US-09-847-946A-75  
OTHER INFORMATION: sequence

Query Match 100.0%; Score 40; DB 9; Length 9;  
Best Local Similarity 100.0%; Pred. No. 3.4e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWA 6  
Db 3 ADMSWA 8

RESULT 9  
US-09-847-946A-76  
; Sequence 76, Application US/09847946A  
; Publication No. US20030054999A1  
; GENERAL INFORMATION:  
; APPLICANT: May, Michael J  
; APPLICANT: Ghosh, Sankar  
; APPLICANT: Findels, Mark A  
; APPLICANT: Phillips, Kathryn  
; APPLICANT: Hannig, Gerhard  
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
; FILE REFERENCE: PFI-119  
; CURRENT APPLICATION NUMBER: US/09/847,946A  
; CURRENT FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: 60/201,261  
; PRIOR FILING DATE: 2000-05-02  
; PRIOR APPLICATION NUMBER: 09/643,260  
; PRIOR FILING DATE: 2000-08-22  
; NUMBER OF SEQ ID NOS: 160  
; SOFTWARE: Patentln Ver. 2.0  
; SEQ ID NO 76  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding  
US-09-847-946A-76  
OTHER INFORMATION: sequence

Query Match 100.0%; Score 40; DB 9; Length 9;

Best Local Similarity 100.0%; Pred. No. 3.4e+05; Indels 0; Gaps 0;  
Matches 6; Conservative 0; Mismatches 0;

QY 1 ADMSWA 6  
111111  
Db 2 ADMSWA 7

## RESULT 10

US-09-847-946A-71  
; Sequence 71, Application US/09847946A  
; Publication No. US20030054999A1  
; GENERAL INFORMATION:

APPLICANT: May, Michael J  
APPLICANT: Ghosh, Sankar  
APPLICANT: Findels, Mark A  
APPLICANT: Phillips, Kathryn  
APPLICANT: Hannig, Gerhard  
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
FILE REFERENCE: PFI-119  
CURRENT APPLICATION NUMBER: US/09/847,946A  
CURRENT FILING DATE: 2001-05-02  
PRIOR APPLICATION NUMBER: 60/201,261  
PRIOR FILING DATE: 2000-05-02  
PRIOR APPLICATION NUMBER: 09/643,260  
PRIOR FILING DATE: 2000-08-22  
NUMBER OF SEQ ID NOS: 160  
SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 71

LENGTH: 10

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence:NEMO binding

US-09-847-946A-71

Query Match 100.0%; Score 40; DB 9; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.2;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWA 6  
111111  
Db 2 ADMSWA 7

## RESULT 11

US-09-847-946A-74  
; Sequence 74, Application US/09847946A  
; Publication No. US20030054999A1  
; GENERAL INFORMATION:

APPLICANT: May, Michael J  
APPLICANT: Ghosh, Sankar  
APPLICANT: Findels, Mark A  
APPLICANT: Phillips, Kathryn  
APPLICANT: Hannig, Gerhard  
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
FILE REFERENCE: PFI-119  
CURRENT APPLICATION NUMBER: US/09/847,946A  
CURRENT FILING DATE: 2001-05-02  
PRIOR APPLICATION NUMBER: 60/201,261  
PRIOR FILING DATE: 2000-05-02  
PRIOR APPLICATION NUMBER: 09/643,260  
PRIOR FILING DATE: 2000-08-22  
NUMBER OF SEQ ID NOS: 160  
SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 74

LENGTH: 10

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence:NEMO binding

US-09-847-946A-74

Query Match 100.0%; Score 40; DB 9; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.2;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWA 6  
111111  
Db 3 ADMSWA 8

## RESULT 12

US-09-847-946A-68  
; Sequence 68, Application US/09847946A  
; Publication No. US20030054999A1  
; GENERAL INFORMATION:

APPLICANT: May, Michael J  
APPLICANT: Ghosh, Sankar  
APPLICANT: Findels, Mark A  
APPLICANT: Phillips, Kathryn  
APPLICANT: Hannig, Gerhard  
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
FILE REFERENCE: PFI-119  
CURRENT APPLICATION NUMBER: US/09/847,946A  
CURRENT FILING DATE: 2001-05-02  
PRIOR APPLICATION NUMBER: 60/201,261  
PRIOR FILING DATE: 2000-05-02  
PRIOR APPLICATION NUMBER: 09/643,260  
PRIOR FILING DATE: 2000-08-22  
NUMBER OF SEQ ID NOS: 160  
SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 68

LENGTH: 11

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence:NEMO binding

US-09-847-946A-68

Query Match 100.0%; Score 40; DB 9; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.4;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWA 6  
111111  
Db 3 ADMSWA 8

## RESULT 13

US-09-815-242-5090  
; Sequence 5090, Application US/09815242  
; Patent No. US20020061569A1  
; GENERAL INFORMATION:

APPLICANT: Haselbeck, Robert  
APPLICANT: Ohlsen, Karl L.  
APPLICANT: Zyskind, Judith W.  
APPLICANT: Wall, Daniel  
APPLICANT: Trawick, John D.  
APPLICANT: Carr, Grant J.  
APPLICANT: Yamamoto, Robert T.  
APPLICANT: Xu, H. Howard  
TITLE OF INVENTION: Identification of Essential Genes in  
FILE REFERENCE: ELITRA.011A  
CURRENT APPLICATION NUMBER: US/09/815,242  
CURRENT FILING DATE: 2001-03-21  
PRIOR APPLICATION NUMBER: 60/191,078  
PRIOR FILING DATE: 2000-03-21  
PRIOR APPLICATION NUMBER: 60/206,848  
PRIOR FILING DATE: 2000-05-23  
PRIOR APPLICATION NUMBER: 60/207,727  
PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/242,578  
PRIOR FILING DATE: 2000-10-23  
PRIOR APPLICATION NUMBER: 60/253,625  
PRIOR FILING DATE: 2000-11-27  
PRIOR APPLICATION NUMBER: 60/257,931  
PRIOR FILING DATE: 2000-12-22  
PRIOR APPLICATION NUMBER: 60/269,308  
PRIOR FILING DATE: 2001-02-16  
NUMBER OF SEQ ID NOS: 1410  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 5090  
LENGTH: 885  
TYPE: PRT  
ORGANISM: Pseudomonas aeruginosa  
US-09-815-242-5090

Query Match 92.5%; Score 37; DB 10; Length 885;  
Best Local Similarity 83.3%; Pred. No. 3.3e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 ADMSA 6  
Db 563 ADMSA 568

RESULT 14  
US-09-847-940B-4  
Sequence 4, Application US/09847940B  
Patent No. US20020156000A1  
GENERAL INFORMATION:  
APPLICANT: May, Michael J.  
APPLICANT: Ghosh, Sankar  
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
FILE REFERENCE: PPI-117CP  
CURRENT APPLICATION NUMBER: US/09/847,940B  
CURRENT FILING DATE: 2001-05-02  
PRIOR APPLICATION NUMBER: 09/643,260  
PRIOR FILING DATE: 2000-08-22  
NUMBER OF SEQ ID NOS: 27  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 4  
LENGTH: 6  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: NBD mutants  
US-09-847-940B-4

Query Match 90.0%; Score 36; DB 9; Length 6;  
Best Local Similarity 100.0%; Pred. No. 3.4e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ADMSW 5  
Db 1 ADMSW 5

RESULT 15  
US-09-847-940B-5  
Sequence 5, Application US/09847940B  
Patent No. US20020156000A1  
GENERAL INFORMATION:  
APPLICANT: May, Michael J.  
APPLICANT: Ghosh, Sankar  
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
FILE REFERENCE: PPI-117CP  
CURRENT APPLICATION NUMBER: US/09/847,940B  
CURRENT FILING DATE: 2001-05-02  
PRIOR APPLICATION NUMBER: 09/643,260  
PRIOR FILING DATE: 2000-08-22  
NUMBER OF SEQ ID NOS: 27  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 5

LENGTH: 6  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: NBD mutants  
US-09-847-940B-5

Query Match 90.0%; Score 36; DB 9; Length 6;  
Best Local Similarity 100.0%; Pred. No. 3.4e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 DMSWA 6  
Db 2 DMSWA 6

Search completed: May 30, 2003, 15:53:16  
Job time : 10.4605 secs



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OM protein - protein search, using sw model

Run on: May 30, 2003, 14:32:11 ; Search time 14.7632 Seconds

(without alignments)  
83.741 Million cell updates/sec

Title: US-09-643-260-6

Perfect score: 40

Sequence: 1 ADMSWA 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPRMBL\_21:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_minc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp Vertebrate:\*  
14: sp\_uniclaffied:\*  
15: sp\_virus:\*  
16: sp\_bacteriaph:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	37	92.5	437	16	Q92K30	Q92K30 rhizobium m
2	37	92.5	548	16	Q92M15	Q92M15 rhizobium m
3	37	92.5	597	5	Q9VGP2	Q9VGP2 dirosophila
4	37	92.5	610	16	Q86712	Q86712 streptomyc
5	37	92.5	885	16	Q91389	Q91389 pseudomonas
6	36	90.0	205	16	Q9ACR5	Q9ACR5 streptomyc
7	36	90.0	242	12	Q919K8	Q919K8 culx nigrl
8	36	90.0	358	10	Q50002	Q50002 prunus arne
9	36	90.0	374	16	Q9H210	Q9H210 pseudomonas
10	36	90.0	452	4	Q96AB7	Q96AB7 homo sapien
11	36	90.0	477	11	Q9CYU6	Q9CYU6 mus musculi
12	36	90.0	484	4	Q9BTV6	Q9BTV6 homo sapien
13	36	90.0	889	16	Q9AAZ6	Q9AAZ6 caulobacter
14	36	90.0	1005	10	Q9XGZ2	Q9XGZ2 arbidopsi
15	36	90.0	5435	2	Q91AX2	Q91AX2 streptomyc
16	34	85.0	273	10	Q94JMA	Q94JMA arabidopsis

17	34	85.0	273	10	Q940D6	Q940D6 arabidopsis
18	34	85.0	275	10	Q65710	Q65710 arabidopsis
19	34	85.0	376	3	Q9UVL4	Q9UVL4 penicillium
20	34	85.0	617	10	P93050	P93050 arabidopsis
21	34	85.0	1842	3	Q96WT8	Q96WT8 schizosach
22	34	85.0	1842	3	Q96WT7	Q96WT7 schizosach
23	34	85.0	1842	3	Q96WT6	Q96WT6 schizosach
24	34	85.0	1842	3	Q96WT5	Q96WT5 equus cabal
25	33	82.5	98	5	Q9VBA5	Q9VBA5 dirosophila
26	33	82.5	161	11	Q921P9	Q921P9 ratius norv
27	33	82.5	198	16	Q9P854	Q9P854 xylella fas
28	33	82.5	213	12	Q9E117	Q9E117 meleagrid h
29	33	82.5	213	12	Q9DPT1	Q9DPT1 trichoderma
30	33	82.5	234	3	Q00095	Q00095 sulfolobus
31	33	82.5	239	17	Q97UT3	Q97UT3 mycobacteri
32	33	82.5	257	16	Q9X787	Q9X787 pseudomonas
33	33	82.5	276	16	Q9RT43	Q9RT43 amycolatops
34	33	82.5	304	16	Q91719	Q91719 rhodococcus
35	33	82.5	309	2	Q9F163	Q9F163 amycolatops
36	33	82.5	310	3	Q8TGE0	Q8TGE0 aspergillus
37	33	82.5	316	2	Q96J74	Q96J74 rhodococcus
38	33	82.5	320	4	Q96J74	Q96J74 homo sapien
39	33	82.5	323	6	Q9T779	Q9T779 ovis aries
40	33	82.5	324	16	Q8YD70	Q8YD70 bruceella me
41	33	82.5	328	16	Q9WXR6	Q9WXR6 thermotoga
42	33	82.5	330	4	Q96M26	Q96M26 homo sapien
43	33	82.5	335	16	Q989F6	Q989F6 rhizobium l
44	33	82.5	338	2	Q46645	Q46645 erwinia amy
45	33	82.5	350	10	Q41057	Q41057 pisum sativ

## ALIGNMENTS

RESULT 1  
ID Q92K30 PRELIMINARY; PRT; 437 AA.  
AC Q92K30;  
DT 01-DEC-2001 (TREMREL. 19, Created).  
DT 01-DEC-2001 (TREMREL. 19, Last sequence update)  
DT 01-MAR-2002 (TREMREL. 20, Last annotation update)  
DE Hypothetical protein R02283.  
GN R02283 OR SMC01671.  
OS Rhizobium melioli (Sinorhizobium melioli).  
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;  
OC Rhizobiaceae; Sinorhizobium.  
OX NCBI\_TaxID=382;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC MEDLINE-21396507; PubMed-11481430;  
RA Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,  
RA Bolstad P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,  
RA Godrie T., Goffeau A., Kahn D., Kiss E., Lelaur V., Masny D.,  
RA Pohl T., Portetlelle D., Puhler A., Punelle B., Ransperger U.,  
RA Renard C., Thebaud P., Vandenbol M., Weidner S., Galibert F.,  
RT "Analysis of the chromosome sequence of the legume symbiont  
Sinorhizobium melioli strain 1021.";  
RL Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).  
DR EMBL; AL591790; CAC46862.1;  
KW Hypothetical protein; Complete proteome.  
SQ SEQUENCE 437 AA; 48372 MW; 950E0B3DA963CE78 CRC64;

Query Match 92.5% Score 37; DB 16; Length 437;  
Best Local Similarity 83.3%; Pred. No. 2.6e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWA 6  
DB 157 ADMSWA 162

RESULT 2

```

092M15
ID 092M15 PRELIMINARY; PRT; 548 AA.
AC 092M15;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DE 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Putative fatty-acid-CoA ligase protein (EC 6.).
GN R02631 OR SMC00741.
OS Rhizobium meliloti (Sinorhizobium meliloti).
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae; Sinorhizobiaceae.
OX NCBI_TaxID=382;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1021;
RX MEDLINE=21396507; PubMed=11481430;
RA Bolstad P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,
RA Godt T., Goffeau A., Kahn D., Kiss E., Leclaire V., Masuy D.,
RA Pohl T., Portetelle D., Puehler A., Purnelle B., Ramsperger U.,
RA Renard C., Thebaud P., Vandenbol M., Weidner S., Galibert F.;
RT "Analysis of the chromosome sequence of the legume symbiont
RT Sinorhizobium meliloti strain 1021."
RT Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
DR EMBL: AL591791; CAC47210.1; -
DR InterPro: IPR003439; ABC-transporter.
DR InterPro: IPR000873; AMP-bind.
DR Pfam: PF00501; AMP-binding; 1.
DR PROSITE: PS00211; ABC-TRANSPORTER; UNKNOWN_1.
DR PROSITE: PS00455; AMP-BINDING; UNKNOWN_1.
KM Ligase: Complete proteome.
SQ SEQUENCE 548 AA; 59383 MW; 659A68C546EA953B CRC64;

Query Match 92.5%; Score 37; DB 16; Length 548;
Best Local Similarity 83.3%; Pred. No. 3.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWA 6
DB 235 ADMSWA 240

RESULT 3
09VGP2 PRELIMINARY; PRT; 597 AA.
ID 09VGP2;
AC 09VGP2;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE CG6728 protein.
GN CG6728.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Baller R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Botkova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
RA Butlis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cavley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

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RA Dodson K., Doup I.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabriellian A.E., Gary N.S., Gelbart W.M., Glasser K.,
RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Kapen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laslo P., Lei Y., Levitsky A.C., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.N., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclet J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svrtkars R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RT Science 287:2185-2195(2000).
RL EMBL: AE003691; AA054634.1; -
DR EMBL: FB90037896; CG6728.
DR InterPro: IPR000172; GMC-oxred.
DR InterPro: IPR000169; SHprol.acetate.
DR Pfam: PF00732; GMC-oxred; 1.
DR PROSITE: PS00624; GMC-oxRED; 2; 1.
DR PROSITE: PS00639; THIOL_PROTEASE_HIS; UNKNOWN_1.
SQ SEQUENCE 597 AA; 65274 MW; 8C4C362AFA90902A CRC64;

Query Match 92.5%; Score 37; DB 5; Length 597;
Best Local Similarity 83.3%; Pred. No. 3.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWA 6
DB 158 SDMSWA 163

RESULT 4
086712 PRELIMINARY; PRT; 610 AA.
ID 086712;
AC 086712;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DE 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Hypothetical protein SC06530.
GN SC06530 OR SC5C7.15.
OS Streptomyces coelicolor.
OC Actinomycetes; Actinobacteria; Actinobacteridae;
OC Bacteria; Firmicutes; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2) / M145;
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
RA Thompson N.R., James K.D., Harris D.E., Quail M.A., Kleser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kleser T., Larke L., Murphy L., Oliver K., O'Neill S.,
RA Rabinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
RT coelicolor A3(2).";
RL Nature 417:141-147(2002).
DR EMBL: AL031515; CAA20627.1; -
KM Hypothetical protein.

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SQ SEQUENCE 610 AA; 67368 MW; 052CEA90DB589021 CRC64;  
 Query Match 92.5%; Score 37; DB 16; Length 610;  
 Best Local Similarity 83.3%; Pred. No. 3.6e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSMA 6  
 111111  
 DB 83 ADMAMA 88

RESULT 5  
 Q91389 PRELIMINARY; PRT; 885 AA.  
 AC Q91389;  
 DT 01-MAR-2001 (TREMBLrel. 16, Created)  
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE Two-component sensor KdpD.  
 GN KDPD OR PA1636.  
 OS Pseudomonas aeruginosa.  
 OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;  
 OC Pseudomonas.  
 OX NCBI\_TaxID=287;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC 15692 / PA01;  
 RX MEDLINE=20437337; PubMed=10984043;  
 RA Stover C.K., Pham X.-O.T., Erwin A.L., Mizoguchi S.D., Warrenner P.,  
 RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lafrou M.,  
 RA Garber R.L., Goltz L., Tolentino E., Westbrock-Wadman S., Yuan Y.,  
 RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,  
 RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,  
 RA Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.;  
 RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an  
 RT opportunistic pathogen.";  
 RT Nature 406:959-964(2000)  
 RL -1- SIMILARITY: TO PROKARYOTE SENSORY TRANSDUCTION PROTEINS.  
 CC EMBL; AEO04591; AAG05025.1; -.  
 DR HSSP; P02933; 1JOY.  
 DR InterPro: IPR003594; ATPbind\_Artpase.  
 DR InterPro: IPR004358; Bact\_sens\_Dr\_C.  
 DR InterPro: IPR003018; GAF.  
 DR InterPro: IPR003661; His\_KinA.  
 DR InterPro: IPR004359; His\_Kin\_s1g.  
 DR InterPro: IPR003852; KdpD.  
 DR Pfam; PF02518; HATPase\_c; 1.  
 DR Pfam; PF02702; KdpD; 1.  
 DR Pfam; PF0512; signal; 1.  
 DR PRINTS; PRO0344; BCTRSENSOR.  
 DR SMART; SM00065; GAF; 1.  
 DR SMART; SM00387; HATPase\_c; 1.  
 DR SMART; SM00388; HlSKA; 1.  
 KW Kinase; Phosphorylation; Sensory transduction; Transferase;  
 KW Complete proteome.  
 SQ SEQUENCE 885 AA; 97019 MW; 20FC8E2B2AB876C0 CRC64;

Query Match 92.5%; Score 37; DB 16; Length 885;  
 Best Local Similarity 83.3%; Pred. No. 5.2e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSMA 6  
 111111  
 DB 563 ADMAMA 568

RESULT 6  
 Q9ACR5 PRELIMINARY; PRT; 205 AA.  
 AC Q9ACR5;  
 DT 01-JUN-2001 (TREMBLrel. 17, Created)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)

DE Hypothetical protein SCPI.253.  
 GN SCPI.253.  
 OS Streptomyces coelicolor.  
 OC Plasmid SCPI.  
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;  
 OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.  
 OX NCBI\_TaxID=1902;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=A3(2);  
 RA Bentley S.D., Chater K.F., Cerdano-Tarraga A.-M., Challis G.L.,  
 RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kleser H.,  
 RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,  
 RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,  
 RA Huang C.-H., Kleser T., Larke L., Murphy L., Oliver K., O'Neill S.,  
 RA Rabinowitz E., Rajandream M.A., Rutherford K., Rutter S.,  
 RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,  
 RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,  
 RA Hopwood D.A.;  
 RT "Complete genome sequence of the model actinomycete Streptomyces  
 RT coelicolor A3(2)."  
 RL Nature 417:141-147(2002).  
 DR EMBL: AF590464; CAC36779.1; -.  
 KW Hypothetical protein; Plasmid.  
 SQ SEQUENCE 205 AA; 23051 MW; 6602396CF93F2D9 CRC64;

Query Match 90.0%; Score 36; DB 16; Length 205;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSW 5  
 111111  
 DB 10 ADMSW 14

RESULT 7  
 Q919K8 PRELIMINARY; PRT; 242 AA.  
 AC Q919K8;  
 DT 01-DEC-2001 (TREMBLrel. 19, Created)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE CUN068 hypothetical protein.  
 GN CUN068.  
 OS Culex nigripalpus baculovirus.  
 OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae.  
 OX NCBI\_TaxID=130556;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=FLORIDA1997;  
 RX MEDLINE=2148685; PubMed=11602755;  
 RA Alonso C.L., Tulman E.R., Lu Z., Balinsky C.A., Moser B.A.,  
 RA Becnel J.J., Rock D.L., Kutish G.F.;  
 RT "Genome Sequence of a Baculovirus Pathogenic for Culex nigripalpus.";  
 RL J. Virol. 75:11157-11165(2001).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=FLORIDA1997;  
 RA Alonso C.L., Tulman E.R., Lu Z., Balinsky C.A., Moser B.A.,  
 RA Becnel J.J., Rock D.L., Kutish G.F.;  
 RT Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF403738; AAR94146.1; -.  
 KW Hypothetical protein.  
 SQ SEQUENCE 242 AA; 27222 MW; 6014967531110E52 CRC64;

Query Match 90.0%; Score 36; DB 12; Length 242;  
 Best Local Similarity 100.0%; Pred. No. 2e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DMSMA 6  
 111111  
 DB 80 DMSMA 84

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RESULT 8
050002 PRELIMINARY; PRT; 358 AA.
ID 050002
AC 050002
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Cysteine protease.
OS Prunus armeniaca (Apricot).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.
OK NCBI_TaxID=36596;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN-BERGERON; TISSUE-MESOCARP PLUS EXOCARP;
RA Mbaguele-A-Mbaguele D., Gomez R.-M., Fils-Lycaon B.;
RT "Sequence of APTP1, a Cysteine Proteinase From Apricot Fruit
RT (Accession No. U93166). Gene Expression During Fruit Ripening. (PGR97-
RT 179)."
RL Plant Physiol. 115:1730-1730(1997).
DR EMBL: U93166; AAB97142.1; -.
DR HSSP: P07711; ICJL.
DR MEROPS: C01.041; -.
DR InterPro: IPR001092; HLH_Basic.
DR InterPro: IPR000668; Peptidase_C1.
DR InterPro: IPR000169; SHprot_acsite.
DR Pfam: PF00112; Peptidase_C1; 1.
DR PRINTS: PR00705; PAPAIN.
DR ProDom: PD000158; Peptidase_C1; 1.
DR PROSITE: PS00038; HELIX_LOOP_HELIX; UNKNOWN_1.
DR PROSITE: PS00640; THIOL_PROTEASE_ASN; 1.
DR PROSITE: PS00139; THIOL_PROTEASE_CYS; 1.
DR PROSITE: PS00639; THIOL_PROTEASE_HIS; 1.
KW Hydrolase; Protease; Thiol protease.
SQ SEQUENCE 358 AA; 39309 MM; C98F78793B002554 CRC64;

Query Match 90.0%; Score 36; DB 10; Length 358;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ADMSW 5
DB 108 ADMSW 112

RESULT 9
09HZ10 PRELIMINARY; PRT; 374 AA.
ID 09HZ10
AC 09HZ10
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-OCT-2001 (TREMBLrel. 18, Last annotation update)
DE Hypothetical protein PA3230.
GN PA3230.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=287;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN-ATCC 15692 / PA01;
RA MEDLINE=20437337; PubMed=10984043;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,
RA Hickey M.J., Birkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Gabler R.L., Goltzy L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Labdig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.;
RA "Complete genome sequence of Pseudomonas aeruginosa PA01, an
RA opportunistic pathogen."
RL Nature 406:959-964(2000).

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DR EMBL: AE004746; AAG06618.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 374 AA; 42269 MM; 31EF185C4F683884 CRC64;

Query Match 90.0%; Score 36; DB 16; Length 374;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 DMSWA 6
DB 81 DMSWA 85

RESULT 10
096AB7 PRELIMINARY; PRT; 452 AA.
ID 096AB7
AC 096AB7
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Hypothetical 50.6 kDa protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN SEQUENCE FROM N.A.
RP TISSUE-SKIN;
RA Strausberg R.;
RT Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
CC -1; SIMILARITY: CONTAINS 3 WD REPEATS (TRP-ASP DOMAINS).
DR EMBL: BC017335; AAH17335.1; -.
DR InterPro: IPR001680; WD40.
DR Pfam: PF00400; WD40; 2.
DR PROSITE: PS00678; WD_REPEATS_1; UNKNOWN_2.
DR PROSITE: PS50082; WD_REPEATS_2; 1.
DR PROSITE: PS50294; WD_REPEATS_REGION; 1.
KW Hypothetical protein; Repeat; WD repeat.
SQ SEQUENCE 452 AA; 50575 MM; B79D25EE38096733 CRC64;

Query Match 90.0%; Score 36; DB 4; Length 452;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ADMSW 5
DB 338 ADMSW 342

RESULT 11
09CY06 PRELIMINARY; PRT; 477 AA.
ID 09CY06
AC 09CY06
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE 2810443U12Rik protein.
GN 2810443U12Rik.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN-C57BL/6J; TISSUE-EMBRYO;
RA MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Aachi J., Fukuda S.,
RA Aizawa K., Izawa Y., Nishi K., Kiyosawa H., Kondo S., Yamana K.I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiya H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

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RA Schriml L.M., Staudt F., Suzuki R., Tomita M., Wagner L., Washio T.,  
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
 RA Blake J., Boiffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
 RA Gustinich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
 RA Suzuki H., Toyooka K., Wang K.H., Weltz C., Whitaker C., Wilming L.,  
 RA Wyszynski-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,  
 RA Hayashizaki Y.,  
 RT "Functional annotation of a full-length mouse cDNA collection.",  
 RL Nature 409:685-690(2001).  
 CC -1- SIMILARITY: CONTAINS 2 WD REPEATS (TRP-ASP DOMAINS).  
 DR EMBL: AK013297; BAB28775.1; -  
 DR MGD: MG1:1914478; 281044312trk.  
 DR InterPro: IPR001680; WD40.  
 DR Pfam: PF00400; WD40; 3.  
 DR SMART: SM00320; WD40; 4.  
 DR PROSITE: PS00678; WD\_REPEATS\_1; UNKNOWN\_1.  
 DR PROSITE: PS50082; WD\_REPEATS\_2; 1.  
 DR PROSITE: PS50294; WD\_REPEATS\_REGION; 1.  
 KM Repeat; WD repeat.  
 SQ SEQUENCE 477 AA; 53201 MW; 2655573524A4BA9C CRC64;

Query Match 90.0%; Score 36; DB 11; Length 477;  
 Best Local Similarity 100.0%; Pred. No. 4e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ADMSW 5  
 DB 337 ADMSW 341

## RESULT 12

O9BTY6 PRELIMINARY; PRT; 484 AA.  
 ID O9BTY6  
 AC O9BTY6; 01-JUN-2001 (TREMblrel. 17, Created)  
 DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)  
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)  
 DE Hypothetical 54.1 kDa protein (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-BRAIN;  
 RA Strausberg R.;  
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: CONTAINS 2 WD REPEATS (TRP-ASP DOMAINS).  
 DR EMBL: BC003123; AA03123.1; -  
 DR InterPro: IPR001680; WD40.  
 DR Pfam: PF00400; WD40; 2.  
 DR SMART: SM00320; WD40; 3.  
 DR PROSITE: PS00678; WD\_REPEATS\_1; UNKNOWN\_2.  
 DR PROSITE: PS50082; WD\_REPEATS\_2; 1.  
 DR PROSITE: PS50294; WD\_REPEATS\_REGION; 1.  
 KM Hypothetical protein; Repeat; WD repeat.  
 FT NON\_TER 1  
 SQ SEQUENCE 484 AA; 54088 MW; 1A2CA3237CB7356E CRC64;

Query Match 90.0%; Score 36; DB 4; Length 484;  
 Best Local Similarity 100.0%; Pred. No. 4e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ADMSW 5  
 DB 370 ADMSW 374

## RESULT 13

O9AAZ6 PRELIMINARY; PRT; 889 AA.  
 ID O9AAZ6  
 AC O9AAZ6; 01-JUN-2001 (TREMblrel. 17, Created)  
 DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)  
 DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)  
 DE TonB-dependent receptor.  
 GN CC0446.  
 OS Caulobacter crescentus.  
 OC Bacteria; Proteobacteria; alpha subdivision; Caulobacter group;  
 OC Caulobacter.  
 OX NCBI\_TaxID=155892;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-ATCC 19089 / CB15;  
 RX MEDLINE: 21173698; PubMed=11259647;  
 RA Niernan W.C., Feldblum T.V., Iash M.T., Paulsen I.T., Nelson K.E.,  
 RA Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,  
 RA Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,  
 RA Deboy R.T., Dodson R.J., Durkin A.S., Gwin M.L., Halt D.H.,  
 RA Kolonay J.F., Smit J., Creaven M.B., Khouri H., Shetty J., Berry K.,  
 RA Ueberlack T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O.,  
 RA Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;  
 RT "Complete genome sequence of Caulobacter crescentus.",  
 RL Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).  
 DR EMBL: AE005717; MAK22433.1; -  
 DR TIGR: CC0446;  
 DR InterPro: IPR00531; TonB\_boxc.  
 DR Pfam: PF00593; TonB\_boxc; 1.  
 KM Receptor; Complete proteome.  
 SQ SEQUENCE 889 AA; 95775 MW; 75FCBD7A726A01A5 CRC64;

Query Match 90.0%; Score 36; DB 16; Length 889;  
 Best Local Similarity 100.0%; Pred. No. 7.4e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ADMSW 5  
 DB 618 ADMSW 622

## RESULT 14

O9XGZ2 PRELIMINARY; PRT; 1005 AA.  
 ID O9XGZ2  
 AC O9XGZ2; 01-NOV-1999 (TREMblrel. 12, Created)  
 DT 01-NOV-1999 (TREMblrel. 12, Last sequence update)  
 DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)  
 DE T1N24.22 protein.  
 GN T1N24.22.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eucosids II; Brassicales; Brassicaceae; Arabidopsis.  
 OX NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-CV. COLUMBIA;  
 RA Wasyu;  
 RT "The A. thaliana Genome Sequencing Project.",  
 RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-CV. COLUMBIA;  
 RA Murray J., Langston Y., Clarke K., Drone K.,  
 RT "The sequence of A. thaliana T1N24.",  
 RL submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-CV. COLUMBIA;  
 RA Waterston R.;  
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

DR EMBL: AF149413; AAD40144.1; -  
 DR InterPro: IPR000719; Euk\_pkinase.  
 DR InterPro: IPR001611; LRR.  
 DR InterPro: IPR003592; LRR\_out.  
 DR InterPro: IPR002290; Ser\_thr\_pkinase.  
 DR Pfam: PF00560; LRR; 19.  
 DR Pfam: PF00069; pkinase; 1.  
 DR PRINTS: PR00019; LEURICHRPT.  
 DR PRODOM: PD000001; Euk\_pkinase; 1.  
 DR SMART: SM00370; LRR; 17.  
 DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP; UNKNOWN\_1.  
 DR PROSITE: PS0011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE: PS00108; PROTEIN\_KINASE\_ST; 1.  
 KW ATP-binding: Serine/threonine-protein kinase; Transferase.  
 SQ SEQUENCE 1005 AA; 111963 MW; BB006438CC9541C9 CRC64;

Query Match 90.0%; Score 36; DB 10; Length 1005;  
 Best Local Similarity 100.0%; Pred. No. 8.4e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 ADMSW 5  
 DB 906 ADMSW 910

## RESULT 15

OSLAX2 PRELIMINARY; PRT; 5435 AA.  
 AC Q9LAX2;  
 DT 01-OCT-2000 (TREMBLrel. 15, Created)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE Nysu.  
 GN NYSU.  
 OS Streptomyces noursei.  
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;  
 OC Actinomycetales; Streptomycetaceae; Streptomyces.  
 OX NCBI\_TaxID:1971;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-ATCC 11455;  
 RX MEDLINE-20334850; PubMed-10873841;  
 RA Brautaset T., Sekurova O.N., Sletta H., Ellingsen T.E., Strom A.R.,  
 RA Valla S., Zotchev S.B.;  
 RT "Biosynthesis of the polyene antifungal antibiotic nystatin in  
 RT Streptomyces noursei ATCC 11455: analysis of the gene cluster and  
 RT deduction of the biosynthetic pathway.";  
 RL Chem. Biol. 7:395-403(2000).  
 DR EMBL: AF263912; AAF71767.1; -  
 DR HSSP: P25715; IMLA.  
 DR InterPro: IPR001227; AC\_transferase.  
 DR InterPro: IPR002198; ADH\_short.  
 DR InterPro: IPR002085; Adh\_zn\_family.  
 DR InterPro: IPR004410; Fadd.  
 DR InterPro: IPR001899; Gram\_pos\_anchor.  
 DR InterPro: IPR000794; Ketoacyl-synt.  
 DR InterPro: IPR003880; ppanine\_attach.  
 DR Pfam: PF00698; Acyl\_transf; 3.  
 DR Pfam: PF00106; adh\_short; 1.  
 DR Pfam: PF00107; adh\_zinc; 1.  
 DR Pfam: PF02801; ketoacyl-synt\_C; 3.  
 DR Pfam: PF00550; pp-binding; 3.  
 DR TIGRfams: TIGR00128; fadd; 3.  
 DR PROSITE: PS50075; ACP\_DOMAIN; 3.  
 DR PROSITE: PS00606; B\_KETOACYL\_SYNTHASE; 3.  
 DR PROSITE: PS00343; GRAM\_POS\_ANCHORING; UNKNOWN\_1.  
 DR PROSITE: PS00012; PHOSPHOPANTHEINE; 3.  
 KW Phosphopantetheine; Transferase.  
 SQ SEQUENCE 5435 AA; 562659 MW; AA55465DE087A38C CRC64;

Query Match 90.0%; Score 36; DB 2; Length 5435;  
 Best Local Similarity 100.0%; Pred. No. 4.5e+03;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 ADMSW 5  
 DB 1525 ADMSW 1529

Search completed: May 30, 2003, 14:38:42  
 Job time: 15.7632 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 30, 2003, 14:41:40 ; Search time 3.11842 Seconds  
(without alignments)

Title: US-09-643-260-6

Sequence: 1 ADWSWA 6

1 ADMSWA 6

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

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Searched:      112892 segs, 41476328 residues
Total number of hits satisfying chosen parameters:  112892
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Minimum DB seq length: 0
Maximum DB seq length: 20000000000
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Post-processing:  Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
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Database : SwlssProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	36	90.0	470	1	NRAM_IADBU	007570 influenza a
2	36	90.0	470	1	NRAM_IADCH	007571 influenza a
3	36	90.0	470	1	NRAM_IADH2	007572 influenza a
4	36	90.0	470	1	NRAM_IADH2	007573 influenza a
5	36	90.0	470	1	NRAM_IADU3	007589 influenza a
6	36	90.0	470	1	NRAM_IADFN	007574 influenza a
7	36	90.0	470	1	NRAM_IADGD	007577 influenza a
8	36	90.0	470	1	NRAM_IADJI	007578 influenza a
9	36	90.0	470	1	NRAM_IADAE	007583 influenza a
10	36	90.0	470	1	NRAM_IADKL	007585 influenza a
11	36	90.0	598	1	MRJ5_APIME	097472 apis mellifera
12	34	85.0	376	1	PGLR_PENGR	093883 penicillium
13	34	85.0	1842	1	FAS2_SCHPO	010289 s faty acti
14	33	82.5	99	1	NOS3_SHEEP	P79209 ovis aries
15	33	82.5	220	1	Y132_MERJA	057566 methanococ
16	33	82.5	232	1	C1B3_SHEEP	080943 ovis aries
17	33	82.5	333	1	C1B2_SHEEP	029422 ovis aries
18	33	82.5	410	1	Y801_DEIRA	097658 delnococtus
19	33	82.5	421	1	YDW4_SCHPO	013911 schizosacch
20	33	82.5	470	1	NRAM_IADIT	007584 influenza a
21	33	82.5	479	1	BGLA_BACSD	P42973 bacillus st
22	33	82.5	492	1	AERA_AERTR	P09166 aeromonas t
23	33	82.5	529	1	GUAA_MYCLE	P46810 mycobacteri
24	33	82.5	579	1	YC20_MERJA	058617 methanococ
25	33	82.5	579	1	YC12_KLEPN	048458 klebsiella
26	33	82.5	914	1	GUX2_CLOS8	P50900 clostridium
27	33	82.5	1201	1	NOS3_MOUSE	P70313 mus musculu
28	33	82.5	1202	1	NOS3_HUDAN	P29474 homo sapien
29	33	82.5	1204	1	NOS3_BOVIN	P29473 bos taurus
30	33	82.5	1204	1	NOS3_PIG	028969 sus scrofa
31	32	80.0	100	1	NOS3_CANVO	P97270 cavia porce
32	32	80.0	107	1	STEL_RHIVE	P00302 rhus vernici
33	32	80.0	125	1	VG61_BPMD2	064253 mycobacteri

34	32	80.0	272	1	CYL RHORI	P23135	rhodospirill
35	32	80.0	282	1	3MG2_ECOLI	P43395	eschschol
36	32	80.0	295	1	X769_HUMAN	Q99871	homo sapien
37	32	80.0	328	1	YUSB_ECOLI	P27280	eschschol
38	32	80.0	339	1	WNT2_ECOLI	P34859	Caenorhabdi
39	32	80.0	362	1	DCUP_YEAST	P32347	saccharomyce
40	32	80.0	375	1	H1S7_XANES	P58882	xanthomonas
41	32	80.0	411	1	FOLC_BUCAL	P57265	buchnera ap
42	32	80.0	418	1	HLF_VIBPA	G99298	vibrio parer
43	32	80.0	453	1	NRAM_TAMIL	P33470	influenza a
44	32	80.0	454	1	NRAM_TAMPE	P33468	influenza a
45	32	80.0	470	1	NOS2_ONCMY	Q92051	oncohyacinth

RESULT 1			
ID	NRAM_IADBU	STANDARD:	PRT: 470 AA.
AC	007570:		
DT	01-FEB-1995 (Rel. 31, Created)		
DT	01-FEB-1995 (Rel. 31, Last sequence update)		
DT	15-JUN-2002 (Rel. 41, Last annotation update)		
DE	Neuraminidase (EC 3.2.1.18).		
GN	NA.		
OS	Influenza A virus (strain A/Duck/Burjatia/652/88).		
OC	Viruses: ssRNA negative-strand viruses: Orthomyxoviridae;		
OC	Influenza A viruses; Influenzavirus A.		
OX	NCBI_TaxID=38956;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=93212520; PubMed=8460490;		
RA	Saito T., Kawasato Y., Webster R.G.;		
RT	"Phylogenetic analysis of the N8 neuraminidase gene of Influenza A		
RT	viruses."		
RL	Virology 193:868-876(1993).		
CC	-1- FUNCTION: Removes the terminal sialic acid from carbohydrate side		
CC	chains of the host cell surface proteins and from the viral		
CC	envelope. Such a reaction prevents self-aggregation and facilitate		
CC	the mobility of the virus to and from the site of infection.		
CC	-1- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-,		
CC	alpha-(2->8)-glycosidic linkages of terminal sialic residues in		
CC	oligosaccharides, glycoproteins, glycolipids, colominic acid and		
CC	synthetic substrates.		
CC	-1- SUBUNIT: HOMOTETRAMER.		
CC	-1- SUBCELLULAR LOCATION: VIRAL MEMBRANE. FORMS A MUSHROOM-SHAPED		
CC	SPIKE ON THE SURFACE OF THE VIRION.		
CC	-1- SIMILARITY: BELONGS TO FAMILY 34 OF GLYCOSYL HYDROLASES.		
CC	-----		
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration		
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -		
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CC	use by non-profit institutions as long as its content is in no way		
CC	modified and this statement is not removed. Usage by and for commercial		
CC	entities requires a license agreement (see <a href="http://www.isb-slb.ch/announce/">http://www.isb-slb.ch/announce/</a>		
CC	or send an email to <a href="mailto:license@isb-slb.ch">license@isb-slb.ch</a> ).		
CC	-----		
DR	EMBL: L06572; AAA43365.1; .		
DR	HSSP: P06820; 2BAT.		
DR	InterPro: IPR001860; GH_34.		
DR	Pfam: PF00064; neur. 1.		
DR	Prodom: PD000431; GH_34; 1.		
KW	TRANSMEM: 7		
FT	TRANSMEM 38		
FT	DOMAIN 39		
FT	DOMAIN 89		
FT	ACT_SITE 273		
FT	ACT_SITE 275		
FT	CARBOHYD 46		
FT	CARBOHYD 54		
FT	CARBOHYD 144		
FT	CARBOHYD 293		
FT	ANCHOR (BY SIMILARITY).		
FT	HYPERVARIABLE STALK REGION.		
FT	BY SIMILARITY.		
FT	BY SIMILARITY.		
FT	N-LINKED (GLCNAC. . .) (POTENTIAL).		
FT	N-LINKED (GLCNAC. . .) (POTENTIAL).		
FT	N-LINKED (GLCNAC. . .) (POTENTIAL).		
FT	N-LINKED (GLCNAC. . .) (POTENTIAL).		

FT CARBOHYD 398 398 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 470 AA: 51989 MW: DIA6F07460F6B8AD CRC64;

Query Match 90.0%; Score 36; DB 1; Length 470;  
Best Local Similarity 100.0%; Pred. No. 57;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ADMSW 5  
DB 453 ADMSW 457

## RESULT 2

NRAM\_IADCH STANDARD: PRT: 470 AA.  
ID NRAM\_IADCH 007571;  
AC 01-FEB-1995 (Rel. 31, Created)  
DT 01-FEB-1995 (Rel. 31, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Neuraminidase (EC 3.2.1.18).  
GN NA.  
OS Influenza A virus (strain A/Duck/Chabarovsk/1610/72).  
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;  
OC Influenza A viruses; Influenzavirus A.  
OX NCBI\_TaxID=38957;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=93212520; PubMed=8460490;  
RA Saito T., Kawoka Y., Webster R.G.;  
RT "Phylogenetic analysis of the N8 neuraminidase gene of Influenza A viruses."  
RL Virology 193:868-876(1993).  
CC -1- FUNCTION: Removes the terminal sialic acid from carbohydrate side chains of the host cell surface proteins and from the viral envelope. Such a reaction prevents self-aggregation and facilitates the mobility of the virus to and from the site of infection.  
CC -1- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2-3)-, alpha-(2-6)-, alpha-(2-8)-glycosidic linkages of terminal sialic residues in oligosaccharides, glycoproteins, glycolipids, colominic acid and synthetic substrates.  
CC -1- SUBUNIT: HOMOTETRAMER.  
CC -1- SUBCELLULAR LOCATION: VIRAL MEMBRANE. FORMS A MUSHROOM-SHAPED SPIKE ON THE SURFACE OF THE VIRION.  
CC -1- SIMILARITY: BELONGS TO FAMILY 34 OF GLYCOSYL HYDROLASES.  
CC -----  
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CC -----  
CC EMBL: L06573; AAA43367.1; .  
DR HSSP: P06820; 2B8T.  
DR InterPro: IPR001860; GH\_34.  
DR Pfam: PF00064; neur; 1.  
DR Prodom: PD000431; GH\_34; 1.  
KW Hydroxylase; Glycosidase; Glycoprotein; Transmembrane.  
FT TRANSMEM 7  
FT DOMAIN 39 88 ANCHOR (BY SIMILARITY).  
FT ACT\_SITE 89 470 HYPERVARIABLE STALK REGION.  
FT ACT\_SITE 273 273 BY SIMILARITY.  
FT ACT\_SITE 275 275 BY SIMILARITY.  
FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 84 84 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 398 398 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 470 AA: 52070 MW: 169AB89FBE8006DC CRC64;

Query Match 90.0%; Score 36; DB 1; Length 470;

Best Local Similarity 100.0%; Pred. No. 57;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ADMSW 5  
DB 453 ADMSW 457

## RESULT 3

NRAM\_IADH2 STANDARD: PRT: 470 AA.  
ID NRAM\_IADH2 007572;  
AC 01-FEB-1995 (Rel. 31, Created)  
DT 01-FEB-1995 (Rel. 31, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Neuraminidase (EC 3.2.1.18).  
GN NA.  
OS Influenza A virus (strain A/Duck/Hokkaido/8/80).  
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;  
OC Influenza A viruses; Influenzavirus A.  
OX NCBI\_TaxID=11358;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=93212520; PubMed=8460490;  
RA Saito T., Kawoka Y., Webster R.G.;  
RT "Phylogenetic analysis of the N8 neuraminidase gene of Influenza A viruses."  
RL Virology 193:868-876(1993).  
CC -1- FUNCTION: Removes the terminal sialic acid from carbohydrate side chains of the host cell surface proteins and from the viral envelope. Such a reaction prevents self-aggregation and facilitates the mobility of the virus to and from the site of infection.  
CC -1- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2-3)-, alpha-(2-6)-, alpha-(2-8)-glycosidic linkages of terminal sialic residues in oligosaccharides, glycoproteins, glycolipids, colominic acid and synthetic substrates.  
CC -1- SUBUNIT: HOMOTETRAMER.  
CC -1- SUBCELLULAR LOCATION: VIRAL MEMBRANE. FORMS A MUSHROOM-SHAPED SPIKE ON THE SURFACE OF THE VIRION.  
CC -1- SIMILARITY: BELONGS TO FAMILY 34 OF GLYCOSYL HYDROLASES.  
CC -----  
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CC -----  
CC EMBL: L06574; AAA43372.1; .  
DR HSSP: P06820; 2B8T.  
DR InterPro: IPR001860; GH\_34.  
DR Pfam: PF00064; neur; 1.  
DR Prodom: PD000431; GH\_34; 1.  
KW Hydroxylase; Glycosidase; Glycoprotein; Transmembrane.  
FT TRANSMEM 7  
FT DOMAIN 39 88 ANCHOR (BY SIMILARITY).  
FT ACT\_SITE 89 470 HYPERVARIABLE STALK REGION.  
FT ACT\_SITE 273 273 BY SIMILARITY.  
FT ACT\_SITE 275 275 BY SIMILARITY.  
FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 84 84 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 398 398 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 470 AA: 52015 MW: E1C1D3E2C650B93C CRC64;

Query Match 90.0%; Score 36; DB 1; Length 470;  
Best Local Similarity 100.0%; Pred. No. 57;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ADMSW 5

DB 453 ADMSW 457

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RESULT 4
NRAM_IADM2 STANDARD: PRT: 470 AA.
ID NRAM_IADM2
AC 007573;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Neuraminidase (EC 3.2.1.18).
GN NA.
OS Influenza A virus (strain A/Duck/Memphis/928/74).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza A viruses; Influenzavirus A.
OX NCBI_TaxID=11367;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93212520; PubMed=8460490;
RA Saito T., Kawoka Y., Webster R.G.;
RT "Phylogenetic analysis of the N8 neuraminidase gene of Influenza A
  viruses.";
RL Virology 193:868-876(1993).
CC -1- FUNCTION: Removes the terminal sialic acid from carbohydrate side
  chains of the host cell surface proteins and from the viral
  envelope. Such a reaction prevents self-aggregation and facilitate
  the mobility of the virus to and from the site of infection.
CC -1- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-,
  alpha-(2->8)-glycosidic linkages of terminal sialic residues in
  oligosaccharides, glycoproteins, glycolipids, colominic acid and
  synthetic substrates.
CC -1- SUBUNIT: HOMOTETRAMER.
CC -1- SUBCELLULAR LOCATION: VIRAL MEMBRANE. FORMS A MUSHROOM-SHAPED
  SPIKE ON THE SURFACE OF THE VIRION.
CC -1- SIMILARITY: BELONGS TO FAMILY 34 OF GLYCOSYL HYDROLASES.
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  or send an email to license@isb-sib.ch).
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CC EMBL: I06575; AAA43404.1; -.
DR HSSP: P06820; 2BAT.
DR InterPro: IPR001860; GH_34.
DR Pfam: PF00064; neur. 1.
KW Hydrolase; Glycosidase; Glycoprotein; Transmembrane.
FT DOMAIN 39 88 ANCHOR (BY SIMILARITY).
FT TRANSMEM 7 38 HYPERVARIABLE STALK REGION.
FT ACT_SITE 273 275 HEAD OF NEURAMINIDASE.
FT ACT_SITE 273 275 BY SIMILARITY.
FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 84 84 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 398 398 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 470 AA; 52146 MW; 30F5F9E364C1F49 CRC64;

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Query Match 90.0%; Score 36; DB 1; Length 470;  
 Best Local Similarity 100.0%; Pred. No. 57;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ADMSW 5  
 |||||  
 DB 453 ADMSW 457

RESULT 5  
 NRAM\_IADU3 STANDARD: PRT: 470 AA.  
 ID NRAM\_IADU3  
 AC 007599;  
 DT 01-OCT-1994 (Rel. 30, Created)  
 DT 01-OCT-1994 (Rel. 30, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Neuraminidase (EC 3.2.1.18).  
 GN NA.  
 OS Influenza A virus (strain A/Duck/Ukraine/1/63).  
 OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;  
 OC Influenza A viruses; Influenzavirus A.  
 OX NCBI\_TaxID=11374;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=93212520; PubMed=8460490;  
 RA Saito T., Kawoka Y., Webster R.G.;  
 RT "Phylogenetic analysis of the N8 neuraminidase gene of Influenza A  
 viruses.";

```

RL Virology 193:868-876(1993).
CC -1- FUNCTION: Removes the terminal sialic acid from carbohydrate side
  chains of the host cell surface proteins and from the viral
  envelope. Such a reaction prevents self-aggregation and facilitate
  the mobility of the virus to and from the site of infection.
CC -1- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-,
  alpha-(2->8)-glycosidic linkages of terminal sialic residues in
  oligosaccharides, glycoproteins, glycolipids, colominic acid and
  synthetic substrates.
CC -1- SUBUNIT: HOMOTETRAMER.
CC -1- SUBCELLULAR LOCATION: VIRAL MEMBRANE. FORMS A MUSHROOM-SHAPED
  SPIKE ON THE SURFACE OF THE VIRION.
CC -1- SIMILARITY: BELONGS TO FAMILY 34 OF GLYCOSYL HYDROLASES.
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  or send an email to license@isb-sib.ch).
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CC EMBL: I06576; AAA16234.1; -.
DR HSSP: P06820; 2BAT.
DR InterPro: IPR001860; GH_34.
DR Pfam: PF00064; neur. 1.
KW Hydrolase; Glycosidase; Glycoprotein; Transmembrane.
FT DOMAIN 37 37 ANCHOR (BY SIMILARITY).
FT TRANSMEM 7 38 HYPERVARIABLE STALK REGION.
FT ACT_SITE 273 275 PROBABLE.
FT ACT_SITE 273 275 PROBABLE.
FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 84 84 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 398 398 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 470 AA; 51960 MW; B46D54A03AC84CCE CRC64;

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Query Match 90.0%; Score 36; DB 1; Length 470;  
 Best Local Similarity 100.0%; Pred. No. 57;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ADMSW 5  
 |||||  
 DB 453 ADMSW 457

RESULT 6  
 NRAM\_IAGFN STANDARD: PRT: 470 AA.  
 ID NRAM\_IAGFN  
 AC 007574;  
 DT 01-FEB-1995 (Rel. 31, Created)

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DT 01-FEB-1995 (Rel. 31, last sequence update)
DE 15-JUN-2002 (Rel. 41, last annotation update)
DE Neuraminidase (EC 3.2.1.18).
GN NA.
OS Influenza A virus (strain A/Guinea fowl/New York/4-3587/84).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza A viruses; Influenzavirus A.
OX NCBI_TaxID=38963;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93212520; PubMed=8460490;
RA Salto T., Kawoka Y., Webster R.G.;
RT "Phylogenetic analysis of the NA neuraminidase gene of Influenza A
  viruses."
RL Virology 193:868-876(1993).
CC -1- FUNCTION: Removes the terminal sialic acid from carbohydrate side
CC chains of the host cell surface proteins and from the viral
CC envelope. Such a reaction prevents self-aggregation and facilitate
CC the mobility of the virus to and from the site of infection.
CC -1- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2-3)-, alpha-(2-6)-,
CC alpha-(2-8)-glycosidic linkages of terminal sialic residues in
CC oligosaccharides, glycoproteins, glycolipids, colominic acid and
CC synthetic substrates.
CC -1- SUBUNIT: HOMOTETRAMER.
CC -1- SUBCELLULAR LOCATION: VIRAL MEMBRANE. FORMS A MUSHROOM-SHAPED
CC SPIKE ON THE SURFACE OF THE VIRION.
CC -1- SIMILARITY: BELONGS TO FAMILY 34 OF GLYCOSYL HYDROLASES.
CC -----
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CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: L06584; AAA43428.1; -
DR HSSP: P06820; 2BAT.
DR InterPro: IPR001860; GH_34.
DR Pfam: PF00064; neur. 1.
DR ProDom: PD000431; GH_34; 1.
KM Hydrolyase; Glycosidase; Glycoprotein; Transmembrane.
FT TRANSMEM 7 38
FT DOMAIN 39 88 ANCHOR (BY SIMILARITY).
FT ACT_SITE 273 275 HYPERVARIABLE STALK REGION.
FT ACT_SITE 273 275 HEAD OF NEURAMINIDASE.
FT ACT_SITE 273 275 BY SIMILARITY.
FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 84 84 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 398 398 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 470 AA; 52348 MW; D3BD2AAC0159FE66 CRC64;

Query Match 90.0%; Score 36; DB 1; Length 470;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 ADMSW 5
DB 453 ADMSW 457

RESULT 7
NRAM_IAGHD STANDARD; PRT; 470 AA.
ID NRAM_IAGHD
AC 007577;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, last sequence update)
DT 15-JUN-2002 (Rel. 41, last annotation update)
DE Neuraminidase (EC 3.2.1.18).
GN NA.

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OS Influenza A virus (strain A/Herring gull/DE/677/88).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza A viruses; Influenzavirus A.
OX NCBI_TaxID=38964;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93212520; PubMed=8460490;
RA Salto T., Kawoka Y., Webster R.G.;
RT "Phylogenetic analysis of the NA neuraminidase gene of Influenza A
  viruses."
RL Virology 193:868-876(1993).
CC -1- FUNCTION: Removes the terminal sialic acid from carbohydrate side
CC chains of the host cell surface proteins and from the viral
CC envelope. Such a reaction prevents self-aggregation and facilitate
CC the mobility of the virus to and from the site of infection.
CC -1- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2-3)-, alpha-(2-6)-,
CC alpha-(2-8)-glycosidic linkages of terminal sialic residues in
CC oligosaccharides, glycoproteins, glycolipids, colominic acid and
CC synthetic substrates.
CC -1- SUBUNIT: HOMOTETRAMER.
CC -1- SUBCELLULAR LOCATION: VIRAL MEMBRANE. FORMS A MUSHROOM-SHAPED
CC SPIKE ON THE SURFACE OF THE VIRION.
CC -1- SIMILARITY: BELONGS TO FAMILY 34 OF GLYCOSYL HYDROLASES.
CC -----
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CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: L06585; AAA43368.1; -
DR HSSP: P06820; 2BAT.
DR InterPro: IPR001860; GH_34.
DR Pfam: PF00064; neur. 1.
DR ProDom: PD000431; GH_34; 1.
KM Hydrolyase; Glycosidase; Glycoprotein; Transmembrane.
FT TRANSMEM 7 38
FT DOMAIN 39 88 ANCHOR (BY SIMILARITY).
FT ACT_SITE 273 275 HYPERVARIABLE STALK REGION.
FT ACT_SITE 273 275 HEAD OF NEURAMINIDASE.
FT ACT_SITE 273 275 BY SIMILARITY.
FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 84 84 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 398 398 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 470 AA; 52265 MW; 28AF0B75E80539B7 CRC64;

Query Match 90.0%; Score 36; DB 1; Length 470;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 ADMSW 5
DB 453 ADMSW 457

RESULT 8
NRAM_IAGHD STANDARD; PRT; 470 AA.
ID NRAM_IAGHD
AC 007578;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, last sequence update)
DT 15-JUN-2002 (Rel. 41, last annotation update)
DE Neuraminidase (EC 3.2.1.18).
GN NA.
OS Influenza A virus (strain A/Egypt/11/89).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza A viruses; Influenzavirus A.
OX NCBI_TaxID=11401;

```

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RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93212520; PubMed=8460490;
RA Saito T., Kawaoka Y., Webster R.G.;
RT "Phylogenetic analysis of the N8 neuraminidase gene of Influenza A
   viruses.";
RL Virology 193:868-876(1993).
CC -1- FUNCTION: Removes the terminal sialic acid from carbohydrate side
   chains of the host cell surface proteins and from the viral
   envelope. Such a reaction prevents self-aggregation and facilitate
   the mobility of the virus to and from the site of infection.
CC -1- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2-3)-, alpha-(2-6)-,
   alpha-(2-8)-glycosidic linkages of terminal sialic residues in
   oligosaccharides, glycoproteins, glycolipids, colominic acid and
   synthetic substrates.
CC -1- SUBUNIT: HOMOTETRAMER.
CC -1- SUBCELLULAR LOCATION: VIRAL MEMBRANE. FORMS A MUSHROOM-SHAPED
   SPIKE ON THE SURFACE OF THE VIRION.
CC -1- SIMILARITY: BELONGS TO FAMILY 34 OF GLYCOSYL HYDROLASES.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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   or send an email to license@isb-sib.ch).
CC
CC EMBL: L06579; AAA3374.1; -.
DR HSSP: P06820; 2BAT.
DR InterPro: IPR001860; GH_34.
DR Pfam: PF00064; neur; 1.
DR ProDom: PD000431; GH_34; 1.
KM Hydrolyase; Glycosidase; Glycoprotein; Transmembrane.
FT TRANSMEM 7 38 ANCHOR (BY SIMILARITY).
FT DOMAIN 39 88 HYPERVARIABLE STALK REGION.
FT ACT_SITE 273 275 HEAD OF NEURAMINIDASE.
FT ACT_SITE 273 275 BY SIMILARITY.
FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 84 84 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 398 398 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 470 AA; 52234 MW; CE50B21050A37668 CRC64;

Query Match 90.0%; Score 36; DB 1; Length 470;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 5; Conservative. 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 ADM5W 5
DB 453 ADM5W 457

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RT "Phylogenetic analysis of the N8 neuraminidase gene of Influenza A
   viruses.";
RL Virology 193:868-876(1993).
CC -1- FUNCTION: Removes the terminal sialic acid from carbohydrate side
   chains of the host cell surface proteins and from the viral
   envelope. Such a reaction prevents self-aggregation and facilitate
   the mobility of the virus to and from the site of infection.
CC -1- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2-3)-, alpha-(2-6)-,
   alpha-(2-8)-glycosidic linkages of terminal sialic residues in
   oligosaccharides, glycoproteins, glycolipids, colominic acid and
   synthetic substrates.
CC -1- SUBUNIT: HOMOTETRAMER.
CC -1- SUBCELLULAR LOCATION: VIRAL MEMBRANE. FORMS A MUSHROOM-SHAPED
   SPIKE ON THE SURFACE OF THE VIRION.
CC -1- SIMILARITY: BELONGS TO FAMILY 34 OF GLYCOSYL HYDROLASES.
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   or send an email to license@isb-sib.ch).
CC
CC EMBL: L06586; AAA3369.1; -.
DR HSSP: P06820; 2BAT.
DR InterPro: IPR001860; GH_34.
DR Pfam: PF00064; neur; 1.
DR ProDom: PD000431; GH_34; 1.
KM Hydrolyase; Glycosidase; Glycoprotein; Transmembrane.
FT TRANSMEM 7 38 ANCHOR (BY SIMILARITY).
FT DOMAIN 39 88 HYPERVARIABLE STALK REGION.
FT ACT_SITE 273 275 HEAD OF NEURAMINIDASE.
FT ACT_SITE 273 275 BY SIMILARITY.
FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 84 84 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 398 398 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 470 AA; 52070 MW; 557630CB11F2765 CRC64;

Query Match 90.0%; Score 36; DB 1; Length 470;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 ADM5W 5
DB 453 ADM5W 457

RESULT 10
ID NRAM_IATKL STANDARD; PRT; 470 AA.
AC 007585;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Neuraminidase (EC 3.2.1.18).
GN NA.
OS Influenza A virus (strain A/Turkey/Minnesota/501/78).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza A viruses; Influenzavirus A.
OX NCBI_TaxID=38984;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93212520; PubMed=8460490;
RA Saito T., Kawaoka Y., Webster R.G.;
RT "Phylogenetic analysis of the N8 neuraminidase gene of Influenza A
   viruses.";
RL Virology 193:868-876(1993).
CC -1- FUNCTION: Removes the terminal sialic acid from carbohydrate side

```

chains of the host cell surface proteins and from the viral envelope. Such a reaction prevents self-aggregation and facilitates the mobility of the virus to and from the site of infection.

-1- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-, alpha-(2->8)-glycosidic linkages of terminal sialic residues in oligosaccharides, glycoproteins, glycolipids, colominic acid and synthetic substrates.

-1- SUBUNIT: HOMOTETRAMER.

-1- SUBCELLULAR LOCATION: VIRAL MEMBRANE. FORMS A MUSHROOM-SHAPED SPIKE ON THE SURFACE OF THE VIRION.

-1- SIMILARITY: BELONGS TO FAMILY 34 OF GLYCOSYL HYDROLASES.

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DR EMBL: L06588; AAA43410.1; -

DR HSSP: P06820; 2BAT.

DR InterPro: IPR001860; GH\_34.

DR Pfam: PF000064; neur: 1.

DR ProDom: PD000431; GH\_34; 1.

KM Hydrolase; Glycosidase; Glycoprotein; Transmembrane.

FT TRANSMEM 7 38 ANCHOR (BY SIMILARITY).

FT DOMAIN 39 88 HYPERVARIABLE STALK REGION.

FT ACT SITE 273 273 HEAD OF NEURAMINIDASE.

FT ACT SITE 275 275 BY SIMILARITY.

FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 84 84 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 398 398 N-LINKED (GLCNAC. . .) (POTENTIAL).

SQ SEQUENCE 470 AA: 52352 MW: 5273742ABFE16B CRC64;

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Query Match 90.0%; Score 36; DB 1; Length 470;

Best Local Similarity 100.0%; Pred. No. 57;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ADMSW 5

DB 453 ADMSW 457

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RESULT 11

MRJ5\_APIME STANDARD; PRT; 598 AA.

AC 097432;

DT 15-JUN-2002 (Rel. 41, Created)

DT 15-JUN-2002 (Rel. 41, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Major royal jelly protein 5 precursor (MRJP-5) (Bee-milk protein).

OS MRJP5.

OS Apis mellifera (Honeybee).

OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;

OC Insecta; Pterygota; Neoptera; Endopterygota; Apocrita;

OC Aculeata; Apoidea; Apidae; Apis.

OC NCB1\_TaxID=7460;

RN NCB1 [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Head;

RA MEDLINE=99373663; PubMed=10441680;

RA Albert S., Bhattacharya D., Klaudiny J., Schmitzova J., Simuth J.,

RT "The family of major royal jelly proteins and its evolution.";

RL J. Mol. Evol. 49:290-297(1999).

CC -1- FUNCTION: MAY PLAY AN IMPORTANT ROLE IN HONEYBEE NUTRITION. IT IS

CC FOUND IN THE ROYAL JELLY WHICH IS THE FOOD OF THE QUEEN HONEY BEE

CC LARVA. THE ROYAL JELLY DETERMINES THE DEVELOPMENT OF THE YOUNG

CC LARVAE AND IS RESPONSIBLE FOR THE HIGH REPRODUCTIVE ABILITY OF THE

HONEYBEE QUEEN.

-1- SUBCELLULAR LOCATION: Extracellular.

-1- TISSUE SPECIFICITY: HYPOPHARYNGEAL GLANDS OF NURSE HONEY BEES.

-1- DEVELOPMENTAL STAGE: PRODUCED BY THE CEPHALIC GLANDULAR SYSTEM OF THE NURSE HONEY BEE.

-1- SIMILARITY: BELONGS TO THE MAJOR ROYAL JELLY PROTEIN FAMILY.

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DR EMBL: AF004842; AAD01205.1; -

DR InterPro: IPR003534; RoyalJelly.

DR Pfam: PR013022; MRJP; 2.

DR PRINTS: PR01366; ROYALJELLY.

KM Signal; Repeat; Glycoprotein.

FT SIGNAL 1 17 POTENTIAL.

FT CHAIN 18 598 MAJOR ROYAL JELLY PROTEIN 5.

FT CARBOHYD 148 148 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 164 164 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 181 181 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 324 324 N-LINKED (GLCNAC. . .) (POTENTIAL).

SQ SEQUENCE 598 AA: 70236 MW: 26030377E7ACDF63 CRC64;

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Query Match 90.0%; Score 36; DB 1; Length 598;

Best Local Similarity 100.0%; Pred. No. 71;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 DMSWA 6

DB 113 DMSWA 117

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RESULT 12

PGLR\_PENGR STANDARD; PRT; 376 AA.

AC 093883;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE Polylacturonase precursor (EC 3.2.1.15) (PG) (Pectinase).

OS PGGL.

OS Penicillium griseoosum.

OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;

OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Penicillium.

OC NCB1\_TaxID=84562;

RN NCB1 [1]

RP SEQUENCE FROM N.A.

RC STRAIN=CGT 6421;

RA Ribon A.B., Coelho J.L.C., Barros E.G., Araujo E.F.;

RT "Cloning and characterization of a gene encoding the

RT endopolylacturonase of Penicillium griseoosum.";

RL Submitted (Aug-1998) to the EMBL/GenBank/DBJ databases.

CC -1- CATALYTIC ACTIVITY: Random hydrolysis of 1,4-alpha-D-

CC galactosiduronic linkages in pectate and other galacturonans.

CC -1- SIMILARITY: BELONGS TO FAMILY 28 OF GLYCOSYL HYDROLASES

CC (POLYGALACTURONASES).

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DR EMBL: AF085238; AAC83692.1; -

DR InterPro: IPR000743; GH28.

DR Pfam: PF00295; Glyco\_hydro\_28; 1.

DR PROSITE: PS00502; POLYGALACTURONASE; 1.  
 KM Hydrolase; Glycosidase; Cell wall; Signal.  
 FT SIGNAL 1 20 POTENTIAL.  
 FT CHAIN 21 376 POLYGALACTURONASE.  
 SQ SEQUENCE 376 AA; 38068 MW; 1EDB1EC56ED56928 CRC64;

Query Match 85.0%; Score 34; DB 1; Length 376;  
 Best Local Similarity 66.7%; Pred. No. 94;  
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 ADMSMA 6  
 DB 349 SDMSMS 354

RESULT 13  
 FAS2\_SCHPO STANDARD; PRT; 1842 AA.  
 AC 010289; P78973; 014163;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Fatty acid synthase subunit alpha (EC 2.3.1.86) [p190/210] [includes:  
 DE Acyl carrier: 3-oxoacyl-[acyl-carrier protein] reductase  
 DE (EC 1.1.1.100) (Beta-ketoacyl reductase); 3-oxoacyl-[acyl-carrier  
 DE protein] synthase (EC 2.3.1.41) (Beta-ketoacyl synthase)].  
 GN FAS2 OR LSI1 OR SPAC48.11C.  
 OS Schizosaccharomyces pombe (Fission yeast).  
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;  
 OC Schizosaccharomycetes; Schizosaccharomycetaceae;  
 OC Schizosaccharomycetes.  
 OX NCBI\_TaxID=4896;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-96354912; PubMed-8769419;  
 RA Saitoh S., Takahashi K., Nabeshima K., Yamashita Y., Nakaseko Y.,  
 RA Hirata A., Yanagida M.,  
 RT Aberrant mitosis in fission yeast mutants defective in fatty acid  
 RT synthetase and acetyl CoA carboxylase.";  
 RL J. Cell Biol. 134:949-961(1996).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-21363051; PubMed-11470243;  
 RA Yokoyama K., Saitoh S., Ishida M., Yamakawa Y., Nakamura K., Inoue K.,  
 RA Taguchi R., Tokumura A., Nishijima M., Yanagida M., Setaka M.,  
 RT Very long-chain fatty-acid-containing phospholipids accumulate in  
 RT fatty acid synthase temperature-sensitive mutant strains of the  
 RT fission yeast Schizosaccharomyces pombe fas2/lsi1.";  
 RL Blochim. Biophys. Acta 1532:223-233(2001).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-972;  
 RX MEDLINE-21848401; PubMed-11859360;  
 RA Wood V., Williams R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,  
 RA Good V., Gwilliam R., Hayles J., Baker S., Basham D., Bowman S.,  
 RA Brooks K., Brown D., Brown N., Chillingworth T., Churcher C.M.,  
 RA Collins M., Connor R., Cronin A., Davis P., Fellwell T., Fraser A.,  
 RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,  
 RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,  
 RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,  
 RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,  
 RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitch E.,  
 RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,  
 RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,  
 RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,  
 RA Woodward J., Volckaert G., Aert R., Robben J., Gymnopoulos B.,  
 RA Wellens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,  
 RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,  
 RA Borzym K., Langer I., Beck A., Lehnach H., Reinhardt R., Pohl T.M.,  
 RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,  
 RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaire V., Mottier S.,  
 RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,  
 RA Lucas M., Rochet M., Gallard C., Tallada V.A., Garzon A., Thode G.,

RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,  
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,  
 RA Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,  
 RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.,  
 RT "The genome sequence of Schizosaccharomyces pombe.";  
 RL Nature 415:871-880(2002).  
 RN [4]  
 RP SEQUENCE OF 1-215 FROM N.A.  
 RA Koken M.H.M., de Rooij J.,  
 RL Submitted (FEB-1997) to the EMBL/Genbank/DBJ databases.  
 RN [5]  
 RP SEQUENCE OF 1-20.  
 RX MEDLINE-94245730; PubMed-8188691;  
 RA Kaeslin E., Heyer W.D.,  
 RT "Schizosaccharomycetes pombe fatty acid synthase mediates DNA strand  
 RT exchange in vitro.";  
 RL J. Biol. Chem. 269:14103-14110(1994).  
 CC -1- FUNCTION: FATTY ACID SYNTHETASE CATALYZES THE FORMATION OF  
 CC LONG-CHAIN FATTY ACIDS FROM ACETYL-COA, MALONYL-COA AND NADPH.  
 CC THE ALPHA SUBUNIT CONTAINS DOMAINS FOR: ACYL CARRIER PROTEIN,  
 CC 3-OXOACYL-[ACYL-CARRIER PROTEIN] REDUCTASE, AND 3-OXOACYL-[ACYL-  
 CC CARRIER-PROTEIN] SYNTHASE. THIS SUBUNIT COORDINATES THE BINDING  
 CC OF THE SIX BETA SUBUNITS TO THE ENZYME COMPLEX.  
 CC -1- CATALYTIC ACTIVITY: Acetyl-CoA + N malonyl-CoA + 2N NADPH -> a  
 CC long-chain fatty acid + (N+1) CO(2) + 2N NADP(+).  
 CC -1- CATALYTIC ACTIVITY: Acyl-[acyl-carrier protein] + malonyl-[acyl-  
 CC carrier protein] -> 3-oxoacyl-[acyl-carrier protein] + CO(2) +  
 CC [acyl-carrier protein].  
 CC -1- CATALYTIC ACTIVITY: (3R)-3-hydroxyacyl-[acyl-carrier protein] +  
 CC NADP(+) -> 3-oxoacyl-[acyl-carrier protein] + NADPH.  
 CC -1- SUBUNIT: [alpha(6)beta(6)] hexamers of two multifunctional  
 CC subunits (alpha and beta).  
 CC -1- SIMILARITY: TO THE FATTY ACID SYNTHETASE, SUBUNIT ALPHA FROM  
 CC OTHER FUNGI.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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 CC use by non-profit institutions as long as its content is in no way  
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 CC entities requires a license agreement (See <http://www.1sb-sib.ch/announce/>  
 CC or send an email to [license@1sb-sib.ch](mailto:license@1sb-sib.ch)).  
 CC -----  
 CC EMBL; D83412; BA11913.1; -;  
 CC EMBL; AB013747; BAB62029.1; -;  
 CC EMBL; Z98762; CAB11481.1; -;  
 CC EMBL; U82216; AAB39943.1; -;  
 CC InterPro: IPR002582; ACPS.  
 CC InterPro: IPR00794; ketoacyl-synt.  
 CC InterPro: IPR004568; pantethn\_tn.  
 CC InterPro: IPR003880; pantethn\_attch.  
 CC Pfam: PF00109; ketoacyl-synt; 1.  
 CC Pfam: PF01648; ACPS; 1.  
 CC Pfam: PF02801; ketoacyl-synt\_C; 1.  
 CC Pfam: PF004282; ACPS; 1.  
 CC TIGRFAMs: TIGR00556; pantethn\_tn; 1.  
 CC PROSITE: PS00012; PHOSPHOPANTETHEINE; 1.  
 CC PROSITE: PS00606; B-KETOACYL-SYNTHASE; 1.  
 CC Fatty acid biosynthesis; Multifunctional enzyme; Oxidoreductase;  
 CC Transferrase; NADP; Phosphopantetheine.  
 FT DOMAIN 1 ?  
 FT DOMAIN 1 ?  
 FT DOMAIN 1 ?  
 FT BINDING 180 ? 1842 BETA-KETOACYL SYNTHASE.  
 FT ACT SITE 1262 1262 PHOSPHOPANTETHEINE (BY SIMILARITY).  
 FT CONFLICT 107 107 BETA-KETOACYL SYNTHASE (BY SIMILARITY).  
 FT CONFLICT 422 422 K -> R (IN REF. 1).  
 SQ SEQUENCE 1842 AA; 202168 MW; E4019F2D133EE571 CRC64;

Query Match 85.0%; Score 34; DB 1; Length 1842;  
 Best Local Similarity 66.7%; Pred. No. 3.9e+02;  
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 ADMSWA 6  
ID 11:11  
DB 400 SDMWMA 405

## RESULT 14

NOS3\_SHEEP STANDARD: PRT; 99 AA.

AC P79209;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE Nitric-oxide synthase, endothelial (EC 1.14.13.39) (EC-NOS) (NOS, type III) (NOSIII) (Endothelial NOS) (eNOS) (Constitutive NOS) (cNOS) (Fragment).  
GN NOS3 OR ENOS.  
OS Ovis aries (Sheep).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Caprinae; Ovis.  
OC NCBI\_TaxID=9940;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE-Endothelial cells;  
RA Aquan K., Weiner C.P.;  
RT Effect of hypoxia on the microvasculature of developing fetal brain of sheep: a studies on the expression pattern of constitutive forms of nitric oxide synthase.  
RL Submitted (OCT-1996) to the EMBL/Genbank/DBJ databases.  
CC -1- FUNCTION: PRODUCES NITRIC OXIDE (NO) WHICH IS IMPLICATED IN VASCULAR SMOOTH MUSCLE RELAXATION THROUGH A CGMP-MEDIATED SIGNAL TRANSDUCTION PATHWAY. NO MEDIATES VASCULAR ENDOTHELIAL GROWTH FACTOR (VEGF)-INDUCED ANGIOGENESIS IN CORONARY VESSELS AND PROMOTES BLOOD CLOTTING THROUGH THE ACTIVATION OF PLATELETS (BY SIMILARITY).  
CC -1- CATALYTIC ACTIVITY: L-arginine + N NADPH + M O(2) = citrulline + nitric oxide + N NADP(+).  
CC -1- COFACTOR: HEME. BINDS ONE MOLE EACH OF FAD AND FMN. ALSO REQUIRES TETRAHYDROBIOTIN (BH4) WHICH MAY STABILIZE THE DIMERIC FORM OF THE ENZYME (BY SIMILARITY).  
CC -1- ENZYME REGULATION: STIMULATED BY CALCIUM/CALMODULIN (BY SIMILARITY).  
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).  
CC -1- SIMILARITY: BELONGS TO THE NOS FAMILY.  
CC -----  
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CC -----  
DR EMBL; U76738; AAB40705.1; -  
DR HSSP; P29473; IDOC.  
DR InterPro: IPR004030; NO\_synthase.  
DR Pfam; PF02898; NO\_synthase; 1.  
DR PROSITE; PS60001; NOS; PARTIAL.  
KW Oxidoreductase; NADP; FAD; FMN; Calmodulin-binding; Calcium-binding; Heme; Multigene family.  
FT NON\_TER 1  
FT NON\_TER 1  
SQ SEQUENCE 99 AA; 11034 MW; 8263C765557031DA CRC64;

Query Match 82.5%; Score 33; DB 1; Length 99;  
Best Local Similarity 80.0%; Pred. No. 40;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 ADMSW 5  
ID 11:11  
DB 65 ADMAM 69

RESULT 15  
Y132\_METJA STANDARD: PRT; 220 AA.

AC 057596;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Hypothetical protein MJ0132.  
GN MJ0132.  
OS Methanococcus jannaschii.  
OC Archaea; Euryarchaeota; Methanococci; Methanococcales; Methanocaldococcaceae; Methanocaldococcus.  
OC NCBI\_TaxID=2190;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-JAL-1 / DSM 2661 / ATCC 43067;  
RX MEDLINE=96337999; PubMed=8688087;  
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D., Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D., Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I., Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A., Scott J.L., Geophagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D., Uterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C., Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M., Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;  
RT "Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii.";  
RL Science 273:1058-1073(1996).  
CC -1- SIMILARITY: TO M. JANNASCHII MJ1220 AND MJEC142.  
CC -1- SIMILARITY: WITH TYPE I RESTRICTION SYSTEM ADENINE METHYLASES (M SUBUNIT).  
CC -----  
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CC -----  
DR EMBL; U67470; AAB98113.1; -  
DR TIGR; MJ0132; -  
DR InterPro: IPR003356; N6\_DNA\_Mtase.  
DR Pfam; PF02384; N6\_Mtase; 1.  
KW Hypothetical protein; Complete proteome.  
SQ SEQUENCE 220 AA; 25766 MW; 710DDAE4C7A47954 CRC64;

Query Match 82.5%; Score 33; DB 1; Length 220;  
Best Local Similarity 80.0%; Pred. No. 82;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 ADMSW 5  
ID 11:11  
DB 33 ADMAM 37

Search completed: May 30, 2003, 15:48:51  
Job time : 4.11842 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 30, 2003, 14:32:12 ; Search time 6.5921 Seconds  
(without alignments)  
87,500 Million cell updates/sec

Title: US-09-643-260-6  
Perfect score: 40  
Sequence: 1 ADMSWA 6

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues  
Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: PIR1:\*  
2: PIR2:\*  
3: PIR3:\*  
4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	37	92.5	610	2 T35222	hypothetical prote
2	37	92.5	885	2 C83441	two-component sens
3	36	90.0	374	2 B83241	conserved hypotet
4	36	90.0	889	2 E87304	TonB-dependent rec
5	34	85.0	275	2 T05822	hypothetical prote
6	34	85.0	617	2 C84922	probable protein k
7	34	85.0	1842	2 T38781	probable fatty-acid
8	34	85.0	1442	2 T38781	fatty acid synthas
9	33	82.5	132	2 S65785	mel-13a protein -
10	33	82.5	198	2 B82531	conserved hypotet
11	33	82.5	220	2 D64316	restriction modifi
12	33	82.5	232	2 S83535	CD1b protein - she
13	33	82.5	239	2 D90470	hypothetical prote
14	33	82.5	257	2 D87152	conserved hypotet
15	33	82.5	276	2 B75337	hypothetical prote
16	33	82.5	304	2 F83632	probable cytochrom
17	33	82.5	324	2 AB3548	vegetable incompe
18	33	82.5	328	2 E72424	oligopeptide ABC t
19	33	82.5	333	2 S47246	gene CDI protein -
20	33	82.5	350	2 S71923	cysteine proteinas
21	33	82.5	368	2 H90998	probable proteinas
22	33	82.5	410	2 D75475	lycopene cyclase -
23	33	82.5	415	2 AE1844	hypothetical prote
24	33	82.5	418	2 AE1460	sugar ABC transpor
25	33	82.5	421	2 AF1097	sugar ABC transpor
26	33	82.5	421	2 T38242	probable phosphata
27	33	82.5	433	2 T31511	hypothetical prote
28	33	82.5	467	2 G82697	hypothetical prote
29	33	82.5	478	2 E89790	6-phospho-beta-glu

30	33	82.5	479	2 T39953	6-phospho-beta-glu
31	33	82.5	492	2 S03098	aerolysin precursor
32	33	82.5	529	2 C86958	probable GMP synth
33	33	82.5	539	2 T15256	hypothetical prote
34	33	82.5	578	2 C64452	restriction modifi
35	33	82.5	590	2 S72813	GMP synthase (glut
36	33	82.5	616	2 C69226	type I restriction
37	33	82.5	623	2 E75221	hypothetical prote
38	33	82.5	765	2 S76795	conserved hypotet
39	33	82.5	836	2 D82177	conserved hypotet
40	33	82.5	1202	2 S71424	nitric-oxide synth
41	33	82.5	1203	1 A47501	nitric-oxide synth
42	33	82.5	1205	1 A38943	nitric-oxide synth
43	33	82.5	1329	2 D87226	conserved hypotet
44	33	82.5	1409	2 S74916	alkaline phosphata
45	33	82.5	1879	2 S74915	extracellular nucl

## ALIGNMENTS

RESULT 1  
T35222  
hypothetical protein SC5C7.15 SC5C7.15 - Streptomyces coelicolor  
C/Species: Streptomyces coelicolor  
C/Date: 05-Nov-1999 #sequence\_revision 05-Nov-1999 #text\_change 05-Nov-1999  
C/Accession: T35222  
R/Seeger, K.J.; Harris, D.; Parkhill, J.; Barrrell, B.G.; Rajandream, M.A.  
submitted to the EMBL Data Library, September 1998  
A/Reference number: Z21572  
A/Accession: T35222  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-610 <SPE>  
A/Cross-references: EMBL:AL031515; PIDN:CA20627.1; GSPDB:GN00070; SCORDB:SC5C7.15  
A/Experimental source: strain A3(2)  
C/Genetics:  
A/Gene: SCORDB:SC5C7.15

Query Match 92.5% Score 37; DB 2; Length 610;  
Best Local Similarity 83.3% Pred. No. 1e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 ADMSWA 6  
Db 83 ADMSWA 88

RESULT 2  
C83441  
two-component sensor KdpD PA1636 [Imported] - Pseudomonas aeruginosa (strain PA01)  
C/Species: Pseudomonas aeruginosa  
C/Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 31-Dec-2000  
C/Accession: C83441  
R/Seeger, C.K.; Pham, X.O.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.;  
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L.  
Nature 406, 959-964, 2000  
A/Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa  
A/Reference number: A82550; MUID:20437337; PMID:10984043  
A/Accession: C83441  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-885 <STO>  
A/Cross-references: GB:AE004591; GB:AE004091; NID:99947599; PIDN:AGC05025.1; GSPDB:GN  
A/Experimental source: strain PA01  
C/Genetics:  
A/Gene: kdpD; PA1636

Query Match 92.5% Score 37; DB 2; Length 885;  
Best Local Similarity 83.3% Pred. No. 1.5e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 ADMSWA 6  
DB 563 ADMWMA 568

## RESULT 3

B83241

Conserved hypothetical protein PA3230 [Imported] - Pseudomonas aeruginosa (strain PA01)  
C:Species: Pseudomonas aeruginosa

C:Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 31-Dec-2000

C:Accession: B83241

R:Stover, C.K.; Plam, X.O.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; B.

adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Latidig, K.; Lim,

Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000

A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho

A:Reference number: A82950; MUID:20437337; PMID:10984043

A:Accession: B83241

A:Status: Preliminary

A:Molecule type: DNA

A:Residues: 1-374 <STO>

A:Cross-references: GB:AE004746; GB:AE004091; NID:9949350; PIDN:AGC0618.1; GSPDB:GN001

A:Experimental source: strain PA01

C:Genetics:

Query Match 90.0%; Score 36; DB 2; Length 374;  
Best Local Similarity 100.0%; Pred. No. 92;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 DMSWA 6  
DB 81 DMSWA 85

## RESULT 4

E87304

ToxB-dependent receptor [Imported] - Caulobacter crescentus

C:Species: Caulobacter crescentus

C:Date: 20-Apr-2001 #sequence\_revision 20-Apr-2001 #text\_change 20-Apr-2001

C:Accession: E87304

R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Neilson, K.E.; Eisen, J.; Heidelberg, J.

B.; Lamb, M.T.; Deboy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolot

n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.

Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001

A:Title: Complete Genome Sequence of Caulobacter crescentus.

A:Reference number: A87249; MUID:21173698; PMID:11259647

A:Accession: E87304

A:Status: Preliminary

A:Molecule type: DNA

A:Residues: 1-889 <STO>

A:Cross-references: GB:AE005673; NID:913421615; PIDN:AAK22433.1; GSPDB:GN00148

C:Genetics:

Query Match 90.0%; Score 36; DB 2; Length 889;  
Best Local Similarity 100.0%; Pred. No. 2.2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ADMSW 5  
DB 618 ADMSW 622

## RESULT 5

T05822

Hypothetical protein TSK18.170 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 13-Aug-1999

C:Accession: T05822

R:Bevan, M.; Van Der Schueren, J.; Chuang, Y.J.; Voelt, M.; Robben, J.; Volckaert, G.; Be

submitted to the Protein Sequence Database, April 1998

A:Reference number: Z15453

A:Accession: T05822

A:Molecule type: DNA

A:Residues: 1-275 <BEV>

A:Cross-references: EMBL:AL022580

A:Experimental source: cultivar Columbia; BAC clone TSK18

C:Genetics:

A:Map position: 4

A:Introns: 103/3; 141/3; 169/1; 206/3

A:Note: TSK18.170

Query Match 85.0%; Score 34; DB 2; Length 275;  
Best Local Similarity 66.7%; Pred. No. 1.4e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 ADMSWA 6  
DB 57 SDMSWS 62

## RESULT 6

C84922

Probable protein kinase [Imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 02-Feb-2001

C:Accession: C84922

R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanden, S.E.; Umayam, L.; Tallon,

euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter

Nature 402, 761-768, 1999

A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A:Reference number: A64420; MUID:20083487; PMID:10617197

A:Accession: C84922

A:Status: Preliminary

A:Molecule type: DNA

A:Residues: 1-617 <STO>

A:Cross-references: GB:AE002093; NID:94249408; PIDN:RAD13705.1; GSPDB:GN00139

C:Genetics:

A:Gene: At2g48010

A:Map position: 2

Query Match 85.0%; Score 34; DB 2; Length 617;  
Best Local Similarity 66.7%; Pred. No. 3.1e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 ADMSWA 6  
DB 500 ADMWMS 505

RESULT 7  
T43409  
Probable fatty-acid synthase (EC 2.3.1.85) alpha chain - fission yeast (Schizosacchar

N) Alternate names: fatty acid synthetase alpha subunit

C:Species: Schizosaccharomyces pombe

C:Date: 21-Jan-2000 #sequence\_revision 21-Jan-2000 #text\_change 21-Jul-2000

C:Accession: T43409

R:Saitoh, S.; Takahashi, K.; Nabeshima, K.; Yamashita, Y.; Nakaseko, Y.; Hirata, A.;

J. Cell Biol. 134, 949-961, 1996

A:Title: Aberrant mitosis in fission yeast mutants defective in fatty acid synthetase

A:Reference number: Z22493; MUID:96354912; PMID:8769419

A:Accession: T43409

A:Status: Preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-1842 <SAI>

A:Cross-references: EMBL:D83412; NID:91199959; PIDN:BAAL1913.1; PID:91199960

C:Genetics:

A:Note: Isd1+

C:Superfamily: yeast fatty-acid synthase

C:Keywords: acyltransferase; coenzyme A

Query Match 85.0%; Score 34; DB 2; Length 1842;  
Best Local Similarity 66.7%; Pred. No. 9.4e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 ADMSWA 6  
: : : :  
Db 400 SDMNWA 405

## RESULT 8

T38781  
fatty acid synthase, subunit alpha - fission yeast (Schizosaccharomyces pombe)  
C:Species: Schizosaccharomyces pombe  
C>Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 21-Jan-2000  
C:Accession: T38781  
R:Skellton, J.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood, V.  
submitted to the EMBL Data Library, August 1997  
A:Reference number: 221751  
A:Accession: T38781  
A>Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: DNA  
A:Residues: 1-1842 <SKED>  
A:Cross-references: EMBL:298762; PIDN:CA811481.1; GSPDB:GN00066; SPDB:SPAC4A8.11c  
A:Experimental source: strain 972h-; cosmid c4A8  
C:Genetics:  
A:Gene: SPDB:SPAC4A8.11c  
A:Map position: 1  
C:Superfamily: yeast fatty-acid synthase

Query Match 85.0%; Score 34; DB 2; Length 1842;  
Best Local Similarity 66.7%; Pred. No. 9.4e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 ADMSWA 6  
: : : :  
Db 400 SDMNWA 405

## RESULT 9

S65785  
mel-13a protein - mouse  
C:Species: Mus musculus (house mouse)  
C>Date: 28-Oct-1996 #sequence\_revision 13-Mar-1997 #text\_change 26-Aug-1999  
C:Accession: S65785  
R:Retzu, O.; Kanno, R.; Isono, K.; Taniguchi, M.; Kanno, M.  
Biochim. Biophys. Acta 1305, 109-112, 1996  
A>Title: Cloning and characterization of two transcripts generated from the mel-13 gene  
A:Reference number: S65785; MID:96180310; PMID:8597592  
A:Accession: S65785  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-132 <TEET>  
A:Cross-references: EMBL:U35309  
C:Genetics:  
A:Gene: mel-13  
C:Superfamily: mouse mel-13a protein  
C:Keywords: alternative splicing

Query Match 82.5%; Score 33; DB 2; Length 132;  
Best Local Similarity 80.0%; Pred. No. 96;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 ADMSW 5  
: : : :  
Db 57 SDMSW 61

## RESULT 10

B82531  
conserved hypothetical protein XF2666 [imported] - Xylella fastidiosa (strain 9a5c)  
C:Species: Xylella fastidiosa  
C>Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 17-Nov-2000  
C:Accession: B82531  
R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequences  
Nature 406, 151-157, 2000  
A>Title: The genome sequence of the plant pathogen Xylella fastidiosa.

A:Reference number: A82515; MID:20365717; PMID:10910347  
A>Note: for a complete list of authors see reference number A59328 below  
A:Accession: B82531  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-198 <SIM>

A:Cross-references: GB:AE004072; GB:AE003849; MID:99107884; PIDN:AAFB5463.1; GSPDB:GN  
A:Experimental source: strain 9a5c  
R:Simpon, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvares, R.  
Brites, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrier  
as-Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S.  
Submitted to Genbank, June 2000  
A:Authors: Ferreira, V.C.A.; Perito, J.A.; Fraga, J.S.; Franco, S.C.; Franco, M.C.; Fr  
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; La  
Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins  
A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.  
Rodrigues, V.; Rosa, A.J. de M.; de Rosa, J.V.; de Sa, R.G.; Santelli, R.V.; Sava  
M.; Tshako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.  
A:Reference number: A59328  
A:Contents: annotation  
C:Genetics:  
A:Gene: XF2666  
C:Superfamily: conserved hypothetical protein MJ1677

Query Match 82.5%; Score 33; DB 2; Length 198;  
Best Local Similarity 80.0%; Pred. No. 1.4e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 DMSWA 6  
: : : :  
Db 135 DNMWA 139

## RESULT 11

D64316  
restriction modification enzyme subunit M1 homolog - Methanococcus jannaschii  
C:Species: Methanococcus jannaschii  
C>Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 16-Aug-2002  
C:Accession: D64316  
R:Balt, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blak  
Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, R.G.; Merrick, J.M.; Glodek,  
rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.  
Science 273, 1058-1073, 1996  
A:Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Frazer, C.M.; Smith, H.O.; Woese  
A>Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannasc  
A:Reference number: A64300; MID:96337999; PMID:8688087  
A:Accession: D64316  
A:Molecule type: DNA  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Residues: 1-220 <BDUL>  
A:Cross-references: GB:U67470; GB:L77117; MID:92826247; PIDN:AB98113.1; PID:91592267  
C:Genetics:  
A:Map position: REV127472-126810  
A:Start codon: TTG  
C:Superfamily: type I site-specific deoxyribonuclease chain hsdM (associate member)

Query Match 82.5%; Score 33; DB 2; Length 220;  
Best Local Similarity 80.0%; Pred. No. 1.6e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 ADMSW 5  
: : : :  
Db 33 ADMNW 37

## RESULT 12

S58353  
CDLP protein - sheep (fragment)  
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)  
C>Date: 14-Jan-1996 #sequence\_revision 01-Mar-1996 #text\_change 21-Jan-2000  
C:Accession: S58353

R.Ferguson, E.D.; Dutta, B.M.; Hein, W.; Hopkins, J.  
 Submitted to the EMBL Data Library, July 1995  
 A:Description: The ovine CDI gene family contains at least four CDIb homologues.  
 A:Reference number: S58353  
 A:Accession: S58353  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-232 <FEK>  
 A:Cross-references: EMBL:X90567; NID:g945010; PIDN:CAA62187.1; PID:g945011  
 C:Superfamily: class I histocompatibility antigen; immunoglobulin homology  
 F:115-180/Domain: immunoglobulin homology <IMM>

Query Match 82.5%; Score 33; DB 2; Length 232;  
 Best Local Similarity 80.0%; Pred. No. 1.7e+02;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 ADMSW 5  
 |||||  
 DB 156 ADMTW 160

## RESULT 13

D90470  
 hypothetical protein cysH [imported] - Sulfolobus solfataricus

C:Species: Sulfolobus solfataricus

C>Date: 24-May-2001 #sequence\_revision 24-May-2001 #text\_change 15-Jun-2001

C:Accession: D90470

R:She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayer, M.J.; Chan-  
 Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thl-Ngoc, H.P.; Redder, F.  
 arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.  
 submitted to GenBank, April 2001

A:Description: Sulfolobus solfataricus complete genome.

A:Reference number: A9139

A:Accession: D90470

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-239 <KUN>

A:Cross-references: GB:AE006641; NID:g13816282; PIDN:AAK43019.1; GSPDB:GN00155

C:Genetics:

A:Gene: cysH

C:Superfamily: 3'-phosphoadenosine 5'-phosphosulfate reductase

Query Match 82.5%; Score 33; DB 2; Length 239;  
 Best Local Similarity 80.0%; Pred. No. 1.7e+02;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 ADMSW 5  
 |||||  
 DB 172 ADMTW 176

## RESULT 14

D87152  
 conserved hypothetical protein ML1945 [imported] - Mycobacterium leprae

C:Species: Mycobacterium leprae

C>Date: 20-Apr-2001 #sequence\_revision 20-Apr-2001 #text\_change 10-May-2001

C:Accession: D87152

R:Cole, S.T.; Elgimeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Ho-  
 R.; Davies, R.M.; Devlin, K.; Duthey, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd,  
 eam, M.A.; Rutherford, K.M.  
 Nature 409, 1007-1011, 2001

A:Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sq

A:Title: Massive gene decay in the leprosy bacillus.

A:Reference number: A86909; MUID:21128732; PMID:11234002

A:Accession: D87152

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-257 <STO>

A:Cross-references: GB:AL450380; NID:g13093601; PIDN:CAC30900.1; GSPDB:GN00147

C:Genetics:

A:Gene: ML1945  
 C:Superfamily: Mycobacterium tuberculosis hypothetical protein RV1100

Query Match 82.5%; Score 33; DB 2; Length 257;  
 Best Local Similarity 83.3%; Pred. No. 1.9e+02;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 ADMSW 6  
 |||||  
 DB 11 ATMSWA 16

## RESULT 15

B75337

hypothetical protein - Deinococcus radiodurans (strain R1)

C:Species: Deinococcus radiodurans

C>Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 31-Mar-2000

C:Accession: B75337

R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.  
 M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Uterback, T.; Zalewski, C.;  
 S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.  
 Science 286, 1571-1577, 1999

A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.

A:Reference number: A75250; MUID:20036896; PMID:10567266

A:Accession: B75337

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-276 <WHI>

A:Cross-references: GB:AE002032; GB:AE000513; NID:g6459715; PIDN:AAFI1479.1; PID:g645

A:Experimental source: strain R1

C:Genetics:

A:Gene: DR1923

A:Map position: 1

Query Match 82.5%; Score 33; DB 2; Length 276;  
 Best Local Similarity 80.0%; Pred. No. 2e+02;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 ADMSW 5  
 |||||  
 DB 84 ADMAW 88

Search completed: May 30, 2003, 14:52:41  
 Job time : 7.5921 secs

GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: May 30, 2003, 14:32:12 ; Search time 6.03947 Seconds.

(without alignments)  
29.231 Million cell updates/sec

Title: US-09-643-260-6

Perfect score: 40

Sequence: 1 ADMSMA 6

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

## Database :

Issued Patents AA:\*  
1: /cgn2\_6/prodata/1/aa/5A.COMB.pep:\*  
2: /cgn2\_6/prodata/1/aa/5B.COMB.pep:\*  
3: /cgn2\_6/prodata/1/aa/6A.COMB.pep:\*  
4: /cgn2\_6/prodata/1/aa/6B.COMB.pep:\*  
5: /cgn2\_6/prodata/1/aa/PCPUS.COMB.pep:\*  
6: /cgn2\_6/prodata/1/aa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	36	90.0	174	4	US-09-325-932A-163
2	36	90.0	225	4	US-09-325-932A-162
3	36	90.0	378	4	US-09-325-932A-158
4	34	85.0	44	4	US-08-905-223-274
5	33	82.5	74	1	US-08-379-538-2
6	33	82.5	136	2	US-08-774-065-2
7	33	82.5	218	1	US-08-032-848C-10
8	33	82.5	218	1	US-08-438-870-10
9	33	82.5	218	2	US-08-169-848B-34
10	33	82.5	218	2	US-08-448-873-34
11	33	82.5	218	4	US-08-382-452D-34
12	33	82.5	218	4	US-09-216-295-1
13	33	82.5	232	4	US-09-146-770-1
14	33	82.5	232	4	US-09-633-084-1
15	33	82.5	234	1	US-08-032-848C-9
16	33	82.5	234	1	US-08-438-870-9
17	33	82.5	234	1	US-09-146-770-3
18	33	82.5	234	4	US-09-216-295-3
19	33	82.5	234	4	US-09-216-295-3
20	33	82.5	234	4	US-09-216-295-4
21	33	82.5	234	4	US-09-633-084-3
22	33	82.5	234	4	US-09-633-084-4
23	33	82.5	239	4	US-09-216-295-15
24	33	82.5	467	1	US-08-140-104A-2
25	33	82.5	1205	1	US-07-908-245-2
26	33	82.5	1205	2	US-08-319-866-10
27	33	82.5	1205	4	US-09-123-708-6

28	33	82.5	1205	4	US-09-123-624-6	Sequence 6, Appl1
29	32	80.0	5	6	5217869-75	Patent No. 5217869
30	32	80.0	100	1	US-08-241-853-28	Sequence 28, Appl1
31	32	80.0	100	1	US-08-241-853-29	Sequence 28, Appl1
32	32	80.0	100	2	US-08-850-917-28	Sequence 28, Appl1
33	32	80.0	100	2	US-08-850-917-29	Sequence 28, Appl1
34	32	80.0	120	1	US-07-942-245-35	Sequence 35, Appl1
35	32	80.0	170	4	US-09-199-637A-339	Sequence 33, Appl1
36	32	80.0	260	4	US-09-216-295-23	Sequence 8, Appl1
37	32	80.0	537	4	US-09-655-270A-11	Sequence 11, Appl1
38	32	80.0	537	4	US-09-651-941-11	Sequence 11, Appl1
39	32	80.0	537	4	US-09-955-587-11	Sequence 47, Appl1
40	32	80.0	616	4	US-09-136-574A-47	Sequence 2, Appl1
41	32	80.0	677	4	US-08-836-567-2	Sequence 3, Appl1
42	32	80.0	745	2	US-08-887-518-3	Sequence 3, Appl1
43	32	80.0	745	2	US-09-023-321-3	Sequence 4, Appl1
44	32	80.0	745	2	US-08-890-853-4	
45	32	80.0	745	2	US-08-890-853-4	

## ALIGNMENTS

RESULT 1  
US-09-325-932A-163  
Sequence 163, Application US/09325932A  
Patent No. 6451604  
GENERAL INFORMATION:  
APPLICANT: Filmm, Barry  
TITLE OF INVENTION: Compositions affecting programmed cell  
FILE REFERENCE: 1022  
CURRENT FILING DATE: 1999-06-04  
NUMBER OF SEQ ID NOS: 206  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 163  
LENGTH: 174  
TYPE: PRT  
ORGANISM: Eucalyptus grandis  
US-09-325-932A-163

Query Match 90.0%; Score 36; DB 4; Length 174;  
Best Local Similarity 100.0%; Pred. No. 62;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSW 5  
Db 109 ADMSW 113

RESULT 2  
US-09-325-932A-162  
Sequence 162, Application US/09325932A  
Patent No. 6451604  
GENERAL INFORMATION:  
APPLICANT: Filmm, Barry  
TITLE OF INVENTION: Compositions affecting programmed cell  
FILE REFERENCE: 1022  
CURRENT FILING DATE: 1999-06-04  
NUMBER OF SEQ ID NOS: 206  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 162  
LENGTH: 225  
TYPE: PRT  
ORGANISM: Eucalyptus grandis  
US-09-325-932A-162

Query Match 90.0%; Score 36; DB 4; Length 225;

Best Local Similarity 100.0%; Pred. No. 79;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSW 5  
Db 100 ADMSW 104

## RESULT 3

US-09-325-932A-158  
Sequence 158, Application US/09325932A  
Patent No. 6451604  
GENERAL INFORMATION:  
APPLICANT: Fliinn, Barry  
APPLICANT: Lasham, Annette  
TITLE OF INVENTION: Compositions affecting programmed cell  
TITLE OF INVENTION: death and their use in the modification of forestry plant develop  
FILE REFERENCE: 1022  
CURRENT APPLICATION NUMBER: US/09/325,932A  
CURRENT FILING DATE: 1999-06-04  
NUMBER OF SEQ ID NOS: 206  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 158  
LENGTH: 378  
TYPE: PRT  
ORGANISM: Eucalyptus grandis  
US-09-325-932A-158

Query Match 90.0%; Score 36; DB 4; Length 378;  
Best Local Similarity 100.0%; Pred. No. 1,3e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSW 5  
Db 128 ADMSW 132

## RESULT 4

US-08-905-223-274  
Sequence 274, Application US/08905223  
Patent No. 6222029  
GENERAL INFORMATION:  
APPLICANT: Edwards, Jean-Baptiste D.  
APPLICANT: Duclert, Aymeric  
APPLICANT: Lacroix, Bruno  
TITLE OF INVENTION: 5' ESTS FOR SECRETED PROTEINS  
NUMBER OF SEQUENCES: 503  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Knobb, Martens, Olson & Bear  
STREET: 501 West Broadway  
CITY: San Diego  
STATE: California  
COUNTRY: USA  
ZIP: 92101-3505  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy Disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: W195  
SOFTWARE: word  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/905,223  
FILING DATE:  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Israelsen, Ned A.  
REGISTRATION NUMBER: 29,655  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 235-8550  
TELEFAX: (619) 235-0176  
INFORMATION FOR SEQ ID NO: 274:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 44 amino acids

TYPE: AMINO ACID  
TOPOLOGY: LINEAR  
MOLECULE TYPE: PROTEIN  
ORIGINAL SOURCE:  
ORGANISM: Homo Sapiens  
TISSUE TYPE: Brain  
FEATURE:

NAME/KEY: sig-peptide  
LOCATION: -26...-1  
IDENTIFICATION METHOD: Von Heljne matrix  
OTHER INFORMATION: score 9.6  
OTHER INFORMATION: seq WLIALASMSMALC/RI  
US-08-905-223-274

Query Match 85.0%; Score 34; DB 4; Length 44;  
Best Local Similarity 83.3%; Pred. No. 32;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ADMSWA 6  
Db 19 ASMSWA 24

## RESULT 5

US-08-379-538-2  
Sequence 2, Application US/08379538  
Patent No. 5804554  
GENERAL INFORMATION:  
APPLICANT: Volkmann, Robert A.  
APPLICANT: Saccamano, Nicholas A.  
APPLICANT: Mason II, Deane M.  
APPLICANT: Heck, Steven D.  
APPLICANT: Ronau, Robert T.  
TITLE OF INVENTION: CALCIUM CHANNEL BLOCKING POLYPEPTIDES  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pfizer Inc  
STREET: 235 East 42nd Street  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10017  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/379,538  
FILING DATE: 3-MAY-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/887073  
FILING DATE: 21-MAY-1992  
APPLICATION NUMBER: PCT/US93/03921  
FILING DATE: 30-APRIL-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Zielinski, Bryan  
REGISTRATION NUMBER: 34,462  
REFERENCE/DOCKET NUMBER: PC8175A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 573-4585  
TELEFAX: (212) 573-1939  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 74 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO

ORIGINAL SOURCE:  
ORGANISM: Filistata hibernalis  
TISSUE TYPE: venom  
US-08-379-538-2

Query Match  
Best Local Similarity 82.5%; Score 33; DB 1; Length 74;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 DMSWA 6  
|||||  
DB 52 DMSWS 56

RESULT 6  
US-08-774-065-2  
Sequence 2, Application US/08774065  
Patent No. 5989899

GENERAL INFORMATION:  
APPLICANT: Bower, Benjamin  
APPLICANT: Clarkson, Kathleen  
APPLICANT: Larenas, Edmund  
APPLICANT: Ward, Michael  
TITLE OF INVENTION: NOVEL OVERSIZED CELLULOSE COMPOSITIONS  
TITLE OF INVENTION: FOR USE IN DETERGENT COMPOSITIONS AND  
NUMBER OF SEQUENCES: 16  
IN THE TREATMENT OF TEXTILES

CORRESPONDENCE ADDRESS:  
ADDRESSEE: GENENCOR INTERNATIONAL  
STREET: 925 PAGE MILL ROAD  
CITY: PALO ALTO  
STATE: CALIFORNIA

COUNTRY: UNITED STATES  
ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/774,065

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Gialster, Debra J.

REGISTRATION NUMBER: 33,888

REFERENCE/DOCKET NUMBER: GC368

TELEPHONE: 415-846-7620

TELEFAX: 415-846-6504

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 136 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-774-065-2

Query Match

Best Local Similarity 82.5%; Score 33; DB 2; Length 136;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 ADMSWA 6  
|||||  
DB 62 ADMSWS 67

RESULT 7  
US-08-032-848C-10  
Sequence 10, Application US/08032848C  
Patent No. 5475101

GENERAL INFORMATION:

APPLICANT: Ward, Michael

APPLICANT: Clarkson, Kathleen A.

APPLICANT: Weiss, Geoffrey L.

APPLICANT: Larenas, Edward

APPLICANT: Lorch, Jeffrey D.

TITLE OF INVENTION: Purification and Molecular Cloning of

EG III Cellulase

NUMBER OF SEQUENCES: 20

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genencor International

STREET: 180 Kinball Way

CITY: South San Francisco

STATE: CA

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/032,848C

FILING DATE: MAR 17 1993

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Horn, Margaret A.

REGISTRATION NUMBER: 33,401

TELEPHONE: 415 742-7356

TELEFAX: 415 742-7217

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 218 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-032-848C-10

Query Match

Best Local Similarity 82.5%; Score 33; DB 1; Length 218;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 ADMSWA 6  
|||||  
DB 46 ADMSWS 51

RESULT 8

US-08-438-870-10

Sequence 10, Application US/08438870

Patent No. 5753484

GENERAL INFORMATION:

APPLICANT: Ward, Michael

APPLICANT: Clarkson, Kathleen A.

APPLICANT: Weiss, Geoffrey L.

APPLICANT: Larenas, Edward

APPLICANT: Lorch, Jeffrey D.

TITLE OF INVENTION: Purification and Molecular Cloning of EG

III Cellulase

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genencor International

STREET: 180 Kinball Way

CITY: South San Francisco

STATE: CA

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/438,870  
FILING DATE: May 10, 1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Christopher L. Stone  
REGISTRATION NUMBER: 35,696  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415 742-7555  
TELEFAX: 415 742-7217  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 218 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-438-870-10

Query Match 82.5%; Score 33; DB 1; Length 218;  
Best Local Similarity 66.7%; Pred. No. 2.1e+02;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ADMSWA 6  
DB 46 ADMQMS 51

RESULT 9  
US-08-169-948B-34  
Sequence 34, Application US/08169948B  
Patent No. 5861271  
GENERAL INFORMATION:  
APPLICANT: Fowler, Timothy  
APPLICANT: Ward, Michael  
APPLICANT: Clarkson, Kathleen  
APPLICANT: Collier, Katherine  
APPLICANT: Larenas, Edmund  
TITLE OF INVENTION: No. 5861271e1 Cellulase Enzymes and Systems  
TITLE OF INVENTION: For Their Expression  
NUMBER OF SEQUENCES: 48  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genencor International  
STREET: 180 Kimball Way  
CITY: South San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/169,948B  
FILING DATE: DEC 17 1993  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Horn, Margaret A.  
REGISTRATION NUMBER: 33,401  
REFERENCE/DOCKET NUMBER: GC226  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 742-7536  
TELEFAX: (415) 742-7217  
INFORMATION FOR SEQ ID NO: 34:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 218 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-169-948B-34

Query Match 82.5%; Score 33; DB 2; Length 218;  
Best Local Similarity 66.7%; Pred. No. 2.1e+02;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ADMSWA 6  
DB 46 ADMQMS 51

RESULT 10  
US-08-448-873-34  
Sequence 34, Application US/08448873  
Patent No. 5874276  
GENERAL INFORMATION:  
APPLICANT: Fowler, Timothy  
APPLICANT: Ward, Michael  
APPLICANT: Clarkson, Kathleen  
APPLICANT: Collier, Katherine A.  
APPLICANT: Larenas, Edmund  
TITLE OF INVENTION: No. 5874276e1 Cellulase Enzymes and Systems  
TITLE OF INVENTION: For Their Expressions  
NUMBER OF SEQUENCES: 48  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genencor International  
STREET: 180 Kimball Way  
CITY: South San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/448,873  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/169,948  
FILING DATE: 17-DEC-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Stone, Christopher L.  
REGISTRATION NUMBER: 35,696  
REFERENCE/DOCKET NUMBER: GC226D14  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 742-7555  
TELEFAX: (415) 742-7217  
INFORMATION FOR SEQ ID NO: 34:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 218 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-448-873-34

Query Match 82.5%; Score 33; DB 2; Length 218;  
Best Local Similarity 66.7%; Pred. No. 2.1e+02;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ADMSWA 6  
DB 46 ADMQMS 51

RESULT 11  
US-08-382-452D-34  
Sequence 34, Application US/08382452D  
Patent No. 6268196  
GENERAL INFORMATION:  
APPLICANT: Fowler, Timothy

APPLICANT: Clarkson, Kathleen A.  
APPLICANT: Ward, Michael  
APPLICANT: Collier, Katherine D.  
APPLICANT: Larenaas, Edmund A.  
TITLE OF INVENTION: NOVEL CELLULOSE ENZYMES AND SYSTEMS  
TITLE OF INVENTION: FOR THEIR EXPRESSION  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genencor International  
STREET: 925 Page Mill Road  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/382,452D  
FILING DATE: February 1, 1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Christopher L. Stone  
REGISTRATION NUMBER: 36,686  
REFERENCE/DOCKET NUMBER: GC226-2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 742-7555  
TELEFAX: (415) 742-7217  
INFORMATION FOR SEQ ID NOS: 34:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 218 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-382-452D-34

Query Match 82.5%; Score 33; DB 4; Length 218;  
Best Local Similarity 66.7%; Pred. No. 2.1e+02;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ADMSWA 6  
DB 46 ADMQWS 51

RESULT 12  
US-09-216-295-1  
Sequence 1, Application US/09216295  
Patent No. 6268328  
GENERAL INFORMATION:  
APPLICANT: Mitchinson, Colin  
APPLICANT: Mendt, Dan J.  
TITLE OF INVENTION: No. 6268328el Variant EGIII-Like Cellulase Compositions  
FILE REFERENCE: GC555  
CURRENT APPLICATION NUMBER: US/09/216,295  
CURRENT FILING DATE: 1998-12-18  
NUMBER OF SEQ ID NOS: 41  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 1  
LENGTH: 218  
TYPE: PRT  
ORGANISM: Trichoderma longibrachiatum  
US-09-216-295-1

Query Match 82.5%; Score 33; DB 4; Length 218;  
Best Local Similarity 66.7%; Pred. No. 2.1e+02;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ADMSWA 6  
DB 46 ADMQWS 51

RESULT 13  
US-09-146-770-1  
Sequence 1, Application US/09146770  
Patent No. 6187732  
GENERAL INFORMATION:  
APPLICANT: Fowler, Timothy  
TITLE OF INVENTION: Mutant EGIII Cellulase, DNA Encoding  
TITLE OF INVENTION: Such EGIII Compositions and Methods for Obtaining Same  
FILE REFERENCE: GC546  
CURRENT APPLICATION NUMBER: US/09/146,770  
CURRENT FILING DATE: 1998-09-03  
SOFTWARE: FastSeq for Windows Version 3.0  
NUMBER OF SEQ ID NOS: 4  
SEQ ID NO 1  
LENGTH: 232  
TYPE: PRT  
ORGANISM: T. reesei  
US-09-146-770-1

Query Match 82.5%; Score 33; DB 4; Length 232;  
Best Local Similarity 66.7%; Pred. No. 2.2e+02;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ADMSWA 6  
DB 60 ADMQWS 65

RESULT 14  
US-09-633-084-1  
Sequence 1, Application US/09633084  
Patent No. 6407046  
GENERAL INFORMATION:  
APPLICANT: Fowler, Timothy  
TITLE OF INVENTION: Mutant EGIII Cellulase, DNA Encoding  
TITLE OF INVENTION: Such EGIII Compositions and Methods for Obtaining Same  
FILE REFERENCE: GC546  
CURRENT APPLICATION NUMBER: US/09/633,084  
CURRENT FILING DATE: 2000-08-04  
PRIOR APPLICATION NUMBER: 09/146,770  
PRIOR FILING DATE: 1998-09-03  
NUMBER OF SEQ ID NOS: 4  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 1  
LENGTH: 232  
TYPE: PRT  
ORGANISM: T. reesei  
US-09-633-084-1

Query Match 82.5%; Score 33; DB 4; Length 232;  
Best Local Similarity 66.7%; Pred. No. 2.2e+02;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ADMSWA 6  
DB 60 ADMQWS 65

RESULT 15  
US-08-032-848C-9  
Sequence 9, Application US/08032848C  
Patent No. 5475101  
GENERAL INFORMATION:  
APPLICANT: Ward, Michael  
APPLICANT: Clarkson, Kathleen A.  
APPLICANT: Weiss, Geoffrey L.  
APPLICANT: Larenaas, Edward  
APPLICANT: Lorch, Jeffrey D.  
TITLE OF INVENTION: Purification and Molecular Cloning of  
TITLE OF INVENTION: EG III Cellulase  
NUMBER OF SEQUENCES: 20

CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Genencor International  
 STREET: 180 Kimball Way  
 CITY: South San Francisco  
 STATE: CA  
 COUNTRY: USA  
 ZIP: 94080  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/032,848C  
 FILING DATE: MAR 17 1993  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Horn, Margaret A.  
 REGISTRATION NUMBER: 33,401  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 415 742-7217  
 TELEFAX: 415 742-7356  
 INFORMATION FOR SEQ ID NO: 9:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 234 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-032-848C-9

Query Match 82.5%; Score 33; DB 1; Length 234;  
 Best Local Similarity 66.7%; Pred. No. 2.3e+02;  
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 ADMSWA 6  
 DB 62 ADMQMS 67

Search completed: May 30, 2003, 14:41:24  
 Job time : 6.03947 secs

PA (UYYA ) UNIV YALE.

XX May MJ, Ghosh S, Findels MA, Phillips K;  
XX WPI; 2002-121889/16.  
XX  
XX  
XX Novel antiinflammatory compound comprising membrane translocation  
PT domain fused to NEMO binding sequence, useful for blocking nuclear  
PT factor kappaB activation, and for treating asthma, lung inflammation,  
PT psoriasis  
XX  
XX  
XX Claim 6; Page 61; 88pp; English.  
XX  
XX The invention relates to an antiinflammatory compound (especially  
CC AAM48628-AAM48645), comprising a membrane translocation domain  
CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15  
CC amino acid residues, fused to a NEMO binding sequence  
CC (AAM48525-AAM48619). The antiinflammatory compounds have antialsthamatic,  
CC cytoskeletal, antipsoriatic, antirheumatic, antiarthritic, osteopathic,  
CC antibacterial, immunosuppressive, dermatological, neuroprotective,  
CC nootropic, antiatherosclerotic, virucide and antiallergic activity. The  
CC compounds act as selective inhibitors of cytokine-mediated NFkappaB  
CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at  
CC the NEMO binding domain that results in inhibition of IKKbeta kinase  
CC activation and subsequent decreased phosphorylation of IkappaB. The  
CC compounds are useful for treating inflammatory disorders, e.g. asthma,  
CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,  
CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,  
CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,  
CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;  
CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia  
CC telangiectasia. The compounds are also useful for treating  
CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,  
CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and  
CC arthritis.  
CC  
XX  
XX Sequence 6 AA;  
SQ  
Query Match 100.0%; Score 40; DB 23; Length 6;  
Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 ADMSWA 6  
DB 1 ADMSWA 6  
RESULT 2  
AAM48570  
ID AAM48570 standard; peptide; 6 AA.  
XX  
XX  
XX AAM48570;  
AC  
XX  
XX 20-MAR-2002 (first entry)  
DT  
XX  
XX Anti-inflammatory peptide SEQ ID NO 73.  
DE  
XX  
XX Antinflammatory; antialsthamatic; cytoskeletal; antipsoriatic; nootropic;  
KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;  
KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;  
KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;  
KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;  
KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
KW autoimmune disorder; multiple sclerosis; transplant rejection;  
KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.  
XX  
XX  
XX Synthetic.  
OS  
XX  
XX W0200183554-A2.  
PN  
XX  
XX 08-NOV-2001.  
PD  
XX  
XX 02-MAY-2001; 2001WO-US14346.  
PF

XX 02-MAY-2000; 2000US-201261P.  
PR 22-AUG-2000; 2000US-0643260.  
XX  
XX  
XX (PRAE-) PRAECIS PHARM INC.  
PA (UYVA ) UNIV YALE.  
XX  
XX May MJ, Ghosh S, Findels MA, Phillips K;  
XX WPI; 2002-121889/16.  
XX  
XX  
XX Novel antiinflammatory compound comprising membrane translocation  
PT domain fused to NEMO binding sequence, useful for blocking nuclear  
PT factor kappaB activation, and for treating asthma, lung inflammation,  
PT psoriasis  
XX  
XX  
XX Claim 6; Page 62; 88pp; English.  
XX  
XX The invention relates to an antiinflammatory compound (especially  
CC AAM48628-AAM48645), comprising a membrane translocation domain  
CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15  
CC amino acid residues, fused to a NEMO binding sequence  
CC (AAM48525-AAM48619). The antiinflammatory compounds have antialsthamatic,  
CC cytoskeletal, antipsoriatic, antirheumatic, antiarthritic, osteopathic,  
CC antibacterial, immunosuppressive, dermatological, neuroprotective,  
CC nootropic, antiatherosclerotic, virucide and antiallergic activity. The  
CC compounds act as selective inhibitors of cytokine-mediated NFkappaB  
CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at  
CC the NEMO binding domain that results in inhibition of IKKbeta kinase  
CC activation and subsequent decreased phosphorylation of IkappaB. The  
CC compounds are useful for treating inflammatory disorders, e.g. asthma,  
CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,  
CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,  
CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,  
CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;  
CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia  
CC telangiectasia. The compounds are also useful for treating  
CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,  
CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and  
CC arthritis.  
CC  
XX  
XX Sequence 6 AA;  
SQ  
Query Match 100.0%; Score 40; DB 23; Length 6;  
Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 ADMSWA 6  
DB 1 ADMSWA 6  
RESULT 3  
AAM48574  
ID AAM48574 standard; peptide; 7 AA.  
XX  
XX  
XX AAM48574;  
AC  
XX  
XX 20-MAR-2002 (first entry)  
DT  
XX  
XX Anti-inflammatory peptide SEQ ID NO 77.  
DE  
XX  
XX Antinflammatory; antialsthamatic; cytoskeletal; antipsoriatic; nootropic;  
KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;  
KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;  
KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;  
KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;  
KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
KW autoimmune disorder; multiple sclerosis; transplant rejection;  
KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.  
XX  
XX  
XX Synthetic.  
OS

XX WO200183554-A2.  
 XX  
 PN  
 XX  
 XX  
 PD 08-NOV-2001. ✓  
 XX  
 XX  
 PF 02-MAY-2001; 2001WO-US14346.  
 XX  
 XX  
 PR 02-MAY-2000; 2000US-201261P.  
 PR 22-AUG-2000; 2000US-0643260.  
 XX  
 XX  
 PA (PRAE-) PRAECIS PHARM INC.  
 PA (UYEA ) UNIV YALE.  
 XX  
 XX  
 P1 May MJ, Ghosh S, Findeis MA, Phillips K;  
 XX  
 XX WPI; 2002-121889/16.  
 DR  
 XX  
 PT Novel antiinflammatory compound comprising membrane translocation  
 XX domain fused to NEMO binding sequence, useful for blocking nuclear  
 XX factor kappaB activation, and for treating asthma, lung inflammation,  
 PT psoriasis -  
 XX  
 ES Claim 6; Page 62; 88pp; English.

CC	The invention relates to an antiinflammatory compound (especially
CC	(AA048628-AA048645), comprising a membrane translocation domain
CC	(AA048620-AA048667 or AA048646-AA048851) which comprises from 6-15
CC	amino acid residues, fused to a NEMO binding sequence
CC	(AA048825-AA0488619). The antiinflammatory compounds have antiaesthetic,
CC	cycostatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,
CC	antibacterial, immunosuppressive, dermatological, neuroprotective,
CC	nootropic, antihypertensive, virocidic and antiallergic activity. The
CC	compounds act as selective inhibitors of cytokine-mediated NFkappaB
CC	activation by blocking interaction of IkappaB kinase beta (IKKbeta) at
CC	the NEMO binding domain that results in inhibition of IKKbeta kinase
CC	activation and subsequent decreased phosphorylation of IkappaB. The
CC	compounds are useful for treating inflammatory disorders, e.g. asthma,
CC	lung inflammation or cancer, psoriasis, rheumatoid arthritis,
CC	osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,
CC	bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,
CC	granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;
CC	Alzheimer's disease; atherosclerosis; viral infections; and ataxia
CC	telangiectasia. The compounds are also useful for treating
CC	pro-inflammatory responses such as allergies, urticaria, anaphylaxis,
CC	drug or food sensitivity, eczema, dermatitis, sunburn, aging and
CC	arthritis.
XX	
Sequence	7 AA;
Query Match	100.0%; Score 40; DB 23; Length 7;
Best Local Similarity	100.0%; Pred. NO. 7.8e+05;
Matches	6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

SQ      Sequence      7 AA;
Query Match      100.0%; Score 40; DB 23; Length 7;
Best Local Similarity: 100.0%; Pred. NO. 7.6e+05;
Matches      6; Conservative      0; Mismatches      0; Indels      0; Gaps      0;
OY      1 ADWSMA 6
        |||||
db      1 ADWSMA 6

```

XX	RESULT 4
AAAM48567	
ID	AAAM48567 standard; Peptide; 8 AA.
XX	
AC	AAAM48567;
XX	
DT	20-MAR-2002 (first entry)
XX	
DE	Anti-inflammatory peptide SEQ ID NO 70.
XX	
KW	Antiinflammatory; antiasthmatic; cyostatic; antipsoriatic; nootropic;
KW	antirheumatic; antiarthritic; osteopathic; anticholesterol; virocidic;
KW	immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
KW	antiallergic; membrane translocation domain; NEMO binding domain; eczema;
KW	cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;

KV	rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
KW	autoimmune disorder; multiple sclerosis; transplant rejection;
KX	osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
KW	ataxia telangiectasia; allergy; anaphylaxis; arthritis.
KX	
OS	Synthetic.
XX	
PN	WO200183554-A2.
XX	
PD	08-NOV-2001. ✓
XX	
PF	02-MAY-2001; 2001WO-US14346.
XX	
PR	02-MAY-2000; 2000US-201261P.
PR	22-AUG-2000; 2000US-0643260.
XX	
PA	(PRAE-) PRAECIS PHARM INC.
PA	(UYVA ) UNIV YALE.
XX	
PI	May MJ, Ghosh S, Findels MA, Phillips K;
XX	
DR	WPI; 2002-121889/16.
XX	
PT	Novel antiinflammatory compound comprising membrane translocation
PT	domain fused to NEMO binding sequence, useful for blocking nuclear
PT	factor kappaB activation, and for treating asthma, lung inflammation,
PT	psoriasis -
XX	
PS	Claim 6; Page 62; 88pp; English.

The invention relates to an antiinflammatory compound (especially AAAM48520-AAAM48645), comprising a membrane translocation domain (AAAM48620-AAAM48627 or AAAM48646-AAAM48651) which comprises from 6-15 amino acid residues, fused to a NEMO binding sequence (AAAM48525-AAAM48619). The antiinflammatory compounds have antiasthmatic, cystostatic, antipsoriatic, antirheumatic, antiarthritic, osteoprotective, antibacterial, immunosuppressive, dermatological, neuroprotective, neurotropic, antiatherosclerotic, virucide and antiallergic activity. The compounds act as selective inhibitors of cytokine-mediated IKK $\beta$  activation by blocking interaction of I $\kappa$ B $\alpha$ p Kinase beta (IKK $\beta$ ) at the NEMO binding domain that results in inhibition of IKK $\beta$  kinase activation and subsequent decreased phosphorylation of I $\kappa$ B $\alpha$ p. The compounds are useful for treating inflammatory disorders, e.g. asthma, lung inflammation or cancer, psoriasis, rheumatoid arthritis, osteoarthritis, inflammatory bowel disease, sepsis, vasculitis, dermatitis, autoimmune diseases such as lupus, polyarthritis, scleroderma, granulomatosis, multiple sclerosis; transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis; viral infections; and ataxia telangiectasia. The compounds are also useful for treating pro-inflammatory responses such as allergies, urticaria, anaphylaxis, drug or food sensitivity, eczema, dermatitis, sunburn, aging and arthritis.

Query Match	100.0%;	Score 40;	DB 23;	length 8;
Best Local	Similarity	100.0%;	Pred. No. 7.8e+05;	
Matches	6; Conservative	0;	Mismatches 0;	Indels 0;
				Gaps 0;

DE	ID	AA	AC	AD	AE	AF	AG	AH	AI	AJ	AK	AL	AM	AN	AO	AP	AQ	AR	AS	AT	AV	AW	AX	AY	AZ	BA	BB	BC	BD	BE	BF	BG	BH	BI	BJ	BK	BL	BM	BN	BO	BP	BQ	BR	BS	BT	BU	BV	BW	BX	BY	BZ	CA	CB	CC	CD	CE	CF	CG	CH	CI	CJ	CK	CL	CM	CN	CO	CP	CQ	CR	CS	CT	CU	CV	CW	CX	CY	CZ	DA	DB	DC	DD	DE	DF	DG	DH	DI	DJ	DK	DL	DM	DN	DO	DP	DQ	DR	DS	DT	DU	DV	DW	DX	DY	DZ	EA	EB	EC	ED	EE	EF	EG	EH	EI	EJ	EK	EL	EM	EN	EO	EP	EQ	ER	ES	ET	EU	EV	EW	EX	EY	EZ	FA	FB	FC	FD	FE	FF	FG	FH	FI	FJ	FK	FL	FM	FN	FO	FP	FQ	FR	FS	FT	FU	FV	FW	FX	FY	FZ	GA	GB	GC	GD	GE	GF	GG	GH	GI	GJ	GK	GL	GM	GN	GO	GP	GQ	GR	GS	GT	GU	GV	GW	GX	GY	GZ	HA	HB	HC	HD	HE	HF	HG	HH	HI	HJ	HK	HL	HM	HN	HO	HP	HQ	HR	HS	HT	HU	HV	HW	HX	HY	HZ	IA	IB	IC	ID	IE	IF	IG	IH	II	IJ	IK	IL	IM	IN	IO	IP	IQ	IR	IS	IT	IU	IV	IW	IX	IY	IZ	JA	JB	JC	JD	JE	JF	JG	JH	JI	IJ	JK	KL	JM	JN	JO	JP	JQ	JR	JS	JT	JU	JV	JW	JX	JY	JZ	KA	KB	KC	KD	KE	KF	KG	KH	KI	KJ	KK	KL	KM	KN	KO	KP	KQ	KR	KS	KT	KU	KV	KW	KX	KY	KZ	LA	LB	LC	LD	LE	LF	LG	LH	LI	LJ	LK	LL	LM	LN	LO	LP	LQ	LR	LS	LT	LU	LV	LW	LX	LY	LZ	MA	MB	MC	MD	ME	MF	MG	MH	MI	MJ	MK	ML	MM	MN	MO	MP	MQ	MR	MS	MT	MU	MV	MW	MX	MY	MZ	NA	NB	NC	ND	NE	NF	NG	NH	NI	NJ	NK	NL	NM	NN	NO	NP	NQ	NR	NS	NT	NU	NV	NW	NX	NY	NZ	OA	OB	OC	OD	OE	OF	OG	OH	OI	OJ	OK	OL	OM	ON	OO	OP	OQ	OR	OS	OT	OU	OV	OW	OX	OY	OZ	PA	PB	PC	PD	PE	PF	PG	PH	PI	PJ	PK	PL	PM	PN	PO	PP	PQ	PR	PS	PT	PU	PV	PW	PX	PY	PZ	QA	QB	QC	QD	QE	QF	QG	QH	QI	QJ	QK	QL	QM	QN	QO	QP	QQ	QR	QS	QT	QU	QV	QW	QX	QY	QZ	RA	RB	RC	RD	RE	RF	RG	RH	RI	RJ	RK	RL	RM	RN	RO	RP	RQ	RR	RS	RT	RU	RV	RW	RX	RY	RZ	SA	SB	SC	SD	SE	SF	SG	SH	SI	SJ	SK	SL	SM	SN	SO	SP	SQ	SR	SS	ST	SU	SV	SW	SX	SY	SZ	TA	TB	TC	TD	TE	TF	TG	TH	TI	TJ	TK	TL	TM	TN	TO	TP	TQ	TR	TS	TT	TU	TV	TW	TX	TY	TZ	UA	UB	UC	UD	UE	UF	UG	UH	UI	UJ	UK	UL	UM	UN	UO	UP	UQ	UR	US	UT	UU	UV	UW	UX	UY	UZ	VA	VB	VC	VD	VE	VF	VG	VH	VI	VJ	VK	VL	VM	VN	VO	VP	VQ	VR	VS	VT	VU	VV	VW	VX	VY	VZ	WA	WB	WC	WD	WE	WF	WG	WH	WI	WJ</
----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	------

XX Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; neutrotropic;  
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;  
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;  
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;  
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;  
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
 KW autoimmune disorder; multiple sclerosis; transplant rejection;  
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.  
 OS Synthetic.  
 XX WO200183554-A2.  
 XX  
 XX 08-NOV-2001.  
 XX  
 XX 02-MAY-2001; 2001WO-US14346.  
 XX  
 XX 02-MAY-2000; 2000US-201261P.  
 XX 22-AUG-2000; 2000US-0643260.  
 XX  
 XX (PRAE-) PRAECIS PHARM INC.  
 XX (UYVA ) UNIV YALE.  
 XX  
 XX May MJ, Ghosh S, Findels MA, Phillips K;  
 XX WPI: 2002-121889/16.  
 XX  
 XX Novel antiinflammatory compound comprising membrane translocation  
 PT domain fused to NEMO binding sequence, useful for blocking nuclear  
 PT factor kappaB activation, and for treating asthma, lung inflammation,  
 PT psoriasis -  
 XX  
 XX Claim 6; Page 62; 88pp; English.  
 XX  
 XX The invention relates to an antiinflammatory compound (especially  
 CC AAM48628-AAM48645), comprising a membrane translocation domain  
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15  
 CC amino acid residues, fused to a NEMO binding sequence  
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,  
 CC cytoskeletal, antipsoriatic, antirheumatic, antiarthritic, osteopathic,  
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,  
 CC neutrotropic, antiatherosclerotic, virucide and antiallergic activity. The  
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB  
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at  
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase  
 CC activation and subsequent decreased phosphorylation of IkappaB. The  
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,  
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,  
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,  
 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,  
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;  
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia  
 CC telangiectasia. The compounds are also useful for treating  
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,  
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and  
 CC arthritis.  
 CC  
 XX Sequence 8 AA;  
 XX  
 XX Query Match 100.0%; Score 40; DB 23; Length 8;  
 XX Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
 XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX AAM48566;  
 AC  
 XX 20-MAR-2002 (first entry)  
 DT  
 XX  
 XX Anti-inflammatory peptide SEQ ID NO 69.  
 DE  
 XX  
 XX Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; neutrotropic;  
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;  
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;  
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;  
 KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;  
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
 KW autoimmune disorder; multiple sclerosis; transplant rejection;  
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.  
 OS Synthetic.  
 XX WO200183554-A2.  
 XX  
 XX 08-NOV-2001.  
 XX  
 XX 02-MAY-2001; 2001WO-US14346.  
 XX  
 XX 02-MAY-2000; 2000US-201261P.  
 XX 22-AUG-2000; 2000US-0643260.  
 XX  
 XX (PRAE-) PRAECIS PHARM INC.  
 XX (UYVA ) UNIV YALE..  
 XX  
 XX May MJ, Ghosh S, Findels MA, Phillips K;  
 XX WPI: 2002-121889/16.  
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 XX Novel antiinflammatory compound comprising membrane translocation  
 PT domain fused to NEMO binding sequence, useful for blocking nuclear  
 PT factor kappaB activation, and for treating asthma, lung inflammation,  
 PT psoriasis -  
 XX  
 XX Claim 6; Page 62; 88pp; English.  
 XX  
 XX The invention relates to an antiinflammatory compound (especially  
 CC AAM48628-AAM48645), comprising a membrane translocation domain  
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15  
 CC amino acid residues, fused to a NEMO binding sequence  
 CC (AAM48525-AAM48619). The antiinflammatory compounds have antiasthmatic,  
 CC cytoskeletal, antipsoriatic, antirheumatic, antiarthritic, osteopathic,  
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,  
 CC neutrotropic, antiatherosclerotic, virucide and antiallergic activity. The  
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB  
 CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at  
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase  
 CC activation and subsequent decreased phosphorylation of IkappaB. The  
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,  
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,  
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,  
 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,  
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;  
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia  
 CC telangiectasia. The compounds are also useful for treating  
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,  
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and  
 CC arthritis.  
 CC  
 XX Sequence 9 AA;  
 XX  
 XX Query Match 100.0%; Score 40; DB 23; Length 9;  
 XX Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
 XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 ADMSWA 6

RESULT 7

AA048569

ID AA048569 standard; Peptide: 9 AA.

AC AA048569;

DT 20-MAR-2002 (first entry)

DE Anti-inflammatory peptide SEQ ID NO 72.

XX

XX Anti-inflammatory; antiaesthetic; cytosolic; antiproliferative; neurotrophic;

XX anti-inflammatory; antiaesthetic; osteoporosis; antiproliferative; neurotrophic;

XX immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;

XX anti-inflammatory; membrane translocation domain; NEMO binding domain; eczema;

XX cytokine; NF-kappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;

XX rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;

XX autoimmune disorder; multiple sclerosis; transplant rejection;

XX osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;

XX ataxia telangiectasia; allergy; anaphylaxis; arthritis.

OS Synthetic.

XX WO200183554-A2.

XX 08-NOV-2001.

XX 02-MAY-2001; 2001WO-US14346.

XX 02-MAY-2000; 2000US-201261P.

XX 22-AUG-2000; 2000US-0643260.

XX (PRAE-) PRAECIS PHARM INC.

XX (UYVA ) UNIV YALE.

XX May MJ, Ghosh S, Finkelstein MA, Phillips K;

XX WPI; 2002-121889/16.

XX Novel anti-inflammatory compound comprising membrane translocation

XX domain fused to NEMO binding sequence, useful for blocking nuclear

XX factor kappaB activation, and for treating asthma, lung inflammation,

XX psoriasis

XX Claim 6; Page 62; 88pp; English.

XX The invention relates to an anti-inflammatory compound (especially

XX AA048628-AA048645), comprising a membrane translocation domain

XX (AA048620-AA048627 or AA048646-AA048651) which comprises from 6-15

XX amino acid residues, fused to a NEMO binding sequence

XX (AA048525-AA048619). The anti-inflammatory compounds have antiasthmatic,

XX cytosolic, antiproliferative, antirheumatic, antiaesthetic, osteopathic,

XX antibacterial, immunosuppressive, dermatological, neuroprotective,

XX neurotrophic, antiatherosclerotic, virucide and antiallergic activity. The

XX compounds act as selective inhibitors of cytokine-mediated NF-kappaB

XX activation by blocking interaction of IkappaB kinase beta (IKKbeta) at

XX the NEMO binding domain that results in inhibition of IKKbeta kinase

XX activation and subsequent decreased phosphorylation of IkappaB. The

XX compounds are useful for treating inflammatory disorders, e.g. asthma,

XX lung inflammation or cancer, psoriasis, rheumatoid arthritis,

XX osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,

XX burstitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,

XX granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;

XX Alzheimer's disease; atherosclerosis; viral infections; and ataxia

XX telangiectasia. The compounds are also useful for treating

XX pro-inflammatory responses such as allergies, urticaria, anaphylaxis,

XX drug or food sensitivity, eczema, dermatitis, sunburn, aging and

XX arthritis.

XX Sequence 9 AA;

Query Match 100.0%; Score 40; DB 23; Length 9;

Best Local Similarity 100.0%; Pred. No. 7.8e+05;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Caps 0;

DB 1 ADMSWA 6

AA048572

ID AA048572 standard; Peptide: 9 AA.

AC AA048572;

DT 20-MAR-2002 (first entry)

DE Anti-inflammatory peptide SEQ ID NO 75.

XX

XX Anti-inflammatory; antiaesthetic; cytosolic; antiproliferative; neurotrophic;

XX anti-inflammatory; antiaesthetic; osteoporosis; antiproliferative; neurotrophic;

XX immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;

XX anti-inflammatory; membrane translocation domain; NEMO binding domain; eczema;

XX cytokine; NF-kappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;

XX rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;

XX autoimmune disorder; multiple sclerosis; transplant rejection;

XX osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;

XX ataxia telangiectasia; allergy; anaphylaxis; arthritis.

OS Synthetic.

XX WO200183554-A2.

XX 08-NOV-2001.

XX 02-MAY-2001; 2001WO-US14346.

XX 02-MAY-2000; 2000US-201261P.

XX 22-AUG-2000; 2000US-0643260.

XX (PRAE-) PRAECIS PHARM INC.

XX (UYVA ) UNIV YALE.

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XX WPI; 2002-121889/16.

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XX domain fused to NEMO binding sequence, useful for blocking nuclear

XX factor kappaB activation, and for treating asthma, lung inflammation,

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XX Claim 6; Page 62; 88pp; English.

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XX (AA048620-AA048627 or AA048646-AA048651) which comprises from 6-15

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XX (AA048525-AA048619). The anti-inflammatory compounds have antiasthmatic,

XX cytosolic, antiproliferative, antirheumatic, antiaesthetic, osteopathic,

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XX neurotrophic, antiatherosclerotic, virucide and antiallergic activity. The

XX compounds act as selective inhibitors of cytokine-mediated NF-kappaB

XX activation by blocking interaction of IkappaB kinase beta (IKKbeta) at

XX the NEMO binding domain that results in inhibition of IKKbeta kinase

XX activation and subsequent decreased phosphorylation of IkappaB. The

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XX osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,

XX burstitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,

XX granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;

XX Alzheimer's disease; atherosclerosis; viral infections; and ataxia

XX telangiectasia. The compounds are also useful for treating

CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,  
CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and  
CC arthritis.

CC Sequence 9 AA;

Query Match 100.0%; Score 40; DB 23; Length 9;  
Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ADMSWA 6  
DB 3 ADMSWA 8

# RESULT 9

AA048573  
ID AA048573 standard; Peptide: 9 AA.

AC AA048573;

DT 20-MAR-2002 (first entry)

DE Anti-Inflammatory peptide SEQ ID NO 76.

XX Anti-inflammatory; antisthmatic; cytostatic; antipsoriatic; nootropic;  
XX antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;  
XX immunosuppressive; dermatological; neuroprotective; antithrombotic;  
XX antiallergic; membrane translocation domain; NEMO binding domain; eczema;  
XX cytokine; NF-kappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;  
XX rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
XX autoimmune disorder; multiple sclerosis; transplant rejection;  
XX osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
XX ataxia telangiectasia; allergy; anaphylaxis; arthritis.

OS Synthetic.

PN WO200183554-A2.

PD 08-NOV-2001.

PF 02-MAY-2001; 2001WO-US14346.

PR 02-MAY-2000; 2000US-201261P.

PR 22-AUG-2000; 2000US-0643260.

PA (PRAE-) PRAECIS PHARM INC.

PI (UYVA) UNIV YALE.

PI May MJ, Ghosh S, Flindeis MA, Phillips K;

DR WPI; 2002-121889/16.

PT Novel anti-inflammatory compound comprising membrane translocation  
PT domain fused to NEMO binding sequence, useful for blocking nuclear  
PT factor kappaB activation, and for treating asthma, lung inflammation,  
PT psoriasis

PS Claim 6; Page 62; 88pp; English.

CC The invention relates to an anti-inflammatory compound (especially  
CC AA048628-AA048645), comprising a membrane translocation domain  
CC (AA048620-AA048627 or AA048646-AA048651) which comprises from 6-15  
CC amino acid residues, fused to a NEMO binding sequence

CC cytoskeletal, antipsoriatic, antirheumatic, antiallergic, osteopathic,  
CC antibacterial, immunosuppressive, dermatological, neuroprotective,  
CC nootropic, antithrombotic, virucide and antiallergic activity. The  
CC compounds act as selective inhibitors of cytokine-mediated NF-kappaB  
CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at  
CC the NEMO binding domain that results in inhibition of IKKbeta kinase  
CC activation and subsequent decreased phosphorylation of IkappaB. The  
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CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,  
CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,  
CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,  
CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;  
CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia  
CC telangiectasia. The compounds are also useful for treating  
CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,  
CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and  
CC arthritis.

CC Sequence 9 AA;

Query Match 100.0%; Score 40; DB 23; Length 9;  
Best Local Similarity 100.0%; Pred. No. 7.8e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ADMSWA 6  
DB 2 ADMSWA 7

# RESULT 10

AA048568  
ID AA048568 standard; Peptide: 10 AA.

AC AA048568;

DT 20-MAR-2002 (first entry)

DE Anti-Inflammatory peptide SEQ ID NO 71.

XX Anti-inflammatory; antisthmatic; cytostatic; antipsoriatic; nootropic;  
XX antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;  
XX immunosuppressive; dermatological; neuroprotective; antithrombotic;  
XX antiallergic; membrane translocation domain; NEMO binding domain; eczema;  
XX cytokine; NF-kappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;  
XX rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
XX autoimmune disorder; multiple sclerosis; transplant rejection;  
XX osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
XX ataxia telangiectasia; allergy; anaphylaxis; arthritis.

OS Synthetic.

PN WO200183554-A2.

PD 08-NOV-2001.

PF 02-MAY-2001; 2001WO-US14346.

PR 02-MAY-2000; 2000US-201261P.

PR 22-AUG-2000; 2000US-0643260.

PA (PRAE-) PRAECIS PHARM INC.

PI (UYVA) UNIV YALE.

PI May MJ, Ghosh S, Flindeis MA, Phillips K;

DR WPI; 2002-121889/16.

PT Novel anti-inflammatory compound comprising membrane translocation  
PT domain fused to NEMO binding sequence, useful for blocking nuclear  
PT factor kappaB activation, and for treating asthma, lung inflammation,  
PT psoriasis

PS Claim 6; Page 62; 88pp; English.

CC The invention relates to an anti-inflammatory compound (especially  
CC AA048628-AA048645), comprising a membrane translocation domain  
CC (AA048620-AA048627 or AA048646-AA048651) which comprises from 6-15  
CC amino acid residues, fused to a NEMO binding sequence  
CC (AA048525-AA048619). The anti-inflammatory compounds have antisthmatic,  
CC cytoskeletal, antipsoriatic, antirheumatic, antiallergic, osteopathic,  
CC antibacterial, immunosuppressive, dermatological, neuroprotective,

CC nootropic, antiatherosclerotic, virucide and antiallergic activity. The  
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB  
 CC activation by blocking interaction of Ikappab kinase beta (IKKbeta) at  
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase  
 CC activation and subsequent decreased phosphorylation of Ikappab. The  
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,  
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,  
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,  
 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,  
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;  
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia  
 CC telangiectasia. The compounds are also useful for treating  
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,  
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and  
 CC arthritis.

CC Sequence 10 AA;  
 SQ

Query Match 100.0%; Score 40; DB 23; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.5;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWA 6  
 Db 2 ADMSWA 7

RESULT 11  
 AAM48571  
 ID AAM48571 standard; Peptide; 10 AA.  
 AC AAM48571;  
 XX  
 DT 20-MAR-2002 (first entry)  
 DE Anti-inflammatory peptide SEQ ID NO 74.  
 XX  
 KW Antinflammatory; antiasthmatic; cytosstatic; antipsoriatic; nootropic;  
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;  
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;  
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;  
 KW cytokine; NFkappaB; Ikappab kinase beta; IKKbeta; cancer; psoriasis;  
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
 KW autoimmune disorder; multiple sclerosis; transplant rejection;  
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200183554-A2.  
 XX  
 PD 08-NOV-2001.  
 XX  
 PF 02-MAY-2001; 2001WO-US14346.  
 XX  
 PR 02-MAY-2000; 2000US-201261P.  
 PR 22-AUG-2000; 2000US-0643260.  
 XX  
 PA (PRAE-) PRAECIS PHARM INC.  
 PA (UYVA ) UNIV YALE.  
 XX  
 PI May MJ, Ghosh S, Flindeis MA, Phillips K;  
 XX  
 DR WPI; 2002-121889/16.  
 XX  
 PT Novel antinflammatory compound comprising membrane translocation  
 PT domain fused to NEMO binding sequence, useful for blocking nuclear  
 PT factor kappaB activation, and for treating asthma, lung inflammation,  
 PT psoriasis  
 XX  
 PS Claim 6; Page 62; 88pp; English.  
 XX  
 CC The invention relates to an antinflammatory compound (especially

CC AAM48628-AAM48645), comprising a membrane translocation domain  
 CC (AAM48620-AAM48627 or AAM48646-AAM48651) which comprises from 6-15  
 CC amino acid residues, fused to a NEMO binding sequence  
 CC (AAM48525-AAM48619). The antinflammatory compounds have antiasthmatic,  
 CC cytosstatic, antipsoriatic, antirheumatic, antiarthritic, osteopathic,  
 CC antibacterial, immunosuppressive, dermatological, neuroprotective,  
 CC nootropic, antiatherosclerotic, virucide and antiallergic activity. The  
 CC compounds act as selective inhibitors of cytokine-mediated NFkappaB  
 CC activation by blocking interaction of Ikappab kinase beta (IKKbeta) at  
 CC the NEMO binding domain that results in inhibition of IKKbeta kinase  
 CC activation and subsequent decreased phosphorylation of Ikappab. The  
 CC compounds are useful for treating inflammatory disorders, e.g. asthma,  
 CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,  
 CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,  
 CC bursitis; autoimmune diseases such as lupus, polymyalgia, scleroderma,  
 CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;  
 CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia  
 CC telangiectasia. The compounds are also useful for treating  
 CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,  
 CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and  
 CC arthritis.

CC Sequence 10 AA;  
 SQ

Query Match 100.0%; Score 40; DB 23; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.5;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ADMSWA 6  
 Db 3 ADMSWA 8

RESULT 12  
 AAM48565  
 ID AAM48565 standard; Peptide; 11 AA.  
 AC AAM48565;  
 XX  
 DT 20-MAR-2002 (first entry)  
 DE Anti-inflammatory peptide SEQ ID NO 68.  
 XX  
 KW Antinflammatory; antiasthmatic; cytosstatic; antipsoriatic; nootropic;  
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;  
 KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;  
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;  
 KW cytokine; NFkappaB; Ikappab kinase beta; IKKbeta; cancer; psoriasis;  
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
 KW autoimmune disorder; multiple sclerosis; transplant rejection;  
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200183554-A2.  
 XX  
 PD 08-NOV-2001.  
 XX  
 PF 02-MAY-2001; 2001WO-US14346.  
 XX  
 PR 02-MAY-2000; 2000US-201261P.  
 PR 22-AUG-2000; 2000US-0643260.  
 XX  
 PA (PRAE-) PRAECIS PHARM INC.  
 PA (UYVA ) UNIV YALE.  
 XX  
 PI May MJ, Ghosh S, Flindeis MA, Phillips K;  
 XX  
 DR WPI; 2002-121889/16.  
 XX  
 PT Novel antinflammatory compound comprising membrane translocation  
 PT domain fused to NEMO binding sequence, useful for blocking nuclear

PT factor kappaB activation, and for treating asthma, lung inflammation,  
PT psoriasis  
XX Claim 6; Page 62; 88pp; English.  
XX  
PS  
CC The invention relates to an antiinflammatory compound (especially  
CC AA48620-AA48645), comprising a membrane translocation domain  
CC (AA48620-AA48627, or AA48646-AA48651) which comprises from 6-15  
CC amino acid residues, fused to a NEMO binding sequence  
CC (AA48525-AA48619). The antiinflammatory compounds have antiasthmatic,  
CC cystostatic, antipsoriatic, antirheumatic, antiarthritic, osteoprotective,  
CC antibacterial, immunosuppressive, dermatological, neuroprotective,  
CC neurotropic, antiatherosclerotic, virocidic and antiallergic activity. The  
CC compounds act as selective inhibitors of cytokine-mediated NF-kappaB  
CC activation by blocking interaction of IkappaB kinase beta (IKKbeta) at  
CC the NEMO binding domain that results in inhibition of IKKbeta kinase  
CC activation and subsequent decreased phosphorylation of IKKbeta. The  
CC compounds are useful for treating inflammatory disorders, e.g. asthma,  
CC lung inflammation or cancer, psoriasis, rheumatoid arthritis,  
CC osteoarthritis, inflammatory bowel disease, sepsis, vasculitis,  
CC bursitis, autoimmune diseases such as lupus, polymyalgia, scleroderma,  
CC granulomatosis, multiple sclerosis; transplant rejection; osteoporosis;  
CC Alzheimer's disease; atherosclerosis; viral infections; and ataxia.  
CC telangiectasia. The compounds are also useful for treating  
CC pro-inflammatory responses such as allergies, urticaria, anaphylaxis,  
CC drug or food sensitivity, eczema, dermatitis, sunburn, aging and  
CC arthritis.  
CC  
SQ Sequence 11 AA;  
  
Query Match 100.0%; Score 40; DB 23; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.7;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 ADMSWA 6  
DB 3 ADMSWA 8  
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ID AAU21305 standard; Protein; 33 AA.  
AC AAU21305;  
XX  
DT 18-DEC-2001 (first entry)  
XX  
DE Human novel foetal antigen, SEQ ID NO 1549.  
XX  
XX Human: foetal tissue antigen; antiinflammatory; neuroprotective;  
KW immunomodulator; cardiovascular; cytosolic; nephrotoxic;  
KW cardiovascular; autoimmune disease; Rheumatoid arthritis;  
KW hyperproliferative disorder; breast neoplasm; cancer;  
KW cardiovascular disorder; cardiac arrest; cerebrovascular disorder;  
KW cerebral ischemia; angiogenesis; nervous system disorder;  
KW Alzheimer's disease; infection; ocular disorder; corneal infection;  
KW wound healing; epithelial cell proliferation; food additive.  
XX  
XX Homo sapiens.  
OS  
XX  
XX MO200155312-A2.  
PN  
XX  
PD 02-AUG-2001.  
XX  
XX 17-JAN-2001; 2001WO-US01321.  
PE  
XX 31-JAN-2000; 2000US-0179065.  
PR 04-FEB-2000; 2000US-0180628.  
PR 24-FEB-2000; 2000US-0184664.  
PR 02-MAR-2000; 2000US-0186350.  
PR 16-MAR-2000; 2000US-0189874.  
PR 17-MAR-2000; 2000US-0190076.  
PR 18-APR-2000; 2000US-0198123.  
PR

PR 19-MAY-2000; 2000US-0205515.  
PR 07-JUN-2000; 2000US-0209467.  
PR 28-JUN-2000; 2000US-0214886.  
PR 30-JUN-2000; 2000US-0215135.  
PR 07-JUL-2000; 2000US-0216647.  
PR 11-JUL-2000; 2000US-0216880.  
PR 11-JUL-2000; 2000US-0217487.  
PR 11-JUL-2000; 2000US-0217496.  
PR 14-JUL-2000; 2000US-0218290.  
PR 26-JUL-2000; 2000US-0220963.  
PR 26-JUL-2000; 2000US-0220964.  
PR 14-AUG-2000; 2000US-0224518.  
PR 14-AUG-2000; 2000US-0224519.  
PR 14-AUG-2000; 2000US-0225213.  
PR 14-AUG-2000; 2000US-0225214.  
PR 14-AUG-2000; 2000US-0225266.  
PR 14-AUG-2000; 2000US-0225267.  
PR 14-AUG-2000; 2000US-0225268.  
PR 14-AUG-2000; 2000US-0225270.  
PR 14-AUG-2000; 2000US-0225447.  
PR 14-AUG-2000; 2000US-0225757.  
PR 14-AUG-2000; 2000US-0225758.  
PR 14-AUG-2000; 2000US-0225759.  
PR 18-AUG-2000; 2000US-0225759.  
PR 22-AUG-2000; 2000US-0225681.  
PR 22-AUG-2000; 2000US-0225681.  
PR 22-AUG-2000; 2000US-0225686.  
PR 23-AUG-2000; 2000US-0227182.  
PR 30-AUG-2000; 2000US-0228924.  
PR 01-SEP-2000; 2000US-0229287.  
PR 01-SEP-2000; 2000US-0229343.  
PR 01-SEP-2000; 2000US-0229344.  
PR 01-SEP-2000; 2000US-0229345.  
PR 05-SEP-2000; 2000US-0229509.  
PR 05-SEP-2000; 2000US-0229513.  
PR 06-SEP-2000; 2000US-0230437.  
PR 06-SEP-2000; 2000US-0230438.  
PR 08-SEP-2000; 2000US-0231242.  
PR 08-SEP-2000; 2000US-0231243.  
PR 08-SEP-2000; 2000US-0231244.  
PR 08-SEP-2000; 2000US-0231413.  
PR 08-SEP-2000; 2000US-0231414.  
PR 08-SEP-2000; 2000US-0232080.  
PR 08-SEP-2000; 2000US-0232081.  
PR 12-SEP-2000; 2000US-0231968.  
PR 14-SEP-2000; 2000US-0232397.  
PR 14-SEP-2000; 2000US-0232398.  
PR 14-SEP-2000; 2000US-0232399.  
PR 14-SEP-2000; 2000US-0232400.  
PR 14-SEP-2000; 2000US-0232401.  
PR 14-SEP-2000; 2000US-0232403.  
PR 14-SEP-2000; 2000US-0233064.  
PR 14-SEP-2000; 2000US-0233065.  
PR 21-SEP-2000; 2000US-0234223.  
PR 21-SEP-2000; 2000US-0234274.  
PR 25-SEP-2000; 2000US-0234997.  
PR 25-SEP-2000; 2000US-0234998.  
PR 26-SEP-2000; 2000US-0234984.  
PR 27-SEP-2000; 2000US-0235834.  
PR 27-SEP-2000; 2000US-0235836.  
PR 29-SEP-2000; 2000US-0236327.  
PR 29-SEP-2000; 2000US-0236367.  
PR 29-SEP-2000; 2000US-0236368.  
PR 29-SEP-2000; 2000US-0236369.  
PR 29-SEP-2000; 2000US-0236370.  
PR 02-OCT-2000; 2000US-0236802.  
PR 02-OCT-2000; 2000US-0237037.  
PR 02-OCT-2000; 2000US-0237038.  
PR 02-OCT-2000; 2000US-0237039.  
PR 02-OCT-2000; 2000US-0237040.  
PR 13-OCT-2000; 2000US-0239935.  
PR 13-OCT-2000; 2000US-0239937.  
PR 20-OCT-2000; 2000US-0240960.  
PR

CC by gene therapy) or ameliorate a medical condition in e.g. humans, mice,  
CC rabbits, goats, horses, cats, dogs, chickens or sheep. They  
CC are also used in diagnosing a pathological condition or susceptibility  
CC to a pathological condition. The antibodies to the antigens can also  
CC be used in alleviating symptoms associated with the disorders and in  
CC diagnostic immunoassays e.g. radioimmunoassays or enzyme linked  
CC immunosorbent assays (ELISA). Disorders which are diagnosed or treated  
CC include autoimmune diseases e.g. rheumatoid arthritis,  
CC hyperproliferative disorders e.g. neoplasms of the breast or liver,  
CC cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders  
CC e.g. cerebral ischemia, angiogenesis, nervous system disorders e.g.  
CC Alzheimer's disease, infections caused by bacteria, viruses and fungi  
CC and ocular disorders e.g. corneal infection. The polypeptides can also  
CC be used to aid wound healing and epithelial cell proliferation, to  
CC prevent skin aging due to sunburn, to maintain organs before  
CC transplantation, for supporting cell culture of primary tissues, to  
CC regenerate tissues and in chemotaxis. The polypeptides can also be used  
CC as a food additive or preservative to increase or decrease storage  
CC capabilities, fat content, lipid, protein, carbohydrate, vitamins,  
CC minerals, cofactors and other nutritional components. Numerous  
CC examples of diseases and disorders treated by the nucleic acids and  
CC proteins are given in the specification. The present sequence

Query Match                      92.5%; Score 37; DB 22; Length 33;  
Best Local Similarity        83.3%; Pred. No. 16;  
Matches    5; Conservative     1; Mismatches    0; Indels     0; Gaps     0;

OY                      1 ADWSMA 6  
                        |||||  
DB                      9 ADMWTWA 14

RESULT 14  
AAV06332  
ID    AAV06332 standard; Protein: 103 AA.

XX                      AAV06332;  
AC                      XX  
AD                      XX  
DT                      DT  
XX                      XX  
DE                      Glucocladium roseum EGIII-like cellulase (partial sequence).  
KW                      Cellulase; endoglucanase; EGIII; textile; feed additive; baking;  
KM                      Food processing; grain wet milling; pulp; paper.  
XX                      XX  
XX                      OS                      Glucocladium roseum.  
XX                      XX                      WO9931255-A2.  
PN                      PD                      24-JUN-1999.  
XX                      XX  
PF                      14-DEC-1998;        98WO-US26552.  
XX                      XX  
PR                      16-DEC-1997;        9TUS-O991720.  
XX                      XX  
PA                      (GENM ) GENENCOR INT INC.  
PI                      Bower BS, Fowler T, Phillips JT;  
PT                      WPI: 1999-395187/33.  
XX                      DR  
EGIII Like cellulase

Example; Fig 3; 47p; English.

The present polypeptide represents a partial sequence of a novel  
EGIII-like cellulase of Glucocladium roseum. It was deduced from  
a partial gene sequence isolated from genomic DNA using PCR  
primers (see AAV59180-91) based on conserved motifs (see AAV06325-29)  
of Trichoderma reesei EGIII cellulase and related enzymes. PCR  
has been used to identify novel EGIII-like enzymes, including the  
present polypeptide, from bacterial and fungal sources (see  
AAV06331-70). Also provided by the invention are vectors, host

CC cells and methods for the recombinant production of such enzymes,  
 CC which can be used in the treatment of cellulose-containing textiles,  
 CC as feed additives, in the treatment of wood pulp, in the reduction  
 CC of biomass to glucose, in the stone washing of indigo dyed denim,  
 CC or as laundry detergent components (all claimed).  
 CC  
 XX

SO Sequence 103 AA;

Query Match 92.5%; Score 37; DB 20; Length 103;  
 Best Local Similarity 83.3%; Pred. No. 53;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 ADMWSMA 6  
 Db 29 ADMWSMS 34

RESULT 15  
 AAY06363  
 ID AAY06363 standard; Protein; 236 AA.

XX AAY06363;

XX 06-SEP-1999 (first entry)

DE Glucocladium roseum EGIII-like cellulase.

XX Cellulase; endoglucanase; EGIII; textile; feed additive; baking;  
 KM food processing; grain wet milling; pulp; paper.

XX Glucocladium roseum.

OS WO9931255-A2.

XX 24-JUN-1999.

XX 14-DEC-1998; 98WO-US26552.

XX 16-DEC-1997; 97US-0991720.

XX (GENV ) GENENCOR INT INC.

XX Bower BS, Fowler T, Phillips Jr;

XX WPI; 1999-395187/33.

PT EGIII like cellulase

XX Example; Fig 6; 47pp; English.

XX The present polypeptide represents a full-length sequence of a  
 CC novel EGIII-like cellulase of Glucocladium roseum. It was deduced  
 CC from a gene sequence isolated from genomic DNA using PCR  
 CC primers (see AAX59180-91) based on conserved motifs (see AAY06325-29)  
 CC of Trichoderma reesei EGIII cellulase and related enzymes. PCR  
 CC has been used to identify novel EGIII-like enzymes, including the  
 CC present protein, from bacterial and fungal sources (see AAY06331-70).  
 CC The sequence shows homology to T. reesei EGIII (see AAY06330). Also  
 CC provided by the invention are vectors, host cells and methods  
 CC for the recombinant production of such enzymes, which can be used  
 CC in the treatment of cellulose-containing textiles, as feed  
 CC additives, in the treatment of wood pulp, in the reduction of  
 CC biomass to glucose, in the stone washing of indigo dyed denim, or  
 CC as laundry detergent components (all claimed).  
 CC  
 XX

SO Sequence 236 AA;

Query Match 92.5%; Score 37; DB 20; Length 236;  
 Best Local Similarity 83.3%; Pred. No. 1.3e+02;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 ADMWSMA 6  
 Db 29 ADMWSMS 34

Db 63 ADMWSMS 68

Search completed: May 30, 2003, 14:49:43  
 Job time : 20.7529 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 30, 2003, 14:50:13 ; Search time 10.4605 Seconds  
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58.060 Million cell updates/sec

Title: US-09-643-260-5  
Perfect score: 40  
Sequence: 1 LDWSMA 6

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 383519 segs, 101223694 residues  
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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	40	100.0	6	9	US-09-847-946A-5
3	40	100.0	6	9	US-09-847-946A-40
4	40	100.0	6	9	US-09-847-946A-62
5	40	100.0	6	9	US-09-847-946A-66
6	40	100.0	6	9	US-09-847-946A-59
7	40	100.0	6	9	US-09-847-946A-67
8	40	100.0	6	9	US-09-847-946A-58
9	40	100.0	6	9	US-09-847-946A-61
10	40	100.0	6	9	US-09-847-946A-64
11	40	100.0	6	9	US-09-847-946A-65
12	40	100.0	6	9	US-09-847-946A-57
13	40	100.0	6	9	US-09-847-946A-60
14	40	100.0	6	9	US-09-847-946A-63
15	36	90.0	6	9	US-09-847-946A-2
16	36	90.0	6	9	US-09-847-946A-33
17	36	90.0	6	9	US-09-847-946A-41
18	36	90.0	6	9	US-09-847-946A-73
19	36	90.0	6	9	US-09-847-946A-73

20	36	90.0	7	9	US-09-847-946A-37	Sequence 37, Appl
21	36	90.0	7	9	US-09-847-946A-77	Sequence 77, Appl
22	36	90.0	8	9	US-09-847-946A-30	Sequence 30, Appl
23	36	90.0	8	9	US-09-847-946A-38	Sequence 38, Appl
24	36	90.0	8	9	US-09-847-946A-70	Sequence 70, Appl
25	36	90.0	8	9	US-09-847-946A-78	Sequence 78, Appl
26	36	90.0	9	9	US-09-847-946A-29	Sequence 29, Appl
27	36	90.0	9	9	US-09-847-946A-32	Sequence 32, Appl
28	36	90.0	9	9	US-09-847-946A-35	Sequence 35, Appl
29	36	90.0	9	9	US-09-847-946A-36	Sequence 36, Appl
30	36	90.0	9	9	US-09-847-946A-69	Sequence 69, Appl
31	36	90.0	9	9	US-09-847-946A-72	Sequence 72, Appl
32	36	90.0	9	9	US-09-847-946A-75	Sequence 75, Appl
33	36	90.0	9	9	US-09-847-946A-76	Sequence 76, Appl
34	36	90.0	10	9	US-09-847-946A-31	Sequence 31, Appl
35	36	90.0	10	9	US-09-847-946A-34	Sequence 34, Appl
36	36	90.0	10	9	US-09-847-946A-71	Sequence 71, Appl
37	36	90.0	10	9	US-09-847-946A-74	Sequence 74, Appl
38	36	90.0	11	9	US-09-847-946A-28	Sequence 28, Appl
39	36	90.0	11	9	US-09-847-946A-68	Sequence 68, Appl
40	36	90.0	11	9	US-09-847-946A-132	Sequence 132, App
41	36	90.0	11	9	US-09-847-946A-140	Sequence 140, App
42	36	90.0	12	9	US-09-847-946A-43	Sequence 43, Appl
43	36	90.0	13	9	US-09-847-946A-143	Sequence 143, App
44	36	90.0	13	9	US-09-847-946A-144	Sequence 144, App
45	36	90.0	13	9	US-09-847-946A-145	Sequence 145, App

## ALIGNMENTS

RESULT 1  
US-09-847-940B-5  
Sequence 5, Application US/09847940B  
Patent No. US20020156000A1  
GENERAL INFORMATION:  
APPLICANT: May, Michael J.  
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
FILE REFERENCE: PPT-117CP  
CURRENT APPLICATION NUMBER: US/09/847, 940B  
CURRENT FILING DATE: 2001-05-02  
PRIOR APPLICATION NUMBER: 09/643, 260  
PRIOR FILING DATE: 2000-08-22  
NUMBER OF SEQ ID NOS: 27  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 5  
LENGTH: 6  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: NBD mutants  
US-09-847-940B-5

Query Match 100.0%; Score 40; DB 9; Length 6;  
Best Local Similarity 100.0%; Pred. No. 3.4e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 LDWSMA 6  
1 LDWSMA 6

RESULT 2  
US-09-847-946A-5

Sequence 5, Application US/09847946A  
Publication No. US20030054999A1  
GENERAL INFORMATION:  
APPLICANT: May, Michael J.  
APPLICANT: Ghosh, Sankar  
APPLICANT: Findeis, Mark A.  
APPLICANT: Phillips, Kathryn  
APPLICANT: Hannig, Gerhard

TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
 FILE REFERENCE: PPI-119  
 CURRENT APPLICATION NUMBER: US/09/847,946A  
 CURRENT FILING DATE: 2001-05-02  
 PRIOR APPLICATION NUMBER: 60/201,261  
 PRIOR FILING DATE: 2000-05-02  
 PRIOR APPLICATION NUMBER: 09/643,260  
 PRIOR FILING DATE: 2000-08-22  
 NUMBER OF SEQ ID NOS: 160  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO 5  
 LENGTH: 6  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Description of Artificial Sequence:NBD peptide  
 US-09-847-946A-5

Query Match 100.0%; Score 40; DB 9; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 3.4e+05;  
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QY 1 LDWSMA 6  
 Db 1 LDWSMA 6

RESULT 3  
 US-09-847-946A-40  
 ; Sequence 40, Application US/09847946A  
 ; Publication No. US20030054999A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: May, Michael J  
 ; APPLICANT: Ghosh, Sankar  
 ; APPLICANT: Flindels, Mark A  
 ; APPLICANT: Phillips, Kathryn  
 ; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
 ; FILE REFERENCE: PPI-119  
 ; CURRENT APPLICATION NUMBER: US/09/847,946A  
 ; CURRENT FILING DATE: 2001-05-02  
 ; PRIOR APPLICATION NUMBER: 60/201,261  
 ; PRIOR FILING DATE: 2000-05-02  
 ; PRIOR APPLICATION NUMBER: 09/643,260  
 ; PRIOR FILING DATE: 2000-08-22  
 ; NUMBER OF SEQ ID NOS: 160  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 40  
 ; LENGTH: 6  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding  
 ; OTHER INFORMATION: sequence  
 US-09-847-946A-40

Query Match 100.0%; Score 40; DB 9; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 3.4e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSMA 6  
 Db 1 LDWSMA 6

RESULT 4  
 US-09-847-946A-62  
 ; Sequence 62, Application US/09847946A  
 ; Publication No. US20030054999A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: May, Michael J  
 ; APPLICANT: Ghosh, Sankar  
 ; APPLICANT: Flindels, Mark A

APPLICANT: Phillips, Kathryn  
 APPLICANT: Hannig, Gerhard  
 TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
 FILE REFERENCE: PPI-119  
 CURRENT APPLICATION NUMBER: US/09/847,946A  
 CURRENT FILING DATE: 2001-05-02  
 PRIOR APPLICATION NUMBER: 60/201,261  
 PRIOR FILING DATE: 2000-05-02  
 PRIOR APPLICATION NUMBER: 09/643,260  
 PRIOR FILING DATE: 2000-08-22  
 NUMBER OF SEQ ID NOS: 160  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO 62  
 LENGTH: 6  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Description of Artificial Sequence:NEMO binding  
 ; OTHER INFORMATION: sequence  
 US-09-847-946A-62

Query Match 100.0%; Score 40; DB 9; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 3.4e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSMA 6  
 Db 1 LDWSMA 6

RESULT 5  
 US-09-847-946A-66  
 ; Sequence 66, Application US/09847946A  
 ; Publication No. US20030054999A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: May, Michael J  
 ; APPLICANT: Ghosh, Sankar  
 ; APPLICANT: Flindels, Mark A  
 ; APPLICANT: Phillips, Kathryn  
 ; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
 ; FILE REFERENCE: PPI-119  
 ; CURRENT APPLICATION NUMBER: US/09/847,946A  
 ; CURRENT FILING DATE: 2001-05-02  
 ; PRIOR APPLICATION NUMBER: 60/201,261  
 ; PRIOR FILING DATE: 2000-05-02  
 ; PRIOR APPLICATION NUMBER: 09/643,260  
 ; PRIOR FILING DATE: 2000-08-22  
 ; NUMBER OF SEQ ID NOS: 160  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 66  
 ; LENGTH: 7  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding  
 ; OTHER INFORMATION: sequence  
 US-09-847-946A-66

Query Match 100.0%; Score 40; DB 9; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 3.4e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDWSMA 6  
 Db 1 LDWSMA 6

RESULT 6  
 US-09-847-946A-59  
 ; Sequence 59, Application US/09847946A  
 ; Publication No. US20030054999A1  
 ; GENERAL INFORMATION:

APPLICANT: May, Michael J  
APPLICANT: Ghosh, Sankar  
APPLICANT: Findels, Mark A  
APPLICANT: Phillips, Kathryn  
APPLICANT: Hannig, Gerhard  
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
FILE REFERENCE: PPI-119  
CURRENT APPLICATION NUMBER: US/09/847,946A  
CURRENT FILING DATE: 2001-05-02  
PRIOR APPLICATION NUMBER: 60/201,261  
PRIOR FILING DATE: 2000-05-02  
PRIOR APPLICATION NUMBER: 09/643,260  
PRIOR FILING DATE: 2000-08-22  
NUMBER OF SEQ ID NOS: 160  
SOFTWARE: Patentln Ver. 2.0  
SEQ ID NO 59  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:NEMO binding  
US-09-847-946A-59

Query Match 100.0%; Score 40; DB 9; Length 8;  
Best Local Similarity 100.0%; Pred. No. 3.4e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDMSWA 6  
|||||  
DB 3 LDMSWA 8

RESULT 7  
US-09-847-946A-67  
Sequence 67, Application US/09847946A  
Publication No. US20030054999A1  
GENERAL INFORMATION:  
APPLICANT: May, Michael J  
APPLICANT: Ghosh, Sankar  
APPLICANT: Findels, Mark A  
APPLICANT: Phillips, Kathryn  
APPLICANT: Hannig, Gerhard  
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
FILE REFERENCE: PPI-119  
CURRENT APPLICATION NUMBER: US/09/847,946A  
CURRENT FILING DATE: 2001-05-02  
PRIOR APPLICATION NUMBER: 60/201,261  
PRIOR FILING DATE: 2000-05-02  
PRIOR APPLICATION NUMBER: 09/643,260  
PRIOR FILING DATE: 2000-08-22  
NUMBER OF SEQ ID NOS: 160  
SOFTWARE: Patentln Ver. 2.0  
SEQ ID NO 67  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:NEMO binding  
US-09-847-946A-67

Query Match 100.0%; Score 40; DB 9; Length 8;  
Best Local Similarity 100.0%; Pred. No. 3.4e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDMSWA 6  
|||||  
DB 1 LDMSWA 6

RESULT 8  
US-09-847-946A-58

Sequence 58, Application US/09847946A  
Publication No. US20030054999A1  
GENERAL INFORMATION:  
APPLICANT: May, Michael J  
APPLICANT: Ghosh, Sankar  
APPLICANT: Findels, Mark A  
APPLICANT: Phillips, Kathryn  
APPLICANT: Hannig, Gerhard  
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
FILE REFERENCE: PPI-119  
CURRENT APPLICATION NUMBER: US/09/847,946A  
CURRENT FILING DATE: 2001-05-02  
PRIOR APPLICATION NUMBER: 60/201,261  
PRIOR FILING DATE: 2000-05-02  
PRIOR APPLICATION NUMBER: 09/643,260  
PRIOR FILING DATE: 2000-08-22  
NUMBER OF SEQ ID NOS: 160  
SOFTWARE: Patentln Ver. 2.0  
SEQ ID NO 58  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:NEMO binding  
US-09-847-946A-58

Query Match 100.0%; Score 40; DB 9; Length 9;  
Best Local Similarity 100.0%; Pred. No. 3.4e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDMSWA 6  
|||||  
DB 1 LDMSWA 6

RESULT 9  
US-09-847-946A-61  
Sequence 61, Application US/09847946A  
Publication No. US20030054999A1  
GENERAL INFORMATION:  
APPLICANT: May, Michael J  
APPLICANT: Ghosh, Sankar  
APPLICANT: Findels, Mark A  
APPLICANT: Phillips, Kathryn  
APPLICANT: Hannig, Gerhard  
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
FILE REFERENCE: PPI-119  
CURRENT APPLICATION NUMBER: US/09/847,946A  
CURRENT FILING DATE: 2001-05-02  
PRIOR APPLICATION NUMBER: 60/201,261  
PRIOR FILING DATE: 2000-05-02  
PRIOR APPLICATION NUMBER: 09/643,260  
PRIOR FILING DATE: 2000-08-22  
NUMBER OF SEQ ID NOS: 160  
SOFTWARE: Patentln Ver. 2.0  
SEQ ID NO 61  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:NEMO binding  
US-09-847-946A-61

Query Match 100.0%; Score 40; DB 9; Length 9;  
Best Local Similarity 100.0%; Pred. No. 3.4e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDMSWA 6  
|||||  
DB 1 LDMSWA 6

## RESULT 10

US-09-847-946A-64  
; Sequence 64, Application US/09847946A  
; Publication No. US20030054999A1  
; GENERAL INFORMATION:  
; APPLICANT: May, Michael J  
; APPLICANT: Ghosh, Sankar  
; APPLICANT: Findels, Mark A  
; APPLICANT: Phillips, Kathryn  
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
; FILE REFERENCE: PPI-119  
; CURRENT APPLICATION NUMBER: US/09/847,946A  
; CURRENT FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: 60/201,261  
; PRIOR FILING DATE: 2000-05-02  
; PRIOR APPLICATION NUMBER: 09/643,260  
; PRIOR FILING DATE: 2000-08-22  
; NUMBER OF SEQ ID NOS: 160  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 64  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding  
; OTHER INFORMATION: sequence  
US-09-847-946A-64

Query Match 100.0%; Score 40; DB 9; Length 9;  
Best Local Similarity 100.0%; Pred. No. 3.4e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSWA 6  
DB 3 LDMSWA 8

## RESULT 11

US-09-847-946A-65  
; Sequence 65, Application US/09847946A  
; Publication No. US20030054999A1  
; GENERAL INFORMATION:  
; APPLICANT: May, Michael J  
; APPLICANT: Ghosh, Sankar  
; APPLICANT: Findels, Mark A  
; APPLICANT: Phillips, Kathryn  
; APPLICANT: Hannig, Gerhard  
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
; FILE REFERENCE: PPI-119  
; CURRENT APPLICATION NUMBER: US/09/847,946A  
; CURRENT FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: 60/201,261  
; PRIOR FILING DATE: 2000-05-02  
; PRIOR APPLICATION NUMBER: 09/643,260  
; PRIOR FILING DATE: 2000-08-22  
; NUMBER OF SEQ ID NOS: 160  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 65  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding  
; OTHER INFORMATION: sequence  
US-09-847-946A-65

Query Match 100.0%; Score 40; DB 9; Length 9;  
Best Local Similarity 100.0%; Pred. No. 3.4e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSWA 6

DB 2 LDMSWA 7

## RESULT 12

US-09-847-946A-57  
; Sequence 57, Application US/09847946A  
; Publication No. US20030054999A1  
; GENERAL INFORMATION:  
; APPLICANT: May, Michael J  
; APPLICANT: Ghosh, Sankar  
; APPLICANT: Findels, Mark A  
; APPLICANT: Phillips, Kathryn  
; APPLICANT: Hannig, Gerhard  
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
; FILE REFERENCE: PPI-119  
; CURRENT APPLICATION NUMBER: US/09/847,946A  
; CURRENT FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: 60/201,261  
; PRIOR FILING DATE: 2000-05-02  
; PRIOR APPLICATION NUMBER: 09/643,260  
; PRIOR FILING DATE: 2000-08-22  
; NUMBER OF SEQ ID NOS: 160  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 57  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding  
; OTHER INFORMATION: sequence  
US-09-847-946A-57

Query Match 100.0%; Score 40; DB 9; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.9;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDMSWA 6  
DB 2 LDMSWA 7

## RESULT 13

US-09-847-946A-60  
; Sequence 60, Application US/09847946A  
; Publication No. US20030054999A1  
; GENERAL INFORMATION:  
; APPLICANT: May, Michael J  
; APPLICANT: Ghosh, Sankar  
; APPLICANT: Findels, Mark A  
; APPLICANT: Phillips, Kathryn  
; APPLICANT: Hannig, Gerhard  
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
; FILE REFERENCE: PPI-119  
; CURRENT APPLICATION NUMBER: US/09/847,946A  
; CURRENT FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: 60/201,261  
; PRIOR FILING DATE: 2000-05-02  
; PRIOR APPLICATION NUMBER: 09/643,260  
; PRIOR FILING DATE: 2000-08-22  
; NUMBER OF SEQ ID NOS: 160  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 60  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding  
; OTHER INFORMATION: sequence  
US-09-847-946A-60

Query Match 100.0%; Score 40; DB 9; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.9;